

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 10, 2004, 11:14:29 ; Search time 5215.6 Seconds
(without alignments)
9953.801 Million cell updates/sec

Title: US-10-763-400-1
Perfect score: 1198
Sequence: 1 tactaagagctccagcatc.....aaaaaaaaaaaaaaaaaaaa 1198

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues
Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

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- 41: em_higo_other.*

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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C 3	1198	100.0	1198	6	AX074287	AX074287 Sequence
C 4	1198	100.0	1198	6	AX074289	AX074289 Sequence
C 5	1198	100.0	1198	6	AX101304	AX101304 Sequence
C 6	1198	100.0	1198	6	AX335821	AX335821 Sequence
C 7	1198	100.0	1198	9	HSFCER1	X03948 Human mRNA
C 8	1186.8	99.1	1198	6	I09686	I09686 Sequence 3
C 9	1144.8	95.6	1174	6	ARI23794	ARI23794 Sequence
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C 11	1079.4	90.1	1106	9	BC015195	BC015195 Homo sapi
C 12	1078	90.0	1102	9	BC005312	BC005312 Homo sapi
C 13	1043.2	87.1	1068	6	A21606	A21606 human PC ep
C 14	1043.2	87.1	1068	6	BD264325	BD264325 Recombina
C 15	1043.2	87.1	1068	6	AX026808	AX026808 Sequence
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C 23	611	51.0	2955	6	ARI175486	ARI175486 Sequence
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C 34	553	46.2	1082	4	OAR18205	Y18205 Ovis aries
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ALIGNMENTS

RESULT 1
ARI175479
LOCUS
DEFINITION Sequence 1 from patent US 6309832.
ACCESSION ARI175479
VERSION ARI175479.1 GI:17916778
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1198)
AUTHORS Frank,G.R., Porter,J.F., Rushlow,K.E. and Wassom,D.L.
TITLE Method to detect IGE
JOURNAL Patent: US 6309832-A 1 30-OCT-2001;
FEATURES Location/Qualifiers

Pred. No. is the number of results predicted by chance to have a

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Query Match 100.0%; Score 1198; DB 6; Length 1198;
Best Local Similarity 100.0%; Pred. No. 5e-266;
Matches 1198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TACTAAGAGTCTCCAGATCTCCACCTGCTGTCTACCAACGAGCATGGCCCTATATTGAAG 60
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LOCUS AR175480 1198 bp DNA linear PAT 17-DEC-2001
DEFINITION Sequence 3 from patent US 6309832.
ACCESSION AR175480
VERSION AR175480.1 GI:17916779
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 1198)
AUTHORS Frank,G.N., Porter,J.P., Rushlow,K.E. and Wasson,D.L.
TITLE Method to detect Ige
JOURNAL Patent: US 6309832-A 3 30-OCT-2001;
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source 1. .1198
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Query Match 100.0%; Score 1198; DB 6; Length 1198;
Best Local Similarity 100.0%; Pred. No. 5e-266;
Matches 1198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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REFERENCE
AUTHORS
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Best Local Similarity 100.0%; Pred. No. 5e-266;
Matches 1198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy      1141  TATAAAACCATGTAACAGAAATGCTTCTGAGTAAAAAATAAAAAAAAAAAAAAAAAAAAA  1198
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RESULT 4
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LOCUS      Sequence 3 from Patent WO0104310.
DEFINITION      AX074289
ACCESSION      AX074289
VERSION      AX074289.1 GI:12710476
KEYWORDS
SOURCE
ORGANISM      Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 Weber, E.R., Wood, K.V. and Hall, M.P.
AUTHORS      Fc epsilon receptor-luminescence inducing protein chimeric nucleic
TITLE      acid molecules, fusion proteins and uses thereof
JOURNAL      Patent: WO 0104310-A 3 18-JAN-2001;
Heska Corporation (US); PROMEGA CORPORATION (US)
FEATURES
Location/Qualifiers
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ORIGIN
Query Match      100.0%; Score 1198; DB 6; Length 1198;
Best Local Similarity 100.0%; Pred. No. 5e-266;
Matches 1198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1  TACTAAGAGTCTCCAGATCTCCACCTGCTTACACCGAGATGGGCTATATTTGAAG  60
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Qy      841  TCTGAACCCACATCTTAAGCCAAACCCCAAAACCACTGATATAATTAATCTCAAGAAAT  900
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LOCUS      Sequence 7 from Patent WO0121816.
DEFINITION      AX101304
ACCESSION      AX101304
VERSION      AX101304.1 GI:13620094
KEYWORDS
SOURCE
ORGANISM      Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 Kinet, J.P., Donnadieu, E., Jouvin, M.H., Cookson, W. and Moffatt, M.F.
AUTHORS      Modulation of Ige receptor cell surface expression
TITLE

```


JOURNAL Patent: WO 0121816-A 7 29-MAR-2001;
ISTS INNOVATION LIMITED (GB) ; Beth Israel Deaconess Medical
Center, Inc. (US)
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Best Local Similarity 100.0%; Pred. No. 5e-266;
Matches 1198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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LOCUS Sequence 6130 from Patent WO0194629.
DEFINITION AX335621
ACCESSION AX335621
VERSION AX335621.1 GI:18126340
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Young, P.E., Augustus, M., Carter, K.C., Ebner, R., Endress, G.,
Horrigan, S., Soppet, D.R. and Weaver, Z.
TITLE Cancer gene determination and therapeutic screening using signature
gene sets
JOURNAL Patent: WO 0194629-A 6130 13-DEC-2001;
Avalon Pharmaceuticals (US)
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Best Local Similarity 100.0%; Pred. No. 5e-266;
Matches 1198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DEFINITION X06948
ACCESSION
VERSION FcER1 gene, IgE receptor alpha-subunit.
KEYWORDS Homo sapiens (human)
SOURCE
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1198)
AUTHORS Kochan,J., Pettine,L.F., Hakimi,J., Kishi,K. and Kinet,J.P.
TITLE Isolation of the gene coding for the alpha subunit of the human

high affinity IgE receptor
Nucleic Acids Res. 16 (8), 3584 (1988)
88233953
2967464
2 (bases 1 to 1198)
Kochan,J.P.
Direct Submission
Submitted (24-FEB-1988) Kochan J. P., Hoffman-La Roche, Dept
Molecular Genetics, 340 Kingsland, Nutley, New Jersey 07110
*source cell line=KU812; library=lamba gt11 cDNA.
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DEFINITION Sequence 3 from Patent WO 9004640.
ACCESSION I09686
VERSION I09686.1 GI:587606
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SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
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Kinet,J.-P. and Metzger,H.
CDNAS CODING FOR THE gamma SUBUNIT OF THE HIGH-AFFINITY RECEPTOR
FOR IMMUNOGLOBULIN E
JOURNAL Patent: WO 9004640-A 3 03-MAY-1990;
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Db	422	CTCAGTCCCATGGTGTGAGGAACCTGGATGCTGACAGGTGATCTATTATAAGGATGGT 481
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Qy	674	CTCAACATTACTGTAAATAAAGCTCCGCGTGAGAGTACTGGCTACAAATTTTATCCCA 733
Db	602	CTCAACATTACTGTAAATAAAGCTCCGCGTGAGAGTACTGGCTACAAATTTTATCCCA 661
Qy	734	TGTTGGTGGTACTCTGTTGCTGTGACACAGATTTATTCTCACTCAGCAGCAG 793
Db	662	TGTTGGTGGTACTCTGTTGCTGTGACACAGATTTATTCTCACTCAGCAGCAG 721
Qy	794	GTCAATTTCTCTTGAAGATTAAAGAACCAAGGAAGCTTTCAGACTTCTGAACCCACAT 853
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Db	782	CCTAAGCCAAACCCCAAAACAACTGATATTAATTAATCTCAAGAAATATTTGCAACATTAGT 841

Qy	914	TTTTTCCAGCATCAGCAATTCCTACTCAATTGTCAAAACACACAGCTTGCATATACATAGA 973
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Qy	974	AACGCTGTGCTCAAGGATTTATAGAAATGCTTCAATTAACCTGAGTGAACCTGGTAACT 1033
Db	902	AACGCTGTGCTCAAGGATTTATAGAAATGCTTCAATTAACCTGAGTGAACCTGGTAACT 961
Qy	1034	GCGATGTAATAGTACTGCTCAATTAACCTGCTTGAATGTAATGAGAGATGAATGATGATT 1093
Db	962	GCGATGTAATAGTACTGCTCAATTAACCTGCTTGAATGTAATGAGAGATGAATGATGATT 1021
Qy	1094	CATTATTAGCATTTGTAAGAGATGTTCAATTTCAATAAATAAATAAATAAATAAATAAATAA 1153
Db	1022	CATTATTAGCATTTGTAAGAGATGTTCAATTTCAATAAATAAATAAATAAATAAATAAATAA 1081
RESULT 11		
BC015195		
LOCUS		
DEFINITION		Homo sapiens Fc fragment of IgE, high affinity I, receptor for; alpha polypeptide, mRNA (cDNA clone MGC:14717 IMAGE:4251469), complete cds.
ACCESSION		BC015195
VERSION		BC015195.1 GI:15929529
KEYWORDS		MGC.
SOURCE		Homo sapiens (human)
ORGANISM		Homo sapiens
REFERENCE		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS		1 (bases 1 to 1106) Straussberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, P., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.P., Casavant, T.L., Schaefer, T.E., Brownstein, M.J., Udwin, T.B., Toshiyuki, S., Carroll, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullaly, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahy, J., Helton, E., Kettner, M., Madan, A., Rodriguez, S., Sanchez, A., Whitting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smalls, D.E., Scherch, A., Schein, J.E., Jones, S.J. and Matra, M.A.
TITLE		Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
JOURNAL		Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
MEDLINE		22388257
PUBMED		12477932
REFERENCE		2 (bases 1 to 1106)
AUTHORS		Straussberg, R.
TITLE		Direct Submission
JOURNAL		Submitted (01-Oct-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
REMARK		NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT		Contact: MGC help desk Email: cgapbs-re@mail.nih.gov Tissue Procurement: CLONTECH cDNA Library Preparation: CLONTECH Laboratories, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Sequencing Group at the Stanford Human Genome Center, Stanford University School of Medicine, Stanford, CA 94305 Web site: http://www-shgc.stanford.edu Contact: (Dickson, Mark) mcd@paxil.stanford.edu Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers,

R. M.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Series: IRAL Plate: 21 Row: a Column: 14
 This clone was selected for full length sequencing because it passed the following selection criteria: Similarity but not identity to protein.

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Matches 1089; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

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DB 1082 AAAAAAAAAAAAAAAAAAAAAA 1106

RESULT 12

BC005912

LOCUS

DEFINITION

Homo sapiens

alpha polypeptide, mRNA (cDNA clone MGC:14507 IMAGE:4294467),

complete cds.

BC005912

VERSION

BC005912.1

GI:13543505

KEYWORDS

MGC.

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1102)

AUTHORS

Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moore J., Wang J., Wang J., Hsieh P.,

Diatchenko L., Marusina K., Farmer A., Rubin G.M., Hong L.,

Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L.,

Scheetz T.E., Brownstein M.J., Usdin F.B., Toshiyuki S.,

Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J.,

Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, D.J., Hulyk, S.W., Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Kettner, M., Madan, A.C., Rodriguez, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, J.S., Krzywicki, M.I., Skalski, U., Smallos, D.E., Schnerch, A., Schein, J.E., Jones, S.J., and Marra, M.A. Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

22388057
12477932
2 (bases 1 to 1102)
Strausberg, R.
Direct Submission
Submitted (02-APR-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
NIH-MGC Project URL: <http://mgc.nci.nih.gov>
Contact: MGC help desk
Email: cgapbs-remail.nih.gov
Tissue Procurement: CLONTECH
cDNA Library Preparation: CLONTECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome Center, Stanford University School of Medicine, Stanford, CA 94305
Web site: <http://www-shgc.stanford.edu>
Contact: (Dickson, Mark) mcd@paxil1.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers, R. M.

REMARK
COMMENT

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Series: IRAL Plate: 21 Row: h Column: 16
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 4503674.

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ORIGIN

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Best Local Similarity 98.6%; Pred. No. 2.6e-238;
Matches 1087; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

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    Best Local Similarity 99.6%; Pred. No. 2.8e-230;
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LOCUS Sequence 14 from Patent EP1006183.
DEFINITION AX026808
ACCESSION AX026808.1 GI:10187941
VERSION AX026808.1
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
REFERENCE
AUTHORS
TITLE Recombinant soluble fc receptors
PATENT: EP 1006183-A 14 07-JUN-2000;
JOURNAL MAX PLANCK GESELLSCHAFT (DE)
FEATURES
    source
        1..1068
        /organism='Homo sapiens'
        /mol_type='unassigned DNA'
        /db_xref='taxon:9606'
ORIGIN
    Query Match      87.1%; Score 1043.2; DB 6; Length 1068;
    Best Local Similarity 99.6%; Pred. No. 2.8e-230;
    Matches 1056; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 74 CAGCACAGTAAGCACCAGGAGTCCATGAAGAAGATGGCTCCGTCATGGAAATCCCTTACT 133
DB 7 CAGCACAGTAAGCACCAGGAGTCCATGAAGAAGATGGCTCCGTCATGGAAATCCCTTACT 66
QY 134 CTACTGTGTGAGCTTACTTCTTCGTCACAGATGGCGTGTAGCAGTCCCTCAGAAA 193
DB 67 CTACTGTGTGAGCTTACTTCTTCGTCACAGATGGCGTGTAGCAGTCCCTCAGAAA 126
QY 194 CCTAAGGTCCTCTTGAACCCCTCCATGGAATAGATATTTAAAGAGAGAAATGTGACTCTT 253
DB 127 CCTAAGGTCCTCTTGAACCCCTCCATGGAATAGATATTTAAAGAGAGAAATGTGACTCTT 186
QY 254 ACATGTAAATGGGAACAATTTCTTTGAAGTCAGTTCCCAAAATGGTTCCCAATGGCAGC 313
DB 187 ACATGTAAATGGGAACAATTTCTTTGAAGTCAGTTCCCAAAATGGTTCCCAATGGCAGC 246
QY 314 CTTTCAGAGAGACAAATTCAGATTTGAATTTGAATGCAATGCAATGCAATGCAATGCA 373
DB 247 CTTTCAGAGAGACAAATTCAGATTTGAATTTGAATGCAATGCAATGCAATGCAATGCA 306
QY 374 GAATACAAATCTCAGCACCAACAAGTTAATGAGAGTGAACCTGTGTACCTGGAGTCTTC 433
DB 307 GAATACAAATCTCAGCACCAACAAGTTAATGAGAGTGAACCTGTGTACCTGGAGTCTTC 366
QY 434 AGTGACTGGCTGCTCTTTCAGGCTCTGCTGAGGTGGTGTAGTGGGCGCAGCCCTCTTC 493
DB 367 AGTGACTGGCTGCTCTTTCAGGCTCTGCTGAGGTGGTGTAGTGGGCGCAGCCCTCTTC 426
```

494	QY	CTCAGGTGCCATCGTTGGAGGAACTGGATGTTGTTACAAGTGATCTATTATTAAGGATGGT	553
427	Db	CTCAGGTGCCATCGTTGGAGGAACTGGATGTTGTTACAAGTGATCTATTATTAAGGATGGT	486
554	QY	GAAGCTCTCAAGTACTGGTATGAGAAACCAACCAATCTCCATTACAAATGCCACAGTTGAA	613
487	Db	GAAGCTCTCAAGTACTGGTATGAGAAACCAACCAATCTCCATTACAAATGCCACAGTTGAA	546
614	QY	GACAGTGGAACTTACTACTCTACGGGCAAGTGTGGCAGCTGCACTATGAGTCTGAGCCC	673
547	Db	GACAGTGGAACTTACTACTCTACGGGCAAGTGTGGCAGCTGCACTATGAGTCTGAGCCC	606
674	QY	CTCAACATTACTGTATAAAAGCTCCGCGTGAGAAGTACTGGCTACAAATTTTATCCCA	733
607	Db	CTCAACATTACTGTATAAAAGCTCCGCGTGAGAAGTACTGGCTACAAATTTTATCCCA	666
734	QY	TTGTTGGTGGTGAATCTGTTTGGCTGTGGACACAGGATTATTATCTCACTCAGCAGCAG	793
667	Db	TTGTTGGTGGTGAATCTGTTTGGCTGTGGACACAGGATTATTATCTCACTCAGCAGCAG	726
794	QY	GTCACATTTCTCTTGAAGATTAAAGAGAAACAGAGAAAGGGCTTCAGACTTCGAAACCCACAT	853
727	Db	GTCACATTTCTCTTGAAGATTAAAGAGAAACAGAGAAAGGGCTTCAGACTTCGAAACCCACAT	786
854	QY	CCTAAGCCAAACCCCAAAACCAACTGATATAATT-ACTCAAGAAATATTTGCAACATTAG	912
787	Db	CCTAAGCCAAACCCCAAAACCAACTGATATAATTAACTCAAGAAATATTTGCAACATTAG	846
913	QY	TTTTTTTTCCAGCATCAGCAATTCCTACTCAATTTGTCAAACACAGCTTGCATATACATAG	972
847	Db	TTTTTTTTCCAGCATCAGCAATTCCTACTCAATTTGTCAAACACAGCTTGCATATACATAG	906
973	QY	AAAACGCTGTGCTCAAGGATTTATAGAAATGCTTTCATTAAACTGAGTGAACCTGGTTAAG	1032
907	Db	AAAACGCTGTGCTCAAGGATTTATAGAAATGCTTTCATTAAACTGAGTGAACCTGGTTAAG	966
1033	QY	TGGCATGTAATAGTAACTGCTCAATTAACATTCGGTTGAATAAATGAGAGAACTGAATAGAT	1092
967	Db	TGGCATGTAATAGTAACTGCTCAATTAACATTCGGTTGAATAAATGAGAGAACTGAATAGAT	1026
1093	QY	TCATTTATTAGCATTTGTTAAAGAGATGTTTCAATTTCAAT	1132
1027	Db	TCATTTATTAGCATTTGTTAAAGAGATGTTTCAATTTTAGAT	1066

Search completed: October 10, 2004, 16:11:54
Job time : 5220.6 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 8, 2004, 15:03:47 ; Search time 582.511 Seconds
(without alignments)
8736.904 Million cell updates/sec

Title: US-10-763-400-1

Perfect score: 1198
Sequence: 1 tactaagagtctccagcatc.....aaaaaaaaaaaaaaaaaaaaa 1198

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_29Jan04.*

- 1: geneseqn1980s.*
- 2: geneseqn1990s.*
- 3: geneseqn2000s.*
- 4: geneseqn2001as.*
- 5: geneseqn2001bs.*
- 6: geneseqn2002s.*
- 7: geneseqn2003as.*
- 8: geneseqn2003bs.*
- 9: geneseqn2003cs.*
- 10: geneseqn2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	1198	100.0	1198	2	AAV36343	AAV36343 CDNA enco
2	1198	100.0	1198	3	AA34813	Aa34813 Human ade
3	1198	100.0	1198	3	AAf20935	Aaf20935 Human hig
4	1198	100.0	1198	4	AAf77692	Aaf77692 Human wil
5	1198	100.0	1198	5	AAf24912	Aaf24912 Complemen
6	1198	100.0	1198	5	AAf24911	Aaf24911 Nucleotid
7	1198	100.0	1198	6	AB167793	AB167793 Cesophagu
8	1198	100.0	1198	7	AB296629	AB296629 Human hig
9	1198	100.0	1198	9	AB85535	AB85535 Human imm
10	1198	100.0	21742	3	AA34816	Aa34816 Human ade
11	1198	100.0	21742	3	AAf20938	Aaf20938 Human hig
12	1198	100.0	21742	7	AB296632	AB296632 Human hig
13	1198	100.0	117608	7	AB297129	AB297129 Human rec
14	1198	100.0	117609	3	AAf21435	Aaf21435 Human rec
15	1190	99.3	1199	2	AAQ14736	Aaql4736 Human Fc(
16	1186	99.0	1197	2	AAf85615	Aaf85615 Alpha sub
17	1183.4	99.8	1193	2	AAQ04644	AaQ04644 Encodes a
18	1144.8	95.6	1174	2	AAQ51020	AaQ51020 Human Fce
19	1083.8	90.5	1088	1	AAf90126	Aaf90126 CDNA enco
20	1043.2	87.1	1068	3	AAa27470	Aaa27470 Human Fc
21	922.2	77.0	1150	2	AAQ34840	AaQ34840 Human hig
22	882.8	73.7	898	8	ACD06182	ACD06182 Human cdn
23	774	64.6	774	4	AAf97964	Aaf97964 Human imm

24	773	64.5	773	6	ABS52959	Human cdn
25	771.4	64.4	773	2	AAV20402	Human IGE
26	705.4	58.9	851	2	AAQ27267	Human FcE
27	697	58.2	713	2	AAQ55969	Human dih
c	696	58.1	696	5	AAf24914	Complemen
28	696	58.1	696	5	AAf24913	Nucleotid
29	630	52.6	757	8	ACD06183	Human cdn
30	630	52.6	757	8	ACD06183	Human cdn
31	611	51.0	2955	2	AAV20404	Plasmid R
32	611	51.0	2955	2	AAV20404	Plasmid R
c	591	49.3	591	5	ABS52957	Human cdn
33	591	49.3	591	5	AAf24916	Complemen
34	591	49.3	591	5	AAf24915	DNA enco
c	591	49.3	1983	5	AAf24927	FC epsilo
35	591	49.3	1983	5	AAf24926	FC epsilo
36	591	49.3	1983	5	AAf24926	FC epsilo
c	591	49.3	2268	5	AAf24921	Complemen
37	591	49.3	2268	5	AAf24921	Complemen
38	591	49.3	2268	5	AAf24920	Nucleotid
c	578.8	48.3	1015	2	AAx89856	Equine Fc
39	578.8	48.3	1015	2	AAx89857	Equine Fc
40	578.8	48.3	1015	2	AAx89857	Equine Fc
41	554	46.2	570	3	AAa27472	Recombina
42	528	44.1	528	3	AAa27301	Human Fce
43	528	44.1	528	4	AAH47768	Nucleotid
44	516	43.1	516	3	AAa27302	Human nhf
45	516	43.1	516	5	AAf24917	DNA enco

ALIGNMENTS

RESULT 1

AAV36343 ID AAV36343 standard; CDNA; 1198 BP.

XX AC AAV36343;

XX DT 07-OCT-1998 (first entry)

XX DE cDNA encoding the alpha chain of a Fc epsilon receptor.

XX KW Alpha chain; human; Fc epsilon receptor; canine; equine; feline;

XX KW Immunoglobulin E; IGE; detection; diagnosis; allergy; atopic disease;

XX KW hyper-IGE syndrome; internal parasitic infection; B cell neoplasia;

XX KW flea allergy; heartworm infection; ds.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

XX FT CDS 107..880

XX FT /*tag= a

XX PN WO9823964-A1.

XX PD 04-JUN-1998.

XX PF 24-NOV-1997; 97WO-US021651.

XX PR 26-NOV-1996; 96US-00756387.

XX PA (HESK-) HESKA CORP.

XX PI Frank RG, Porter JP, Rushlow KE, Wassom DL;

XX DR WPI; 1998-322873/28.

XX DR P-PSDB; AAW61190.

XX PT Detection of non-human immunoglobulin E - by complex formation with human

XX PT Fc epsilon receptor, used for, e.g. diagnosis of allergy and atopic

XX PT disease.

XX PS Claim 11; Page 36-37; 70pp; English.

XX CC The present sequence encodes the alpha chain of the human Fc epsilon

XX CC receptor. Detection of canine, equine or feline immunoglobulin E (IGE)

XX CC comprises reacting isolated human Fc epsilon receptor with the test

XX CC sample and detecting formation of a IGE-receptor complex. Detection of

CC IgE is used to diagnose allergy, atopic disease, hyper-IgE syndrome,
 CC internal parasitic infections or B cell neoplasia, and for measuring
 CC effect of treatments. Most particularly flea allergy in dogs and cats is
 CC detected, and also heartworm infection
 XX
 SQ

Sequence 1198 BP; 389 A; 243 C; 245 G; 321 T; 0 U; 0 Other;

Query Match 100.0%; Score 1198; DB 2; Length 1198;

Best Local Similarity 100.0%; Pred. No. 2.3e-230;

Matches 1198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TACTAAGAGTCTCCAGCAGCTCCACCTGCTTACACCGAGCATGGGCTATATTGAAG 60
 DB 1 TACTAAGAGTCTCCAGCAGCTCCACCTGCTTACACCGAGCATGGGCTATATTGAAG 60
 QY 61 CTTTAGATCTCTCCAGCAGTAAGCACCAGGAGTCCATGAAGAAGATGGCTCTGCCAT 120
 DB 61 CTTTAGATCTCTCCAGCAGTAAGCACCAGGAGTCCATGAAGAAGATGGCTCTGCCAT 120
 QY 121 GGAATCCCTACTCTACTGTGTGTAGCTTACTGTCTTCGCTCCAGATGGGCTGTAGC 180
 DB 121 GGAATCCCTACTCTACTGTGTGTAGCTTACTGTCTTCGCTCCAGATGGGCTGTAGC 180
 QY 181 AGTCCCTCAGAACCTTAAGTCTCTCTGAAACCTCCATGGAATAGATATTTAAAGGAGA 240
 DB 181 AGTCCCTCAGAACCTTAAGTCTCTCTGAAACCTCCATGGAATAGATATTTAAAGGAGA 240
 QY 241 GAATGTGACTCTTACATGTAATGGGAACAAATTTCTTGAAGTCAGTCCACCAATGGTT 300
 DB 241 GAATGTGACTCTTACATGTAATGGGAACAAATTTCTTGAAGTCAGTCCACCAATGGTT 300
 QY 301 CCACATGTCAGCTTCCAGAGAGACAAATTCAGATTTGAATATTTGAATGCCAAAT 360
 DB 301 CCACATGTCAGCTTCCAGAGAGACAAATTCAGATTTGAATATTTGAATGCCAAAT 360
 QY 361 TGAAGCAGTGGAGATACAAATGTGAGCACCACCAAGTTAATGAGATGAACCTGTGTA 420
 DB 361 TGAAGCAGTGGAGATACAAATGTGAGCACCACCAAGTTAATGAGATGAACCTGTGTA 420
 QY 421 CCTGGAAGTCTTCAAGTACTGCTGCTCCTTCAAGCTCTGCTGAGTGGTGTAGTGAGGG 480
 DB 421 CCTGGAAGTCTTCAAGTACTGCTGCTCCTTCAAGCTCTGCTGAGTGGTGTAGTGAGGG 480
 QY 481 CCAGCCCTCTTCTCAGTGCATGGTTGGAGGAACCTGGGATGTGTACAAAGGTGATCTA 540
 DB 481 CCAGCCCTCTTCTCAGTGCATGGTTGGAGGAACCTGGGATGTGTACAAAGGTGATCTA 540
 QY 541 TTATAAGATGGTGAAGCTCTCAAGTACTGTTGATGAGAACCAACATCTCCATTACAAA 600
 DB 541 TTATAAGATGGTGAAGCTCTCAAGTACTGTTGATGAGAACCAACATCTCCATTACAAA 600
 QY 601 TGCACAGTTGAAGCAGTGGAACTTACTGTTGAGGCAAGTGTGGCAGCTGGACTA 660
 DB 601 TGCACAGTTGAAGCAGTGGAACTTACTGTTGAGGCAAGTGTGGCAGCTGGACTA 660
 QY 661 TGAGTCTGAGCCCTCAACATTTACTGTATATAAAGCTCCGCTGAGAGATGCTGCTACA 720
 DB 661 TGAGTCTGAGCCCTCAACATTTACTGTATATAAAGCTCCGCTGAGAGATGCTGCTACA 720
 QY 721 ATTTTATCCCATTTGCTGGTGTGATCTGTTGCTGGAACAGGATTTATCTC 780
 DB 721 ATTTTATCCCATTTGCTGGTGTGATCTGTTGCTGGAACAGGATTTATCTC 780
 QY 781 AACTCAGCAGAGGTCACATTTCTCTTGAAGATTAAGAGAACCCAGGAAGGCTTCAGACT 840
 DB 781 AACTCAGCAGAGGTCACATTTCTCTTGAAGATTAAGAGAACCCAGGAAGGCTTCAGACT 840
 QY 841 TGTGAACCCACATCTTAAGCCAAACCCAAACAACTGATATATTTACTCAAGAAATAT 900
 DB 841 TGTGAACCCACATCTTAAGCCAAACCCAAACAACTGATATATTTACTCAAGAAATAT 900
 QY 901 TTGCAACATAGTTTTTTTCCAGCATCAGCAATTTGCTCAATTTGTCAAAACAGCTTG 960

DB 901 TTGCAACATAGTTTTTTTCCAGCATCAGCAATTCCTACTCAATTTGCAAAACAGCTTG 960
 QY 961 CAATATACATAGAAAGCTGTGCTCAAGAGATTTATAGAAATGCTTCATTAACATGAGTG 1020
 DB 961 CAATATACATAGAAAGCTGTGCTCAAGAGATTTATAGAAATGCTTCATTAACATGAGTG 1020
 QY 1021 AAATCGTTAAGTGGCATGTAAATAGTAAGTGTCAATTAACATTTGCTCAATAAATGAGA 1080
 DB 1021 AAATCGTTAAGTGGCATGTAAATAGTAAGTGTCAATTAACATTTGCTCAATAAATGAGA 1080
 QY 1081 GAATGAATAGATTCATTTATAGCATTTTGAAGAAGAGATGTTCAATTTCAATAAATAAA 1140
 DB 1081 GAATGAATAGATTCATTTATAGCATTTTGAAGAAGAGATGTTCAATTTCAATAAATAAA 1140
 QY 1141 TATAAAACCATGTAAACAGATGCTTCTGAGTAAACAAAAAATAAATAAATAAATAA 1198
 DB 1141 TATAAAACCATGTAAACAGATGCTTCTGAGTAAACAAAAAATAAATAAATAAATAA 1198

RESULT 2

AAA34813

ID AAA34813 standard; DNA; 1198 BP.

XX AAA34813;

XX AC

XX 28-JUL-2000 (first entry)

XX Human adenosine receptor related polynucleotide SEQ ID NO:2502.

XX Human; adenosine receptor; low adenosine antisense oligonucleotide;
 KW phosphorothioate; impaired respiration; inflammation; allergy;
 KW allergic disease; bronchoconstriction; inhibitor; antiinflammatory;
 KW antiallergic; antihistaminic; cytostatic; analgesic; impaired airway;
 KW lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;
 KW respiratory distress syndrome; pain; cystic fibrosis; emphysema;
 KW pulmonary hypertension; chronic obstructive pulmonary disease; COPD;
 KW cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.

XX Homo sapiens.

OS W0200009525-A2.

PN 24-FEB-2000.

XX 03-AUG-1999; 99WO-US017712.

XX 03-AUG-1998; 98US-0095212P.

XX (UYEC-) UNIV EAST CAROLINA.

XX Nyce JW;

XX WPI; 2000-205971/18.

XX New antisense oligonucleotides useful for treating e.g. pulmonary
 DR vasoconstriction, inflammation, allergies, asthma, hypertension,
 PT bronchitis, emphysema, respiratory distress syndrome, ischemia or
 PT cancers.

XX Disclosure; Page 655; 1343pp; English.

XX The present invention describes a new composition comprising an antisense
 CC oligonucleotide (ON) with low adenosine (up to 15%), which targets
 CC nucleic acids involved in bronchoconstriction, allergies, and/or
 CC inflammation. The ON can have antiinflammatory, antiallergic,
 CC antihistaminic, cytostatic and analgesic activities. The compositions are
 CC useful for the treatment of diseases associated with inflammation,
 CC impaired airways, including lung disease and diseases whose secondary
 CC effects afflict the lungs of a subject. They can be used for treating
 CC e.g. ischaemic conditions, pulmonary vasoconstriction, allergies, asthma,
 CC impeded respiration, respiratory distress syndrome, pain, cystic
 CC fibrosis, pulmonary hypertension, emphysema, chronic obstructive
 CC pulmonary disease (COPD), and cancers such as leukaemias, lymphomas,

CC carcinomas, and cancers which may metastasize to the lungs, including
CC breast and prostate cancer. The reduction of the adenosine content of the
CC ONs reduces side effects. The A-containing ONs break down with the
CC release of deoxyadenosine which activates adenosine receptors causing
CC bronchoconstriction and inflammation. AAA32313 to AAA35312 represent the
CC nucleotide sequences given in the sequence listing from the present
CC invention, which correspond to SEQ ID NO:1 to 2815, and then the last 185
CC sequences are also called SEQ ID NO:1 to 185, but the sequences differ
CC from the previously named sequences. SEQ ID NO:11 to 1680 (AAA32323 to
CC AAA33992) are specifically claimed ONs from the present invention. N.B.
CC Sequences given in the disclosure of the present invention do not match
CC up with their corresponding SEQ ID NO: sequences given in the sequence
CC listing
XX
XX
SQ Sequence 1198 BP; 389 A; 243 C; 245 G; 321 T; 0 U; 0 Other;

Query Match 100.0%; Score 1198; DB 3; Length 1198;
Best Local Similarity 100.0%; Pred. No. 2.3e-230;
Matches 1198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TACTAAGAGTCTCCAGCATCTCCACCTGTCTACCGCGAGCATGGCGCTATATTGAAG 60
DB 1 TACTAAGAGTCTCCAGCATCTCCACCTGTCTACCGCGAGCATGGCGCTATATTGAAG 60

QY 61 CTTTAGATCTCTCCAGCACAGTAAAGCACCGAGGATCCATGAAGAAGATGCTCTGCCAT 120
DB 61 CTTTAGATCTCTCCAGCACAGTAAAGCACCGAGGATCCATGAAGAAGATGCTCTGCCAT 120

QY 121 GGAATCCCTACTACTGTGTGTAGCTTACTGTCTTCCGCTCCAGATGGCGGTGAGC 180
DB 121 GGAATCCCTACTACTGTGTGTAGCTTACTGTCTTCCGCTCCAGATGGCGGTGAGC 180

QY 181 AGTCCTCAGAAACCTAAGGTCTCTTGAACCTCCATGGAATAGATATTTAAAGGAGA 240
DB 181 AGTCCTCAGAAACCTAAGGTCTCTTGAACCTCCATGGAATAGATATTTAAAGGAGA 240

QY 241 GAATGTGACTCTTACATGTAATGGGAACAATTTCTTGAAGTCAAGTCCACCAATGGT 300
DB 241 GAATGTGACTCTTACATGTAATGGGAACAATTTCTTGAAGTCAAGTCCACCAATGGT 300

QY 301 CCACAATGGCGCCTTTTCCAGAGAGACAAATTTCAAGTTGTAATTTGTAATGCAAAAT 360
DB 301 CCACAATGGCGCCTTTTCCAGAGAGACAAATTTCAAGTTGTAATTTGTAATGCAAAAT 360

QY 361 TGAAGACAGTGGAGAAATACAAATGTCCAGCACCAACAAAGTTAATGAGAGTGAACCTGTGA 420
DB 361 TGAAGACAGTGGAGAAATACAAATGTCCAGCACCAACAAAGTTAATGAGAGTGAACCTGTGA 420

QY 421 CCTGGAAGTCTTCAAGTGAAGTGGCTGCTCTTCAAGCCTCTGCTGAGGTGGTGAAGGG 480
DB 421 CCTGGAAGTCTTCAAGTGAAGTGGCTGCTCTTCAAGCCTCTGCTGAGGTGGTGAAGGG 480

QY 481 CCAGCCCTCTTCTCAGGTGCCATGGTTGGAGAACTGGGATGTGTACAAGGTGATCTA 540
DB 481 CCAGCCCTCTTCTCAGGTGCCATGGTTGGAGAACTGGGATGTGTACAAGGTGATCTA 540

QY 541 TTATAAGAGTGGTGAAGCTTCAAGTACTGTGTATGAGAACCAACAATCTCCATTACAAA 600
DB 541 TTATAAGAGTGGTGAAGCTTCAAGTACTGTGTATGAGAACCAACAATCTCCATTACAAA 600

QY 601 TGCCACAGTGAAGACAGTGAACCTACTACTGTACGGGCAAGTGGCGAGCTGGACTA 660
DB 601 TGCCACAGTGAAGACAGTGAACCTACTACTGTACGGGCAAGTGGCGAGCTGGACTA 660

QY 661 TGAGTCTGAGCCCTCAACATTACTGTAAATAAAGCTCCGCGTGAAGAAGTACTGGCTACA 720
DB 661 TGAGTCTGAGCCCTCAACATTACTGTAAATAAAGCTCCGCGTGAAGAAGTACTGGCTACA 720

QY 721 ATTTTATCCATTGTTGGTGGTGAATCTGTTGCTGTGACACAGGATTTATTTCTC 780
DB 721 ATTTTATCCATTGTTGGTGGTGAATCTGTTGCTGTGACACAGGATTTATTTCTC 780

QY 781 AACTCAGCAGCAGGTTCACATTTCTTGAAGATTAAGAGAACCCAGGAAAGGCTTCAGACT 840

DB 781 AACTCAGCAGCAGGTTCACATTTCTTGAAGATTAAGAGAACCCAGGAAAGGCTTCAGACT 840
QY 841 TGTGAACCCACATCTCTAAGCCAAACCCCAAAACAACTGATATTAATTACTCAAGAAATAT 900
DB 841 TGTGAACCCACATCTCTAAGCCAAACCCCAAAACAACTGATATTAATTACTCAAGAAATAT 900
QY 901 TTGCAACATTTAGTTTTCAGCATCAGCAATTCCTACTCAATTTGTCAAAACACAGCTTG 960
DB 901 TTGCAACATTTAGTTTTCAGCATCAGCAATTCCTACTCAATTTGTCAAAACACAGCTTG 960
QY 961 CAATATACATAGAAACGCTGTGCTCAAGGATTTATAGAAATGCTTCAATTTCAATTTAA 1020
DB 961 CAATATACATAGAAACGCTGTGCTCAAGGATTTATAGAAATGCTTCAATTTCAATTTAA 1020
QY 1021 AAATGTTTAACTGGCATGTAACTAGTCTCAATTAAGCATTTGTTTCAATTTCAATTTAA 1080
DB 1021 AAATGTTTAACTGGCATGTAACTAGTCTCAATTTAACTAGTCTCAATTTCAATTTAA 1080
QY 1081 GAATGAATAGATTCATTTATTAGCATTTGTTAAAGAGATGTTTCAATTTCAATTTAA 1140
DB 1081 GAATGAATAGATTCATTTATTAGCATTTGTTAAAGAGATGTTTCAATTTCAATTTAA 1140
QY 1141 TATAAAACCATGTAAACAGATGCTTCTGAGTAAAAAAGAGATGTTTCAATTTCAATTTAA 1198
DB 1141 TATAAAACCATGTAAACAGATGCTTCTGAGTAAAAAAGAGATGTTTCAATTTCAATTTAA 1198

RESULT 3
AAF20935
ID AAF20935 standard; DNA; 1198 BP.
XX
XX AAF20935;
XX
XX 14-MAR-2001 (first entry)
XX
XX Human high affinity IgE receptor polynucleotide fragment #2502.
DE
KW Low adenosine antisense oligonucleotide; phosphorothioate; allergy;
KW human; airway disorder; bronchoconstriction; lung inflammation;
KW surfactant depletion; respiratory; bronchodilator; antiinflammatory;
KW immunosuppressive; antiaesthetic; analgesic; hypotensive; cyclostatic;
KW respiratory obstruction; pulmonary obstruction; impeded respiration;
KW surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;
KW respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;
KW pulmonary hypertension; emphysema; pulmonary transplantation rejection;
KW chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
KW cancer; ss.
XX
XX Homo sapiens.
OS
XX WO200062736-A2.
PN
XX 26-OCT-2000.
XX
XX 24-MAR-2000; 2000WO-US008020.
PF
XX 06-APR-1999; 99US-0127958P.
PR
XX (UYEC-) UNIV EAST CAROLINA.
PA
XX (NYCE/) NYCE J W.
PI
XX Nyce JW;
XX
XX WPI; 2000-679539/66.
DR
XX
XX Low adenosine (A) content antisense oligonucleotides which do not trigger
PT adenosine receptors during metabolism, useful e.g. for treating cancers
PT and respiratory obstructions.
XX
XX Disclosure; Page 138; 1592pp; English.
PS
XX The present invention describes low adenosine (A) content antisense
CC

CC oligonucleotides and compositions (I) comprising them. In the antisense
 CC oligonucleotides the A is replaced by a 'Universal' or alternative base.
 CC (i) can have respiratory, bronchodilator, antiinflammatory, analgesic,
 CC immunosuppressive, antidiabetic, hypotensive and cytostatic activities.
 CC The antisense oligonucleotides and (i) can be used to down-regulate the
 CC expression and/or activity of target polypeptides associated with
 CC lung/respiratory disorders and malignancies, such as stimulating and
 CC activating peptide factors and transmitters, transcription factors,
 CC immunoglobulins and antibodies, antibody receptors, cytokines and
 CC chemokines, endogenously produced specific and non-specific enzymes,
 CC binding proteins, adhesion molecules and their receptors, cytokine and
 CC chemokine receptors, adenosine receptors, bradykinin receptors, central
 CC nervous system (CNS) and peripheral nervous and non-nervous system
 CC receptors, CNS and peripheral nervous and non-nervous system peptide
 CC transmitters, defensins, growth factors, vasoactive peptides and
 CC receptors, binding proteins and malignancy associated proteins. The
 CC antisense oligonucleotides may be used in this way to treat disorders
 CC including respiratory obstruction (especially pulmonary obstruction
 CC and/or bronchoconstriction) and/or lung inflammation, allergy(ies) and/or
 CC surfactant hypoproduction which are associated with a disease or
 CC condition selected from pulmonary vasoconstriction, inflammation,
 CC allergies, asthma, impeded respiration, respiratory distress syndrome
 CC (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary
 CC hypertension, emphysema, chronic obstructive pulmonary disease (COPD),
 CC pulmonary transplantation rejection, pulmonary infections, bronchitis,
 CC and/or cancer. AAF18434 to AAF21543 represent human polynucleotide
 CC fragments and antisense oligonucleotides used in the exemplification of
 CC the present invention

XX SQ Sequence 1198 BP; 389 A; 243 C; 245 G; 321 T; 0 U; 0 Other;

Query Match 100.0%; Score 1198; DB 3; Length 1198;

Best Local Similarity 100.0%; Pred. No. 2.3e-230;

Matches 1198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TACTAAGAGTCTCCAGCATCTCCACCTGCTTACCACGAGCATGGGCTATATTGAAG 60
 DB 1 TACTAAGAGTCTCCAGCATCTCCACCTGCTTACCACGAGCATGGGCTATATTGAAG 60
 QY 61 CCTTAGATCTCTCCAGCAGTAAGCACCAGGAGTCCATGAAGAGATGGCTCCCTGCCAT 120
 DB 61 CCTTAGATCTCTCCAGCAGTAAGCACCAGGAGTCCATGAAGAGATGGCTCCCTGCCAT 120
 QY 121 GGAATCCCTCTACTACTGTGTGTAGCTTACTGTCTTCTCGCTCCAGATGGCTGTAGC 180
 DB 121 GGAATCCCTCTACTACTGTGTGTAGCTTACTGTCTTCTCGCTCCAGATGGCTGTAGC 180
 QY 181 AGTCCCTCAGAAACCTAAGTCTCTCTGAAACCTCCATGGAATAGATATTAAAGGAGA 240
 DB 181 AGTCCCTCAGAAACCTAAGTCTCTCTGAAACCTCCATGGAATAGATATTAAAGGAGA 240
 QY 241 GAATGTGACTCTTATCATGTAATGGGAAACAATTTCTTTGAAGTCAGTCCACCAATGGTT 300
 DB 241 GAATGTGACTCTTATCATGTAATGGGAAACAATTTCTTTGAAGTCAGTCCACCAATGGTT 300
 QY 301 CCACATGGCAGCCTTTCCAGAGAGACAAATTCAGATTTGAATTTGATGCAATTT 360
 DB 301 CCACATGGCAGCCTTTCCAGAGAGACAAATTCAGATTTGAATTTGATGCAATTT 360
 QY 361 TGAAGACAGTGGAGAAATCAATGTCCAGCACCACCAAGTTAATGAGAGTGAACCTGTGTA 420
 DB 361 TGAAGACAGTGGAGAAATCAATGTCCAGCACCACCAAGTTAATGAGAGTGAACCTGTGTA 420
 QY 421 CCTGGAAGTCTTCACTGAGTGGCTCTCTCTCAGGCTCTCTGAGGTGGTGTAGGAGG 480
 DB 421 CCTGGAAGTCTTCACTGAGTGGCTCTCTCTCAGGCTCTCTGAGGTGGTGTAGGAGG 480
 QY 481 CCAGGCCCTCTCTCCTCAGTGCCTAGTGTGGAGGAACCTGGGATGTGTACAAAGGTGATCTA 540
 DB 481 CCAGGCCCTCTCTCCTCAGTGCCTAGTGTGGAGGAACCTGGGATGTGTACAAAGGTGATCTA 540
 QY 541 TTATAGAGTGTGAGTCTCAAGTACTGTGTATGAGAACCAACATCTCCATTACAA 600

Db 541 TTATAGAGTGTGAGTCTCAAGTCTCAAGTACTGTGTATGAGAACCAACATCTCCATTACAA 600
 QY 601 TGGCAGAGTTGAAGACAGTGGAACTTACTACTGTAGCGGCAAGTGTGGCAGCTGGACTA 660
 Db 601 TGGCAGAGTTGAAGACAGTGGAACTTACTACTGTAGCGGCAAGTGTGGCAGCTGGACTA 660
 QY 661 TGAGTCTGAGCCCTCAACATTTACTCTAATAAAGCTCCGCGTGAAGAGTACTGGCTACA 720
 Db 661 TGAGTCTGAGCCCTCAACATTTACTCTAATAAAGCTCCGCGTGAAGAGTACTGGCTACA 720
 QY 721 ATTTTATATCCCATTTGTTGGTGTGATCTGTTTGTCTGTGGACACAGGATTTATCTCTC 780
 Db 721 ATTTTATATCCCATTTGTTGGTGTGATCTGTTTGTCTGTGGACACAGGATTTATCTCTC 780
 QY 781 AACTCAGCAGCAGTCCACATTTCTCTTGAAGATTAAAGAACCCAGGAAAGGCTTCAGACT 840
 Db 781 AACTCAGCAGCAGTCCACATTTCTCTTGAAGATTAAAGAACCCAGGAAAGGCTTCAGACT 840
 QY 841 TCTGAACCCACATCTTAAAGCCAAACCCCAAAACCACTGATATAATTACTCAAGAAATAT 900
 Db 841 TCTGAACCCACATCTTAAAGCCAAACCCCAAAACCACTGATATAATTACTCAAGAAATAT 900
 QY 901 TTGCAACATTTAGTTTTCCTCAGCATCAGCAATTTGCTCAATTTGCTCAAAACACAGCTTG 960
 Db 901 TTGCAACATTTAGTTTTCCTCAGCATCAGCAATTTGCTCAATTTGCTCAAAACACAGCTTG 960
 QY 961 CAATATACATAGAAACGCTGCTGCTCAAGGATTTATAGAAATGCTTTCATTAACATGAGTG 1020
 Db 961 CAATATACATAGAAACGCTGCTGCTCAAGGATTTATAGAAATGCTTTCATTAACATGAGTG 1020
 QY 1021 AAATCGTTAAGTGGCATGTAATAGTGAATGCTCAATTAACATTTGTTGAATAATGAGA 1080
 Db 1021 AAATCGTTAAGTGGCATGTAATAGTGAATGCTCAATTAACATTTGTTGAATAATGAGA 1080
 QY 1081 GAATGAATAGATTCATTTATTAGCATTTTGTAAAAGAGATGTTCAATTTCAATAAATAAA 1140
 Db 1081 GAATGAATAGATTCATTTATTAGCATTTTGTAAAAGAGATGTTCAATTTCAATAAATAAA 1140
 QY 1141 TATAAAACCATGTAACAGAAATGCTTCTGAGTAAAAAATAAATAAATAAATAAATAA 1198
 Db 1141 TATAAAACCATGTAACAGAAATGCTTCTGAGTAAAAAATAAATAAATAAATAAATAA 1198
 RESULT 4
 AAF77692
 ID AAF77692 standard; cDNA; 1198 BP.
 XX AAF77692;
 XX AC
 XX 29-MAY-2001 (first entry)
 XX Human wild-type FeepsilonRialpha chain coding sequence.
 DE Human; FeepsilonRiBeta chain; immunoglobulin E; allergy; atopy;
 KW conjunctivitis; rhinitis; anaphylaxis; urticaria; angioedema; ss.
 KW
 XX Homo sapiens.
 OS
 XX WC200121816-A1.
 PN
 XX 29-MAR-2001.
 PD
 XX 21-SEP-2000; 2000WO-US025877.
 PF
 XX 21-SEP-1999; 99US-0154924P.
 PR
 XX (ISIS-) ISIS INNOVATION LTD.
 PA (BETH-) BETH ISRAEL DEACONESS MEDICAL CENT.
 PI Kinet J, Donnadieu E, Jouvin M, Cookson W, Moffatt MF;
 XX WPI; 2001-266077/27.
 DR
 XX

PT Inhibiting expression of high affinity receptors for immunoglobulin (Ig)
PT E, in cell or in subject to treat atopy, anaphylaxis mediated by IgE, by
PT contacting cell or administering to subject, a Fc epsilon chain variant.
XX
PS Disclosure; Page 52; 55pp; English.

XX The present invention describes a method of inhibiting the expression of
CC the Fc epsilon chain variant. The Fc epsilon chain variant is a high affinity
CC receptor for immunoglobulin E. The method is useful in the treatment of
CC allergic conditions such as rhinitis, conjunctivitis, atopy, anaphylaxis,
CC urticaria and angioedema. The present sequence is the wild-type human
CC Fc epsilon chain coding sequence

SQ Sequence 1198 BP; 389 A; 243 C; 245 G; 321 T; 0 U; 0 Other;

Query March 100.0%; Score 1198; DB 4; Length 1198;
Best Local Similarity 100.0%; Pred. No. 2.3e-230;
Matches 1198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TACTAAGAGTCTCCAGCATCTCCACCTGCTACACCGAGCATGGCCCTATATTGAAG 60
DB 1 TACTAAGAGTCTCCAGCATCTCCACCTGCTACACCGAGCATGGCCCTATATTGAAG 60
QY 61 CCTTAGATCTCCAGCAGTACAGCAGGAGTCCATGAGAGATGCTCTGCTCCAT 120
DB 61 CCTTAGATCTCCAGCAGTACAGCAGGAGTCCATGAGAGATGCTCTGCTCCAT 120
QY 121 GGAATCCCTACTCTACTGCTGAGCTTACTGCTTCTGCTCCAGATGGCGTGTAGC 180
DB 121 GGAATCCCTACTCTACTGCTGAGCTTACTGCTTCTGCTCCAGATGGCGTGTAGC 180
QY 181 AGTCCCTCAGAACTAAGGCTCTCCTTGAACCTCCATGGAATAGATATTTAAAGGAGA 240
DB 181 AGTCCCTCAGAACTAAGGCTCTCCTTGAACCTCCATGGAATAGATATTTAAAGGAGA 240
QY 241 GAAATGAGCTTACATGTAATGGACAAATTTCTTGAAGTCAAGTTCACCAATGTT 300
DB 241 GAAATGAGCTTACATGTAATGGACAAATTTCTTGAAGTCAAGTTCACCAATGTT 300
QY 301 CCACAAATGGCAGCTTTTCCAGAGAGACAAATTTCAAGTTCAAGTTCAAGTTCAAGTT 360
DB 301 CCACAAATGGCAGCTTTTCCAGAGAGACAAATTTCAAGTTCAAGTTCAAGTTCAAGTT 360
QY 361 TGAAGACAGTGGAGAAATACAAATGTGACACCAACAAATGTAAGAGTGAACCTGTGTA 420
DB 361 TGAAGACAGTGGAGAAATACAAATGTGACACCAACAAATGTAAGAGTGAACCTGTGTA 420
QY 421 CCTGGAAGTCTTCAAGTCAAGTCTGCTCTTCCAGGCTCTGCTGAGTGGTGGAGGG 480
DB 421 CCTGGAAGTCTTCAAGTCAAGTCTGCTCTTCCAGGCTCTGCTGAGTGGTGGAGGG 480
QY 481 CCAGCCCTCTTCTCAGTGGTCCATGTTGGAGAACTGGGATGTGTACAAAGTGTACTTA 540
DB 481 CCAGCCCTCTTCTCAGTGGTCCATGTTGGAGAACTGGGATGTGTACAAAGTGTACTTA 540
QY 541 TTATAGAGATGGTGAAGCTCTCAAGTCAAGTCTGTAAGACCAACATCTCCATTACAAA 600
DB 541 TTATAGAGATGGTGAAGCTCTCAAGTCAAGTCTGTAAGACCAACATCTCCATTACAAA 600
QY 601 TGCCACAGTGAAGACAGTGAACCTACTACTGACGGGAAAGTGGCAGCTGGACTA 660
DB 601 TGCCACAGTGAAGACAGTGAACCTACTACTGACGGGAAAGTGGCAGCTGGACTA 660
QY 661 TGAGTCTGAGCCCTCAACATCTGTAATTAAGAGTCCGCTGAGAGTACTGGCTACA 720
DB 661 TGAGTCTGAGCCCTCAACATCTGTAATTAAGAGTCCGCTGAGAGTACTGGCTACA 720
QY 721 ATTTTATCCATTTGTTGGTGGTATCTGTTGCTGTGACACAGGATTTATCTC 780
DB 721 ATTTTATCCATTTGTTGGTGGTATCTGTTGCTGTGACACAGGATTTATCTC 780
QY 781 AACTCAGCAGCAGGTCACTTTCTTGAAGATTAAGAGAACCCAGGAAAGGCTTCAGACT 840

DB 781 AACTCAGCAGCAGGTCACTTTCTTGAAGATTAAGAGAACCCAGGAAAGGCTTCAGACT 840
QY 841 TCTGAAACCCACATCTTAAGCCAAACCCCAAAACCACTGATATATTAATCAAGAAATAT 900
DB 841 TCTGAAACCCACATCTTAAGCCAAACCCCAAAACCACTGATATATTAATCAAGAAATAT 900
QY 901 TTGCAACATTTAGTCTTTTCCAGCATCAGCAATTTCTACTCAATTTCAACACAGCTTG 960
DB 901 TTGCAACATTTAGTCTTTTCCAGCATCAGCAATTTCTACTCAATTTCAACACAGCTTG 960
QY 961 CAATATACATAGAAACGCTGCTGCTCAAGGATTTATAGAAATGCTTCAATTAAGTGGTG 1020
DB 961 CAATATACATAGAAACGCTGCTGCTCAAGGATTTATAGAAATGCTTCAATTAAGTGGTG 1020
QY 1021 AAACTGGTTAAGTGGCATGTAATAGTAGTCTCAATTAACATTTGTTGAATAATGAGA 1080
DB 1021 AAACTGGTTAAGTGGCATGTAATAGTAGTCTCAATTAACATTTGTTGAATAATGAGA 1080
QY 1081 GAATGAATAGATTCATTTTATTAGCATTTTGTAAAGAGATGTTCAATTTCAATAAATAA 1140
DB 1081 GAATGAATAGATTCATTTTATTAGCATTTTGTAAAGAGATGTTCAATTTCAATAAATAA 1140
QY 1141 TATAAAACCATCTTAACAGATGCTTCTGAGTAAAAAATAAATAAATAAATAAATAA 1198
DB 1141 TATAAAACCATCTTAACAGATGCTTCTGAGTAAAAAATAAATAAATAAATAAATAA 1198

RESULT 5

AAF24912/c

ID AAF24912 standard; DNA; 1198 BP.

XX AAF24912;

XX AAF24912;

DT 30-APR-2001 (first entry)

XX Complement sequence of a human Fc epsilon receptor alpha-chain gene.

DE Fc epsilon receptor; Fc epsilonR; immunoglobulin E; IgE; atopic disease;

XX Fc epsilon receptor; Fc epsilonR; immunoglobulin E; IgE; atopic disease;

XX Fc epsilon receptor; Fc epsilonR; immunoglobulin E; IgE; atopic disease;

XX Fc epsilon receptor; Fc epsilonR; immunoglobulin E; IgE; atopic disease;

XX Fc epsilon receptor; Fc epsilonR; immunoglobulin E; IgE; atopic disease;

XX Fc epsilon receptor; Fc epsilonR; immunoglobulin E; IgE; atopic disease;

XX Fc epsilon receptor; Fc epsilonR; immunoglobulin E; IgE; atopic disease;

XX Fc epsilon receptor; Fc epsilonR; immunoglobulin E; IgE; atopic disease;

XX Fc epsilon receptor; Fc epsilonR; immunoglobulin E; IgE; atopic disease;

XX Fc epsilon receptor; Fc epsilonR; immunoglobulin E; IgE; atopic disease;

XX Fc epsilon receptor; Fc epsilonR; immunoglobulin E; IgE; atopic disease;

XX Fc epsilon receptor; Fc epsilonR; immunoglobulin E; IgE; atopic disease;

XX Fc epsilon receptor; Fc epsilonR; immunoglobulin E; IgE; atopic disease;

XX Fc epsilon receptor; Fc epsilonR; immunoglobulin E; IgE; atopic disease;

XX Fc epsilon receptor; Fc epsilonR; immunoglobulin E; IgE; atopic disease;

XX Fc epsilon receptor; Fc epsilonR; immunoglobulin E; IgE; atopic disease;

XX Fc epsilon receptor; Fc epsilonR; immunoglobulin E; IgE; atopic disease;

XX Fc epsilon receptor; Fc epsilonR; immunoglobulin E; IgE; atopic disease;

XX Fc epsilon receptor; Fc epsilonR; immunoglobulin E; IgE; atopic disease;

XX Fc epsilon receptor; Fc epsilonR; immunoglobulin E; IgE; atopic disease;

XX Fc epsilon receptor; Fc epsilonR; immunoglobulin E; IgE; atopic disease;

XX Fc epsilon receptor; Fc epsilonR; immunoglobulin E; IgE; atopic disease;

XX Fc epsilon receptor; Fc epsilonR; immunoglobulin E; IgE; atopic disease;

XX Fc epsilon receptor; Fc epsilonR; immunoglobulin E; IgE; atopic disease;

XX Fc epsilon receptor; Fc epsilonR; immunoglobulin E; IgE; atopic disease;

XX Fc epsilon receptor; Fc epsilonR; immunoglobulin E; IgE; atopic disease;

XX Fc epsilon receptor; Fc epsilonR; immunoglobulin E; IgE; atopic disease;

XX Fc epsilon receptor; Fc epsilonR; immunoglobulin E; IgE; atopic disease;

XX Fc epsilon receptor; Fc epsilonR; immunoglobulin E; IgE; atopic disease;

XX Fc epsilon receptor; Fc epsilonR; immunoglobulin E; IgE; atopic disease;

XX Fc epsilon receptor; Fc epsilonR; immunoglobulin E; IgE; atopic disease;

XX Fc epsilon receptor; Fc epsilonR; immunoglobulin E; IgE; atopic disease;

XX Fc epsilon receptor; Fc epsilonR; immunoglobulin E; IgE; atopic disease;

XX Fc epsilon receptor; Fc epsilonR; immunoglobulin E; IgE; atopic disease;

XX Fc epsilon receptor; Fc epsilonR; immunoglobulin E; IgE; atopic disease;

XX Fc epsilon receptor; Fc epsilonR; immunoglobulin E; IgE; atopic disease;

XX Fc epsilon receptor; Fc epsilonR; immunoglobulin E; IgE; atopic disease;

XX Fc epsilon receptor; Fc epsilonR; immunoglobulin E; IgE; atopic disease;

XX Fc epsilon receptor; Fc epsilonR; immunoglobulin E; IgE; atopic disease;

XX Fc epsilon receptor; Fc epsilonR; immunoglobulin E; IgE; atopic disease;

XX Fc epsilon receptor; Fc epsilonR; immunoglobulin E; IgE; atopic disease;

XX Fc epsilon receptor; Fc epsilonR; immunoglobulin E; IgE; atopic disease;

XX Fc epsilon receptor; Fc epsilonR; immunoglobulin E; IgE; atopic disease;

XX Fc epsilon receptor; Fc epsilonR; immunoglobulin E; IgE; atopic disease;

XX Fc epsilon receptor; Fc epsilonR; immunoglobulin E; IgE; atopic disease;

XX Fc epsilon receptor; Fc epsilonR; immunoglobulin E; IgE; atopic disease;

XX Fc epsilon receptor; Fc epsilonR; immunoglobulin E; IgE; atopic disease;

XX Fc epsilon receptor; Fc epsilonR; immunoglobulin E; IgE; atopic disease;

CC be used to identify a compound capable of inhibiting Fc epsilon R protein
 CC activity. Ige antibody production is indicative of diseases such as
 CC allergies, atopic disease, hyper Ige syndrome, internal parasite
 CC infections and B cell neoplasia. Detection of Ige production in an animal
 CC following therapy is indicative of the efficacy of the treatment, for
 CC example when using treatments intended to disrupt Ige production
 XX

Sequence 1198 BP; 321 A; 245 C; 243 G; 389 T; 0 U; 0 Other;

Query Match 100.0%; Score 1198; DB 5; Length 1198;

Best Local Similarity 100.0%; Pred. No. 2.3e-230;

Matches 1198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TACTAAGAGTCTCCAGCATCTCCACCTGTCTACACCGAGCATGGGCTATATTGAAG 60
 DB 1198 TACTAAGAGTCTCCAGCATCTCCACCTGTCTACACCGAGCATGGGCTATATTGAAG 1139
 QY 61 CCTTAGATCTCTCCAGCAGTAAGCACCAGGAGTCCATGAAGAAGATGGCTCTGCCAT 120
 DB 1138 CCTTAGATCTCTCCAGCAGTAAGCACCAGGAGTCCATGAAGAAGATGGCTCTGCCAT 1079

QY 121 GGAATCCCTACTCTACTGTGTAGCTTCTTCCATGAGTCTTCCAGATGGCGTTAGC 180
 DB 1078 GGAATCCCTACTCTACTGTGTAGCTTCTTCCATGAGTCTTCCAGATGGCGTTAGC 1019

QY 181 AGTCCCTCAGAACCTTAAGTCTCTTGAACCTCCATGGAATGAATATTAAGGAGA 240
 DB 1018 AGTCCCTCAGAACCTTAAGTCTCTTGAACCTCCATGGAATGAATATTAAGGAGA 959

QY 241 GAATGTGACTCTTACATGTAATGGAACAATTTCTTTGAAGTCAGTTCCACCAATGTT 300
 DB 958 GAATGTGACTCTTACATGTAATGGAACAATTTCTTTGAAGTCAGTTCCACCAATGTT 899

QY 301 CCACATGCGACCTTCCAGAGACAAATTCAGTTTGAATATGTAATGGAATGCCAATT 360
 DB 898 CCACATGCGACCTTCCAGAGACAAATTCAGTTTGAATATGTAATGGAATGCCAATT 839

QY 361 TGAAGCAGTGGAGATAACAATGTTCAGCAACAAGTTAATGAGAGTGAACCTGTGA 420
 DB 838 TGAAGCAGTGGAGATAACAATGTTCAGCAACAAGTTAATGAGAGTGAACCTGTGA 779

QY 421 CTGGAAGTCTTCAGTACTGCTGCTCTTCCAGCCCTCTGCTGAGTGGTGTAGGAGG 480
 DB 778 CTGGAAGTCTTCAGTACTGCTGCTCTTCCAGCCCTCTGCTGAGTGGTGTAGGAGG 719

QY 481 CCAGCCCTCTTCTCAGTGCATGTTGGAGGAACCTGGATGTACAAGGTGATCTA 540
 DB 718 CCAGCCCTCTTCTCAGTGCATGTTGGAGGAACCTGGATGTACAAGGTGATCTA 659

QY 541 TTATAAGATGTGAGTCTCAAGTACTGATGATGAGAACCAACAATCTCCATCAAAA 600
 DB 658 TTATAAGATGTGAGTCTCAAGTACTGATGATGAGAACCAACAATCTCCATCAAAA 599

QY 601 TCCACAGTGAAGCAGTGGAGTCTTACTGACGGCAAGTGTGCGAGCTGACTA 660
 DB 598 TCCACAGTGAAGCAGTGGAGTCTTACTGACGGCAAGTGTGCGAGCTGACTA 539

QY 661 TGAGTCTGAGCCCTCAACATTTACTGTATATAAAGCTCCCGGTGAGAGTACTGGCTACA 720
 DB 538 TGAGTCTGAGCCCTCAACATTTACTGTATATAAAGCTCCCGGTGAGAGTACTGGCTACA 479

QY 721 ATTTTATCCATTTGTTGGTGAATTTCTGTTGCTGTGACACAGAGTATTTATCTC 780
 DB 478 ATTTTATCCATTTGTTGGTGAATTTCTGTTGCTGTGACACAGAGTATTTATCTC 419

QY 781 AACTCAGCAGGTCACATTTCTCTTGAAGTAAAGAGAACCCAGGAAGCTTCAGACT 840
 DB 418 AACTCAGCAGGTCACATTTCTCTTGAAGTAAAGAGAACCCAGGAAGCTTCAGACT 359

QY 841 TGTGAACCCACATCTTAAGCCMAACCCCAAAAACAACTGATATATTAATCTCAAGAAATAT 900
 DB 358 TGTGAACCCACATCTTAAGCCMAACCCCAAAAACAACTGATATATTAATCTCAAGAAATAT 299

QY 901 TTGCAACATTAGTTTTTTTCCAGCATCAGCAATTGCTACTCAATTGCTCAACACAGCTTG 960
 DB 298 TTGCAACATTAGTTTTTTTCCAGCATCAGCAATTGCTACTCAATTGCTCAACACAGCTTG 239
 QY 961 CAATATACATAGAAAACGTCTGCTCAAGGATTTATAGAAATGCTTCATTAAACTGAGTG 1020
 DB 238 CAATATACATAGAAAACGTCTGCTCAAGGATTTATAGAAATGCTTCATTAAACTGAGTG 179
 QY 1021 AAATGTTAAAGTGGCATGTAATAGTCTCAATTAACTAACTGGTTGAATAAATGAGA 1080
 DB 178 AAATGTTAAAGTGGCATGTAATAGTCTCAATTAACTAACTGGTTGAATAAATGAGA 119
 QY 1081 GAATGAATGATTCATTATTAGCATTTGTAAAAGAGATGTTCAATTTCAATAAATAA 1140
 DB 118 GAATGAATGATTCATTATTAGCATTTGTAAAAGAGATGTTCAATTTCAATAAATAA 59
 QY 1141 TATAAACCATGTAAACAGATGCTTCTGAGTAAAAAATAAATAAATAAATAA 1198
 DB 58 TATAAACCATGTAAACAGATGCTTCTGAGTAAAAAATAAATAAATAAATAAATAA 1

RESULT 6

AAF24911

ID AAF24911 standard; DNA; 1198 BP.

XX AAF24911;

XX 30-APR-2001 (first entry)

XX Nucleotide sequence of a human Fc epsilon receptor alpha-chain.

XX Fc epsilon receptor; Fc epsilon R; immunoglobulin E; IGE; atopic disease;

XX luminescence inducing protein; allergy; hyper IGE syndrome;

XX internal parasite infection; B cell neoplasia; ss.

XX Homo sapiens.

XX Key Location/Qualifiers

XX CDS 107..880

XX FT /*tag= a

XX PT /product= "Fc epsilon receptor alpha-chain"

XX WO200104310-A1.

XX 18-JAN-2001.

XX 13-JUL-2000; 2000WO-US019070.

XX 13-JUL-1999; 99US-0143612P.

XX 02-MAR-2000; 2000US-0186412P.

XX (HESK-) HESKA CORP.

XX (PROM-) PROMEGA CORP.

XX Weber ER, Wood KV, Hall MP;

XX WPI; 2001-103082/11.

XX P-PSDB; AAB31584.

XX A fusion protein, comprising an Fc epsilon receptor domain and a

XX luminescence inducing protein domain that induces a LP substrate to emit

XX light when contacted with the LP domain, useful for detecting

XX immunoglobulin (Ig) E.

XX Claim 17; Page 58-59; 105pp; English.

XX The present sequence encodes a human Fc epsilon receptor (Fc epsilon R)

XX alpha-chain protein, that binds to immunoglobulin (Ig) E. The Fc epsilon R

XX domain is used to produce a fusion protein, which also comprises a

XX luminescence inducing protein domain that induces a substrate to emit

XX light when contacted with the luminescence inducing protein domain. The

XX fusion protein may be used to detect IGE. It may also be used to identify

XX a compound capable of inhibiting Fc epsilon R protein activity. IGE

CC antibody production is indicative of diseases such as allergies, atopic
CC disease, hyper IGE syndrome, internal parasite infections and B cell
CC neoplasia. Detection of IGE production in an animal following therapy is
CC indicative of the efficacy of the treatment, for example when using
CC treatments intended to disrupt IGE production
XX
SQ Sequence 1198 BP; 389 A; 243 C; 245 G; 321 T; 0 U; 0 Other;

Query Match 100.0%; Score 1198; DB 5; Length 1198;
Best Local Similarity 100.0%; Pred. No. 2.3e-230;
Matches 1198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TACTAAGAGTCTCCAGCATCCTCAGCTGTCTACCCAGAGCATGGCCCTATATTGAAG 60
Db 1 TACTAAGAGTCTCCAGCATCCTCAGCTGTCTACCCAGAGCATGGCCCTATATTGAAG 60
Qy 61 CCTTAGATCTCTCCAGCAGATGAACAGGAGTCCATGAAGATGCTCCTCCCAT 120
Db 61 CCTTAGATCTCTCCAGCAGATGAACAGGAGTCCATGAAGATGCTCCTCCCAT 120
Qy 121 GGAATCCCTTACTTACTGTGTAGCTTACTGTCTTTCGCTCCAGATGGCGTGTAGC 180
Db 121 GGAATCCCTTACTTACTGTGTAGCTTACTGTCTTTCGCTCCAGATGGCGTGTAGC 180
Qy 181 AGTCCCTCAGAAACCTTAAGTCTCCTTGAACCTCCATGAATAGATATTAAAGAGA 240
Db 181 AGTCCCTCAGAAACCTTAAGTCTCCTTGAACCTCCATGAATAGATATTAAAGAGA 240
Qy 241 GAATGTGACTCTTACATGTAAATGGAAACAATTTCTTGAAGTCAGTTCACCAAAATGGTT 300
Db 241 GAATGTGACTCTTACATGTAAATGGAAACAATTTCTTGAAGTCAGTTCACCAAAATGGTT 300
Qy 301 CCACATGGGAGCCTTTTCAAGAGAGCAAAATTCAGTTTGAATTTGTGAATGCCAAAT 360
Db 301 CCACATGGGAGCCTTTTCAAGAGAGCAAAATTCAGTTTGAATTTGTGAATGCCAAAT 360
Qy 361 TGAAGACAGTGGAGATACAAATGTGACGACCAACAGTTAAATGAGAGTGAACCTGTGA 420
Db 361 TGAAGACAGTGGAGATACAAATGTGACGACCAACAGTTAAATGAGAGTGAACCTGTGA 420
Qy 421 CCTGGAAGTCTTCAGTGACTGGTCTGCTTCCAGGCTCTGCTGAGGTGGTGAAGGG 480
Db 421 CCTGGAAGTCTTCAGTGACTGGTCTGCTTCCAGGCTCTGCTGAGGTGGTGAAGGG 480
Qy 481 CCAGCCCTCTTCTCAGGTGCCATGTTGGAGAACTGGATGTGTACAGGTGATCTA 540
Db 481 CCAGCCCTCTTCTCAGGTGCCATGTTGGAGAACTGGATGTGTACAGGTGATCTA 540
Qy 541 TTATAAGATGGTGAAGCTCTCAAGTACTGCTATGAGAACCAACAATCTCCATTACAA 600
Db 541 TTATAAGATGGTGAAGCTCTCAAGTACTGCTATGAGAACCAACAATCTCCATTACAA 600
Qy 601 TGCCACAGTTGAAGACAGTGAACCTTACTGTAGCGGCAAAAGTGGCAGCTGACTA 660
Db 601 TGCCACAGTTGAAGACAGTGAACCTTACTGTAGCGGCAAAAGTGGCAGCTGACTA 660
Qy 661 TGAGTCTGAGCCCTCAACATTAATGTAATAAGCTCCGCTGAGAGTACTGGGTACA 720
Db 661 TGAGTCTGAGCCCTCAACATTAATGTAATAAGCTCCGCTGAGAGTACTGGGTACA 720
Qy 721 ATTTTATCCATTTGTGGTGGTATCTGTTTGTGTCGACACAGGATTTATTTCTC 780
Db 721 ATTTTATCCATTTGTGGTGGTATCTGTTTGTGTCGACACAGGATTTATTTCTC 780
Qy 781 AACTCAGCAGGCTCAGTCTTCTTCTGAGATTAAGAGAACAGGAAAGGCTTCAGACT 840
Db 781 AACTCAGCAGGCTCAGTCTTCTTCTGAGATTAAGAGAACAGGAAAGGCTTCAGACT 840
Qy 841 TCTGAACCCATCCTTAAGCCAAACCCCAACAACTGATATAATTTACTCAAGAAATAT 900
Db 841 TCTGAACCCATCCTTAAGCCAAACCCCAACAACTGATATAATTTACTCAAGAAATAT 900
Qy 901 TTGCAACATTAAGTTTTTTCAGCATCAGCAATTTGCTACTCAATTTCAACACAGCTTG 960

Db 901 TTGCAACATTAAGTTTTTTCAGCATCAGCAATTTGCTACTCAATTTGCAACACAGCTTG 960
Qy 961 CAATATACATAGAAAGCTGTCTGCTCAAGGATTTATAGAAATGCTTCATTAACTGAGTG 1020
Db 961 CAATATACATAGAAAGCTGTCTGCTCAAGGATTTATAGAAATGCTTCATTAACTGAGTG 1020
Qy 1021 AAATCGTGAAGTGGCATGTAATAGTCTCAATTAACATTTGTTGAATAAATGAGA 1080
Db 1021 AAATCGTGAAGTGGCATGTAATAGTCTCAATTAACATTTGTTGAATAAATGAGA 1080
Qy 1081 GAATGAATAGATTCATTTATTAGCATTTTGTAAAGAGAGTTCATTTCAATAAATAA 1140
Db 1081 GAATGAATAGATTCATTTATTAGCATTTTGTAAAGAGAGTTCATTTCAATAAATAA 1140
Qy 1141 TATATAAACCATGTAAACAGATCTTCTGAGTAAATAAATAAATAAATAAATAA 1198
Db 1141 TATATAAACCATGTAAACAGATCTTCTGAGTAAATAAATAAATAAATAAATAA 1198

RESULT 7

ABL67793

ID ABL67793 standard; DNA; 1198 BP.

AC ABL67793;

XX DT 15-MAY-2002 (first entry)

XX Oesophagus cancer related gene sequence SEQ ID NO:6130.

XX Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;
XX stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;
XX cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;
XX gene; ds.

OS Homo sapiens.

XX WO200194629-A2.

XX PD 13-DEC-2001.

XX 30-MAY-2001; 2001WO-US010838.

XX 05-JUN-2000; 2000US-0209473P.

PR 05-JUN-2000; 2000US-0209531P.

PR 18-SEP-2000; 2000US-0231133P.

PR 18-SEP-2000; 2000US-0233611P.

PR 20-SEP-2000; 2000US-0234009P.

PR 20-SEP-2000; 2000US-0234034P.

PR 22-SEP-2000; 2000US-0234052P.

PR 22-SEP-2000; 2000US-0234509P.

PR 22-SEP-2000; 2000US-0234567P.

PR 25-SEP-2000; 2000US-0234923P.

PR 25-SEP-2000; 2000US-0234924P.

PR 25-SEP-2000; 2000US-0235077P.

PR 25-SEP-2000; 2000US-0235082P.

PR 25-SEP-2000; 2000US-0235134P.

PR 25-SEP-2000; 2000US-0235280P.

PR 26-SEP-2000; 2000US-0235637P.

PR 26-SEP-2000; 2000US-0235638P.

PR 27-SEP-2000; 2000US-0235711P.

PR 27-SEP-2000; 2000US-0235720P.

PR 27-SEP-2000; 2000US-0235840P.

PR 27-SEP-2000; 2000US-0235863P.

PR 28-SEP-2000; 2000US-0236028P.

PR 28-SEP-2000; 2000US-0236032P.

PR 28-SEP-2000; 2000US-0236033P.

PR 28-SEP-2000; 2000US-0236034P.

PR 28-SEP-2000; 2000US-0236109P.

PR 28-SEP-2000; 2000US-0236111P.

PR 29-SEP-2000; 2000US-0236842P.

PR 29-SEP-2000; 2000US-0236891P.

PR 02-OCT-2000; 2000US-0237172P.

KW antiallergic; allergic response; drug screening assay; immunoglobulin E;
 KW human; gene; ss.
 XX Homo sapiens.

OS

FH Key Location/Qualifiers
 FT CDS 107..880

FT /tag= a

FT /product= "Human FcERI receptor"

FT /transl_except= (767..769, aa:Glu)

FT /transl_except= (863..865, aa:Asp)

XX US6602983-B1.

PN

XX 05-AUG-2003.

PD

XX 22-SEP-1994; 94US-00310902.

XX 24-FEB-1988; 88US-00160457.

PR 30-OCT-1991; 91US-00785127.

PR 29-MAY-1993; 93US-00066640.

XX (USSH) US DEPT HEALTH & HUMAN SERVICES.

PA

XX Kinet JP, Kochan JP;

PI

XX WPI; 2003-669612/63.

DR P-PSDB; ADB5536.

XX

PT New alpha subunit of the human high affinity receptor for immunoglobulin
 PT E polypeptides, useful as antagonists to prevent allergic response, as
 PT reagents in drug screening assays, or for monitoring immunoglobulin E
 PT levels in patients.

XX Claim 1; Fig 1; 9pp; English.

PS

CC This invention relates to a novel purified polypeptide corresponding to
 CC the alpha subunit of the human high affinity receptor for immunoglobulin
 CC E (FcERI) and the DNA sequence which encodes it. The receptor of the
 CC invention is found exclusively on mast cells, basophils and related
 CC cells. Activation of the receptor triggers the release of preformed
 CC mediators such as histamine and serotonin which may result in allergic
 CC conditions. Compounds which modulate FcERI activity may have an antiallergic
 CC activity. The polypeptide of the invention may be useful as an antagonist
 CC for preventing allergic response, as a reagent in drug screening assays,
 CC as a therapeutic or for monitoring immunoglobulin E levels in patients.
 CC The DNA sequences may be useful for producing the polypeptide or for
 CC synthesising cDNA sequences to construct DNA probes used in diagnostic
 CC assays. The present sequence is the cDNA sequence encoding the alpha
 CC subunit of the human FcERI receptor of the invention.

XX Sequence 1198 BP; 389 A; 243 C; 245 G; 321 T; 0 U; 0 Other;

SQ Query Match 100.0%; Score 1198; DB 9; Length 1198;

Best Local Similarity 100.0%; Pred. No. 2.3e-230;

Matches 1198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TACTAAGAGTCTCCAGCATCTCCACCTGTCTACCCGAGCATGGCCCTATATTGAAAG 60

DB 1 TACTAAGAGTCTCCAGCATCTCCACCTGTCTACCCGAGCATGGCCCTATATTGAAAG 60

QY 61 CCTTAGATCTCTCCAGCAGTAAGCACCAGAGTCCCATGAAGAAGATGGCTCTCGCCAT 120

DB 61 CCTTAGATCTCTCCAGCAGTAAGCACCAGAGTCCCATGAAGAAGATGGCTCTCGCCAT 120

QY 121 GGAATCCCTACTCTACTGTGTGTAGCTTACTGTTCTTCTGCTCCAGATCGCGTTAGC 180

DB 121 GGAATCCCTACTCTACTGTGTGTAGCTTACTGTTCTTCTGCTCCAGATCGCGTTAGC 180

QY 181 AGTCCTCTCAGAAACCTTAGGTCCTCTTGAACCCCTCCCATGGAATAGATATTAAAGAGGA 240

DB 181 AGTCCTCTCAGAAACCTTAGGTCCTCTTGAACCCCTCCCATGGAATAGATATTAAAGAGGA 240

QY 241 GAATGTGACTCTTACATGTAATGGGAACAATTTCTTGAAGTCAGTTCCACCAAAATGGTT 300

DB 241 GAATGTGACTCTTACATGTAATGGGAACAATTTCTTGAAGTCAGTTCCACCAAAATGGTT 300

QY 301 CCACANTGCGAGCCTTTGAGAGAGACAAATTCAGTTTGAATATGTAATGTCACCAATTT 360

DB 301 CCACANTGCGAGCCTTTGAGAGAGACAAATTCAGTTTGAATATGTAATGTCACCAATTT 360

QY 361 TGAAGACAGTGGAGAAATACAAATGTGAGCACCACCAAGTTAATGAGAGTGAACCTGTGTA 420

DB 361 TGAAGACAGTGGAGAAATACAAATGTGAGCACCACCAAGTTAATGAGAGTGAACCTGTGTA 420

QY 421 CTTGGAAGTCTTCAGTGACTGGCTGCTCTCAGGCTCTGCTGAGGTGGTGTGATGGAGG 480

DB 421 CTTGGAAGTCTTCAGTGACTGGCTGCTCTCAGGCTCTGCTGAGGTGGTGTGATGGAGG 480

QY 481 CCAGCCCTCTTCCCTCAGTGCCATGTTGGAGGAACCTGGGATGTGTACAAGTGTATCTA 540

DB 481 CCAGCCCTCTTCCCTCAGTGCCATGTTGGAGGAACCTGGGATGTGTACAAGTGTATCTA 540

QY 541 TTATAAGATGCTGAAGCTCTCAAGTACTGTGATGAGAACCAACAATCTCCATTACAAA 600

DB 541 TTATAAGATGCTGAAGCTCTCAAGTACTGTGATGAGAACCAACAATCTCCATTACAAA 600

QY 601 TGCCACAGTTGAAGACAGTGGAACTTACTGTACGGGCAAGTGTGCGAGCTGGACTA 660

DB 601 TGCCACAGTTGAAGACAGTGGAACTTACTGTACGGGCAAGTGTGCGAGCTGGACTA 660

QY 661 TGAGTCTGAGCCCTCAACATTACTGTAAATAAAGCTCCGGGTGAGAAAGTACTGCTACA 720

DB 661 TGAGTCTGAGCCCTCAACATTACTGTAAATAAAGCTCCGGGTGAGAAAGTACTGCTACA 720

QY 721 ATTTTATCCCATTTGTTGGTGGTGAATTTCTGTTGCTGTGACACAGATTTATTTATCTC 780

DB 721 ATTTTATCCCATTTGTTGGTGGTGAATTTCTGTTGCTGTGACACAGATTTATTTATCTC 780

QY 781 AACTCAGCAGCAGGTTCACATTTCTCTGAAGATTGAAGAAACCCAGAAAGGCTTCAGACT 840

DB 781 AACTCAGCAGCAGGTTCACATTTCTCTGAAGATTGAAGAAACCCAGAAAGGCTTCAGACT 840

QY 841 TGTGAACCCACATCTTAAAGCCAAACCCCAAAACCACTGATATATTAATTAATCAAGAAATAT 900

DB 841 TGTGAACCCACATCTTAAAGCCAAACCCCAAAACCACTGATATATTAATTAATCAAGAAATAT 900

QY 901 TTGCAACATTAGTTTTTTTCCAGCATCAGCAATTCCTACTCAATTTGTCAAAACACAGCTTG 960

DB 901 TTGCAACATTAGTTTTTTTCCAGCATCAGCAATTCCTACTCAATTTGTCAAAACACAGCTTG 960

QY 961 CAATATACATAGAAACGTCCTGTGCTCAAGGATTTATAGAAATGCTTCAATTAACCTGAGTG 1020

DB 961 CAATATACATAGAAACGTCCTGTGCTCAAGGATTTATAGAAATGCTTCAATTAACCTGAGTG 1020

QY 1021 AAACCTGGTTAAGTGGCATGTATAGTAAAGTGTCTCAATTAACCTGGTTGAATAATGAGA 1080

DB 1021 AAACCTGGTTAAGTGGCATGTATAGTAAAGTGTCTCAATTAACCTGGTTGAATAATGAGA 1080

QY 1081 GAATGAATAGATTCATTTATTAGCATTTGTAAAAGAGATGTTCAATTTCAATAAATAAAA 1140

DB 1081 GAATGAATAGATTCATTTATTAGCATTTGTAAAAGAGATGTTCAATTTCAATAAATAAAA 1140

QY 1141 TATTAACCATGTAAACAGATGCTTCTGAGTAAATAAAAAAAAAAAAAAAAAAAAAA 1198

DB 1141 TATTAACCATGTAAACAGATGCTTCTGAGTAAATAAAAAAAAAAAAAAAAAAAAAA 1198

RESULT 10

AAA34816

ID AAA34816 standard; DNA; 21742 BP.

XX AAA34816;

XX AC

XX AC

DT 28-JUL-2000 (first entry)

XX

DE Human adenosine receptor related polynucleotide SEQ ID NO:2505.
 XX Human; adenosine receptor; low adenosine antisenese oligonucleotide;
 KW phosphorothioate; impaired respiration; inflammation; allergy;
 KN antiallergic; bronchoconstriction; inhibitor; antiinflammatory;
 KW allergic disease; bronchoconstriction; analgesic; impaired airway;
 KW antiallergic; antiasthmatic; cytotatic; analgesic; impaired airway;
 KW lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;
 KW respiratory distress syndrome; pain; cystic fibrosis; emphysema;
 KW pulmonary hypertension; chronic obstructive pulmonary disease; COPD;
 KW cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.
 XX Homo sapiens.
 OS
 XX
 XX WO200009525-A2.
 PN
 XX 24-FEB-2000.
 PD
 XX
 XX 03-AUG-1999; 99WO-US017712.
 FF
 XX
 XX 03-AUG-1998; 98US-0095212P.
 PR
 XX (UYEC-) UNIV EAST CAROLINA.
 PA
 XX
 XX Nyce JW;
 PI
 XX WPI; 2000-205971/18.
 DR
 XX
 XX New antisenese oligonucleotides useful for treating e.g. pulmonary
 PT vasoconstriction, inflammation, allergies, asthma, hypertension, or
 PT bronchitis, emphysema, respiratory distress syndrome, ischemia or
 PT cancers.
 PT
 XX
 XX Disclosure; Page 658-664; 1343pp; English.
 PS
 XX
 XX The present invention describes a new composition comprising an antisenese
 CC oligonucleotide (ON) with low adenosine (up to 15%), which targets
 CC nucleic acids involved in bronchoconstriction, allergies, and/or
 CC inflammation. The ON can have antiinflammatory, antiallergic,
 CC antiasthmatic, cytotatic and analgesic activities. The compositions are
 CC useful for the treatment of diseases associated with inflammation,
 CC impaired airways, including lung disease and diseases whose secondary
 CC effects afflict the lungs of a subject. They can be used for treating
 CC e.g. ischaemic conditions, pulmonary vasoconstriction, allergies, asthma,
 CC impeded respiration, respiratory distress syndrome, pain, cystic
 CC fibrosis, pulmonary hypertension, emphysema, chronic obstructive
 CC pulmonary disease (COPD), and cancers such as leukaemias, lymphomas,
 CC carcinomas, and cancers which may metastasize to the lungs, including
 CC breast and prostate cancer. The reduction of the adenosine content of the
 CC ONs reduces side effects. The A-containing ONs break down with the
 CC release of deoxyadenosine which activates adenosine receptors causing
 CC bronchoconstriction and inflammation. AAA32313 to AAA35312 represent the
 CC nucleotide sequences given in the sequence listing from the present
 CC invention, which correspond to SEQ ID NO:1 to 2815, and then the last 185
 CC sequences are also called SEQ ID NO:1 to 185, but the sequences differ
 CC from the previously named sequences. SEQ ID NO:11 to 1690 (AAA32323 to
 CC AAA33992) are specifically claimed ONs from the present invention. N.B.
 CC Sequences given in the disclosure of the present invention do not match
 CC up with their corresponding SEQ ID NO: sequences given in the sequence
 CC listing
 XX
 XX Sequence 21742 BP; 6598 A; 4107 C; 4408 G; 6612 T; 0 U; 17 Other;
 SQ
 Query Match 100.0%; Score 1198; DB 3; Length 21742;
 Best Local Similarity 100.0%; Pred. No. 3.8e-230;
 Matches 1198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 1 TACTAAGAGTCTCCAGCATCTCCACCTGTCTACCCGAGCATGGCGCTATATTTGAAG 60
 8353 TACTAAGAGTCTCCAGCATCTCCACCTGTCTACCCGAGCATGGCGCTATATTTGAAG 8412
 51 CCTTAGATCTCTCAGCAGCATAGCAGGATCCATGAGAGATGGCTCTCTGCCAT 120
 8413 CCTTAGATCTCTCAGCAGCATAGCAGGATCCATGAGAGATGGCTCTCTGCCAT 8472

QY 121 GGAATCCCTACTCTACTGTGTAGCTTACTGTCTTCTCGCTCCAGATGCGGTGTAGC 180
 DB 8473 GGAATCCCTACTCTACTGTGTAGCTTACTGTCTTCTCGCTCCAGATGCGGTGTAGC 8532
 QY 181 AGTCCTCAGAAACCTAAGGTCTCTTGAACCCCTCCATGGATAGATATTTAAAGGAGA 240
 DB 8533 AGTCCTCAGAAACCTAAGGTCTCTTGAACCCCTCCATGGATAGATATTTAAAGGAGA 8592
 QY 241 GAATGTGACTCTTACATGTAATGGGAAACAAATTTCTTTGAAGTCTAGTTCACCAATGGTT 300
 DB 8593 GAATGTGACTCTTACATGTAATGGGAAACAAATTTCTTTGAAGTCTAGTTCACCAATGGTT 8652
 QY 301 CCACAAATGGAGCCCTTTCAGAGAGAGACAAATTCAGATTTGAATATTTGGAATGCCAAAT 360
 DB 8653 CCACAAATGGAGCCCTTTCAGAGAGAGACAAATTCAGATTTGAATATTTGGAATGCCAAAT 8712
 QY 361 TGAACACAGTGGAGAAATACAAATGTCAGCACCAACAGTTAATGAGAGTGAACCTGTGTA 420
 DB 8713 TGAACACAGTGGAGAAATACAAATGTCAGCACCAACAGTTAATGAGAGTGAACCTGTGTA 8772
 QY 421 COTGGAAGTCTTCACTGAGTGGCTCTCTTCAAGCCCTCTCTGAGGTGGTGTAGGAGGG 480
 DB 8773 COTGGAAGTCTTCACTGAGTGGCTCTCTTCAAGCCCTCTCTGAGGTGGTGTAGGAGGG 8832
 QY 481 CCAGCCCTCTCTTCCAGGTGCCATGGTGGAGAACTGGGATGTGTACAAAGGTGATCTA 540
 DB 8833 CCAGCCCTCTCTTCCAGGTGCCATGGTGGAGAACTGGGATGTGTACAAAGGTGATCTA 8892
 QY 541 TTATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCAACACATCTCCATTACAAA 600
 DB 8893 TTATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCAACACATCTCCATTACAAA 8952
 QY 601 TGCCACAGTGAAGACAGTGGAAACCTACTACTGTACGGGCAAGTGTGGCAGCTGACTA 660
 DB 8953 TGCCACAGTGAAGACAGTGGAAACCTACTACTGTACGGGCAAGTGTGGCAGCTGACTA 9012
 QY 661 TGAGTCTGAGCCCTCAACATTTCTTGAAGTAAATAAAGCTCCGGTGGAGAGTACTGGCTACA 720
 DB 9013 TGAGTCTGAGCCCTCAACATTTCTTGAAGTAAATAAAGCTCCGGTGGAGAGTACTGGCTACA 9072
 QY 721 ATTTTATCCCATTTGGTGGTGAATTTCTTGTCTGTGGACACAGATTTATTTATCTC 780
 DB 9073 ATTTTATCCCATTTGGTGGTGAATTTCTTGTCTGTGGACACAGATTTATTTATCTC 9132
 QY 781 AACTCAGCAGCAGTCAATTTCTTGAAGTAAATAAAGCTCCGGTGGAGAGTACTGGCTACA 840
 DB 9133 AACTCAGCAGCAGTCAATTTCTTGAAGTAAATAAAGCTCCGGTGGAGAGTACTGGCTACA 9192
 QY 841 TCTGAAACCCACATCTTAAGCCAAACCCCAAAACCACTGATATATTTACTCAAGAAATAT 900
 DB 9193 TCTGAAACCCACATCTTAAGCCAAACCCCAAAACCACTGATATATTTACTCAAGAAATAT 9252
 QY 901 TTGCAACATTTATTTTTCAGATCAGCAATTTCTTGAAGTAAATAAAGCTCCGGTGGAGAGT 960
 DB 9253 TTGCAACATTTATTTTTCAGATCAGCAATTTCTTGAAGTAAATAAAGCTCCGGTGGAGAGT 9312
 QY 961 CAATATACATAGAAACGCTGTGTCTCAAGGATTTATAGAAATGCTTCAATTAACCTGAGTG 1020
 DB 9313 CAATATACATAGAAACGCTGTGTCTCAAGGATTTATAGAAATGCTTCAATTAACCTGAGTG 9372
 QY 1021 AAATGGTTTAACTGGCATGTAAATAGTGTCTCAATTAACATTTGGTGTGAATTAATGAGA 1080
 DB 9373 AAATGGTTTAACTGGCATGTAAATAGTGTCTCAATTAACATTTGGTGTGAATTAATGAGA 9432
 QY 1081 GAATGATAGATTCATTTATTTAGCATTTGTAAAGAGATGTTCAATTTCAATAAATAAAA 1140
 DB 9433 GAATGATAGATTCATTTATTTAGCATTTGTAAAGAGATGTTCAATTTCAATAAATAAAA 9492
 QY 1141 TATAAAACCATGTAAACAGATGCTTCTGAGTAAAAAATAAAAAAAAAAAAAAAAAAAAAA 1198
 DB 9493 TATAAAACCATGTAAACAGATGCTTCTGAGTAAAAAATAAAAAAAAAAAAAAAAAAAAAA 9550

RESULT 11	CC	the present invention	
AAF20938	XX		
ID AAF20938 standard; DNA; 21742 BP.	SQ	Sequence 21742 BP; 6598 A; 4107 C; 4408 G; 6612 T; 0 U; 17 Other;	
AC AAF20938;		Query Match 100.0%; Score 1198; DB 3; Length 21742;	
XX		Best Local Similarity 100.0%; Pred. No. 3.8e-230;	
DT 14-MAR-2001 (first entry)		Matches 1199; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
XX			
DE Human high affinity IgE receptor polynucleotide fragment #2505.	QY	1 TACTAAGAGTCTCCAGCATCTCCACCTGTCTACCAACCGAGCATGGGCTATATTGAAG 60	
XX	DB	8353 TACTAAGAGTCTCCAGCATCTCCACCTGTCTACCAACCGAGCATGGGCTATATTGAAG 8412	
KW Low adenosine antisense oligonucleotide; phosphorothioate; allergy;	QY	61 CTTATAGATCTCTCCAGCAGCATGAGCAGCAGAGTCCATGAAGAGATGGCTCTCCGCCAT 120	
KW human; airway disorder; bronchoconstriction; lung inflammation;	DB	8413 CTTATAGATCTCTCCAGCAGCATGAGCAGCAGAGTCCATGAAGAGATGGCTCTCCGCCAT 8472	
KW surfactant depletion; respiratory; bronchodilator; antiinflammatory;	QY	121 GGAATCCCTACTCTACTGTGTAGCCTTACTGTCTTCGCTCCAGATGGCGTGTAGC 180	
KW immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatic;	DB	8473 GGAATCCCTACTCTACTGTGTAGCCTTACTGTCTTCGCTCCAGATGGCGTGTAGC 8532	
KW respiratory obstruction; pulmonary obstruction; impeded respiration;	QY	181 AGTCCCTCAGAAACCTTAAGTCTCTTGAACCTCTCATGGAATAGAAATATTAAAGGAGA 240	
KW surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;	DB	8533 AGTCCCTCAGAAACCTTAAGTCTCTTGAACCTCTCATGGAATAGAAATATTAAAGGAGA 8592	
KW respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;	QY	241 GAATGTGACTCTTACATGTAATGGGAACAATTTCTTGAAGTCAGTTCACCAAAATGGTT 300	
KW pulmonary hypertension; emphysema; pulmonary transplantation rejection;	DB	8593 GAATGTGACTCTTACATGTAATGGGAACAATTTCTTGAAGTCAGTTCACCAAAATGGTT 8652	
KW chronic obstructive pulmonary disease; pulmonary infection; bronchitis;	QY	301 CCACAAATGGCAGCCTTTTCAAGAGAGACAAATTCAGATTTGAATATGTGAATGCCAAATTT 360	
XX	DB	8653 CCACAAATGGCAGCCTTTTCAAGAGAGACAAATTCAGATTTGAATATGTGAATGCCAAATTT 8712	
OS Homo sapiens.	QY	361 TGAAGACAGTGGAGAAATACAAATGTGAGCAGCAACCAAGTAAATAGAGAGTGAACCTGTGTA 420	
XX	DB	8713 TGAAGACAGTGGAGAAATACAAATGTGAGCAGCAACCAAGTAAATAGAGAGTGAACCTGTGTA 8772	
XX	QY	421 CTTGGAAGTCTTTTCAAGTGTGCTCTCTTCAAGTGTGCTCTCTGAGGTGGTGAAGGG 480	
XX	DB	8773 CTTGGAAGTCTTTTCAAGTGTGCTCTCTTCAAGTGTGCTCTCTGAGGTGGTGAAGGG 8832	
XX	QY	481 CCAGCCCCCTCTTCTCAGTGTGCTCTCTTCAAGTGTGCTCTCTGAGGTGGTGAAGGGTGAATCTA 540	
XX	DB	8833 CCAGCCCCCTCTTCTCAGTGTGCTCTCTTCAAGTGTGCTCTCTGAGGTGGTGAAGGGTGAATCTA 8892	
XX	QY	541 TTATAGAGTGTGGAAGCTCTCAAGTGTGCTCTCTTCAAGTGTGCTCTCTGAGGTGGTGAAGGG 600	
XX	DB	8893 TTATAGAGTGTGGAAGCTCTCAAGTGTGCTCTCTTCAAGTGTGCTCTCTGAGGTGGTGAAGGG 8952	
XX	QY	601 TGCCACAGTTGAAGACAGTGGAACTCTACTGTGTACGGGCAAGTGTGGCAGCTGGACTA 660	
XX	DB	8953 TGCCACAGTTGAAGACAGTGGAACTCTACTGTGTACGGGCAAGTGTGGCAGCTGGACTA 9012	
XX	QY	661 TGAGTCTGAGCCCCCTCAACATTTACTGTATATAAAGCTCCGCTGAGAGTACTGGCTACA 720	
XX	DB	9013 TGAGTCTGAGCCCCCTCAACATTTACTGTATATAAAGCTCCGCTGAGAGTACTGGCTACA 9072	
XX	QY	721 ATTTTATPCCCATTTGTTGGTGAATCTGTTGCTGTGGACACAGGATTTATTTATCTC 780	
XX	DB	9073 ATTTTATPCCCATTTGTTGGTGAATCTGTTGCTGTGGACACAGGATTTATTTATCTC 9132	
XX	QY	781 AACTCAGCAGCAGTGCACATTTCTTGAAGATTAAGAGAACCCAGGAAGCTTCAGACT 840	
XX	DB	9133 AACTCAGCAGCAGTGCACATTTCTTGAAGATTAAGAGAACCCAGGAAGCTTCAGACT 9192	
XX	QY	841 TCTGAACCCACATCTCTAAGCAGCAACCCCAAAACCACTGATATATTTACTCAAGAAATAT 900	
XX	DB	9193 TCTGAACCCACATCTCTAAGCAGCAACCCCAAAACCACTGATATATTTACTCAAGAAATAT 9252	
XX	QY	901 TTGCAACATTTAGTTTTTTTTCAGGATCAGCAATGTCTACTCAATGTCAACACAGCTTG 960	
XX	DB	9253 TTGCAACATTTAGTTTTTTTTCAGGATCAGCAATGTCTACTCAATGTCAACACAGCTTG 9312	
XX	QY	961 CAATATACATAGAAACGCTCTGTGCTCAAGGATTTATAGAAATGCTTCAATTAAGTGTG 1020	

Db 9313 CAATATACATAGAAACCTCTGTCTCAAGGATTATAGAAATCTTCATTAATACTGAGTG 9372
Qy 1021 AAACCTGGTTAAGTGGCATGTAATAGTAAGTGCCTCAATTAAACATTTGGTTGAATAAATGAGA 1080
Db 9373 AAACCTGGTTAAGTGGCATGTAATAGTAAGTGCCTCAATTAAACATTTGGTTGAATAAATGAGA 9432
Qy 1081 GAATGAATAGATTCATTTATTTAGCATTTGTAAGAGATGTTCAATTTCAATTAATAATATAA 1140
Db 9433 GAATGAATAGATTCATTTATTTAGCATTTGTAAGAGATGTTCAATTTCAATTAATAATATAA 9492
Qy 1141 TATAAAACCATGTAAACAGATGCTTCTGAGTAAATATAAATAAATAAATAAATAAATAA 1198
Db 9493 TATAAAACCATGTAAACAGATGCTTCTGAGTAAATATAAATAAATAAATAAATAAATAA 9550

RESULT 12
ID ABZ96632 standard; DNA; 21742 BP.
XX AC ABZ96632;
XX DT 17-OCT-2003 (first entry)
XX DE Human high affinity IGE receptor oligonucleotide fragment.
XX KW Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX OS Homo sapiens.
XX WO200285308-A2.
XX 31-OCT-2002.
XX 23-APR-2002; 2002WO-US013135.
XX 24-APR-2001; 2001US-0286137P.
XX (EPIG-) EPIGENESIS PHARM INC.
XX Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
XX Miller S, Tang L, Shahabuddin S;
XX WPI; 2003-229219/22.
XX Pharmaceutical composition for treating ailments associated with impaired
XX respiration, has oligo(s) antisense to specific gene(s) or its
XX corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
XX ubiquinone.
XX Disclosure; SEQ ID NO 11874; 872bp; English.
XX The invention relates to a novel pharmaceutical composition, which has a
XX first active agent comprising an oligonucleotide antisense to the
XX initiation codon, coding region, 5' or 3' end genomic flanking regions,
XX 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
XX junctions of genes encoding a polypeptide associated with lung and/or
XX nasal airway dysfunction and a second active agent comprising an
XX antiinflammatory steroid and ubiquinone. A composition of the invention
XX has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
XX immunosuppressive, and cytostatic activity. The composition may have a
XX use in antisense gene therapy. The composition is useful for treating or
XX preventing a respiratory, lung or malignant disease or condition, also
XX for enhancing the prophylactic or therapeutic respiratory effect of an
XX antiinflammatory steroid in a subject, for reducing or depleting levels
XX of, or reducing sensitivity to adenosine, reducing levels of adenosine
XX receptor, producing bronchodilation, increasing levels of ubiquinone or
XX lung surfactant in a subject's tissue, or treating bronchoconstriction,

CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: the sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 21742 BP; 6598 A; 4107 C; 4408 G; 6612 T; 0 U; 17 Other;
Query Match 100.0%; Score 1198; DB 7; Length 21742;
Best Local Similarity 100.0%; Pred. No. 3.8e-230; Indels 0; Gaps 0;
Matches 1198; Conservative 0; Mismatches 0;
Qy 1 TACTAAGAGTCTCCAGCATCTCCACCTGTCTACCCAGCAGCATGGGCTATATTGAAG 60
Db 8353 TACTAAGAGTCTCCAGCATCTCCACCTGTCTACCCAGCAGCATGGGCTATATTGAAG 8412
Qy 61 CTTTATAGATCTCTCCAGCAGTAAACACAGAGTCCATGAAGAAGATGGCTCTGCCAT 120
Db 8413 CTTTATAGATCTCTCCAGCAGTAAACACAGAGTCCATGAAGAAGATGGCTCTGCCAT 8472
Qy 121 GGAATCCCTACTCTACTGTGTAGCTTACTGTCTTCTCGCTCCAGATGGCTGTAGC 180
Db 8473 GGAATCCCTACTCTACTGTGTAGCTTACTGTCTTCTCGCTCCAGATGGCTGTAGC 8532
Qy 181 AGTCCCTCAGAAACCTAAAGTCTCTTGAACCTCCATGGAATAGAAATATTTAAAGGAGA 240
Db 8533 AGTCCCTCAGAAACCTAAAGTCTCTTGAACCTCCATGGAATAGAAATATTTAAAGGAGA 8592
Qy 241 GAATGTACTCTTACATGTAAATGGGAACAATTTCTTTGAAGTCAGTCCACCAATGGTT 300
Db 8593 GAATGTACTCTTACATGTAAATGGGAACAATTTCTTTGAAGTCAGTCCACCAATGGTT 8652
Qy 301 CCACATATGTCAGCCTTTTCCAGAAAGACAAATTTCAAGTTTGAATATTTGAATGCCAAAT 360
Db 8653 CCACATATGTCAGCCTTTTCCAGAAAGACAAATTTCAAGTTTGAATATTTGAATGCCAAAT 8712
Qy 361 TGAAGCAGTGGAGAAATACAAATGTGCAGCACCACCAAGTTAATAGAGTGAACCTGTCTA 420
Db 8713 TGAAGCAGTGGAGAAATACAAATGTGCAGCACCACCAAGTTAATAGAGTGAACCTGTCTA 8772
Qy 421 CTTGGAAGTCTTCAAGTACTGGCTCTCTCAGGCTCTCTGCTGAGGTGGTCAATGAGGG 480
Db 8773 CTTGGAAGTCTTCAAGTACTGGCTCTCTCAGGCTCTCTGCTGAGGTGGTCAATGAGGG 8832
Qy 481 CCAGCCCTCTTCTCAGTGCCATGGTTGGAGAACTGGGATGTGTACAGGTGATCTA 540
Db 8833 CCAGCCCTCTTCTCAGTGCCATGGTTGGAGAACTGGGATGTGTACAGGTGATCTA 8892
Qy 541 TTATAGAGTGGTGAAGTCTCAAGTACTGTATGAGAACCAACATCTCCATTACAAA 600
Db 8893 TTATAGAGTGGTGAAGTCTCAAGTACTGTATGAGAACCAACATCTCCATTACAAA 8952
Qy 601 TGCCACAGTTGAAGCAGTGGAACTTACTACTGTACGGGCAAGTGTGGCAGCTGACTA 660
Db 8953 TGCCACAGTTGAAGCAGTGGAACTTACTACTGTACGGGCAAGTGTGGCAGCTGACTA 9012
Qy 661 TGAGTCTGAGCCCTCAACATTTACTGTATTAAGCTCCGCTGAGAGTACTGGCTACA 720
Db 9013 TGAGTCTGAGCCCTCAACATTTACTGTATTAAGCTCCGCTGAGAGTACTGGCTACA 9072
Qy 721 ATTTTATCCCATTTGCTGTGATTTCTGTTGCTGGACACAGAGTATTTATCTC 780
Db 9073 ATTTTATCCCATTTGCTGTGATTTCTGTTGCTGGACACAGAGTATTTATCTC 9132
Qy 781 AACTCAGCAGCGGTTCATATTCTCTTGAAGTAAAGAGAACACAGGAAGGCTTCAGACT 840
Db 9133 AACTCAGCAGCGGTTCATATTCTCTTGAAGTAAAGAGAACACAGGAAGGCTTCAGACT 9192
Qy 841 TCTGACCCACATCTTAAGCCAAACCCCAAAACCACTGATATATTTACTCAAGAAATAT 900
Db 9193 TCTGACCCACATCTTAAGCCAAACCCCAAAACCACTGATATATTTACTCAAGAAATAT 9252
Qy 901 TTGCAACATTTAGTTTTTTTCCAGCATTCAGCAATTCCTACTCAATTTGTCAACACAGCTTG 960

Db 9253 TTGCAACATTAGTATTTTCCAGCATCAGCAATTGCTACTCAATTGTCAAACACAGCTTG 9312
 Qy 961 CAAATACATAGAAACGCTGCTCAAGGATTTATAGAAATGCTTCAATTAACCTGAGTG 1020
 Db 9313 CAAATACATAGAAACGCTGCTCAAGGATTTATAGAAATGCTTCAATTAACCTGAGTG 9372
 Qy 1021 AAACCTGGTTAAGTGGCATGTAATAGTAAGTGTCTCAATTAACATTTGGTTGAATAAATGAGA 1080
 Db 9373 AAACCTGGTTAAGTGGCATGTAATAGTAAGTGTCTCAATTAACATTTGGTTGAATAAATGAGA 9432
 Qy 1081 GAATGAATAGATTCATTTATAGCAATTTGTAAGAGATGTTCAATTTCAATAAATAAAA 1140
 Db 9433 GAATGAATAGATTCATTTATAGCAATTTGTAAGAGATGTTCAATTTCAATAAATAAAA 9492
 Qy 1141 TATAAAACCATGTAACAGAAATGCTTCTGAGTAAAAAATAAAAAAAAAAAAAAAAAAAAA 1198
 Db 9493 TATAAAACCATGTAACAGAAATGCTTCTGAGTAAAAAATAAAAAAAAAAAAAAAAAAAAA 9550

RESULT 13

ABZ97129

ID ABZ97129 standard; DNA; 117608 BP.

XX AC ABZ97129;

XX DT 17-OCT-2003 (first entry)

XX DE Human receptor-related antisense polynucleotide.

XX KW Human; antisense; lung dysfunction; nasal airway dysfunction;
 KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
 KW antiasthmatic; hypotensive; immunosuppressive; cyclostatic; gene therapy;
 KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
 KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
 KW lung inflammation; respiratory disease; ds.
 XX OS Homo sapiens.

XX PN WO200285308-A2.

XX PD 31-OCT-2002.

XX PF 23-APR-2002; 2002WO-US013135.

XX PR 24-APR-2001; 2001US-0286137P.

XX PA (EPIG-) EPIGENESIS PHARM INC.

XX PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;

XX PI Miller S, Tang L, Shahabuddin S;

XX DR WPI; 2003-229219/22.

XX PT Pharmaceutical composition for treating ailments associated with impaired
 PT respiration, has oligo(s) antisense to specific gene(s) or its
 PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
 PT ubiquinone.

XX PS Disclosure; SEQ ID NO 12371; 872pp; English.

XX CC The invention relates to a novel pharmaceutical composition, which has a
 CC first active agent comprising an oligonucleotide antisense to the
 CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
 CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
 CC junctions of genes encoding a polypeptide associated with lung and/or
 CC nasal airway dysfunction and a second active agent comprising an
 CC antiinflammatory steroid and ubiquinone. A composition of the invention
 CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
 CC immunosuppressive, and cyclostatic activity. The composition may have a
 CC use in antisense gene therapy. The composition is useful for treating or
 CC preventing a respiratory, lung or malignant disease or condition, also
 CC for enhancing the prophylactic or therapeutic respiratory effect of an
 CC antiinflammatory steroid in a subject, for reducing or depleting levels

CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
 CC receptor, producing bronchodilation, increasing levels of ubiquinone or
 CC lung surfactant in a subject's tissue, or treating bronchoconstriction.
 CC lung inflammation, lung allergies, or a respiratory disease or condition.
 CC Note: The sequence data for this patent is not represented in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences
 XX SQ Sequence 117608 BP; 27528 A; 29941 C; 30321 G; 29442 T; 0 U; 376 Other;

Query Match 100.0%; Score 1198; DB 7; Length 117608;

Best Local Similarity 100.0%; Pred. No. Se-230;

Matches 1198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TACTAAGAGTCTCCAGCATCCTCCACCTGCTCTACCAACCGAGCATGGCCCTATATTGAAG 60
 Db 100755 TACTAAGAGTCTCCAGCATCCTCCACCTGCTCTACCAACCGAGCATGGCCCTATATTGAAG 100814
 Qy 61 CTTAGATCTCTCCAGCACAGTAAGCACAGAGTCCATGAAGAGATGGCTCTGCCAT 120
 Db 100815 CTTAGATCTCTCCAGCACAGTAAGCACAGAGTCCATGAAGAGATGGCTCTGCCAT 100874
 Qy 121 GGAATCCCTACTCTACTGCTGTAGTACCTTACTGTTCTTCGCTCCAGATGGCGTGTAGC 180
 Db 100875 GGAATCCCTACTCTACTGCTGTAGTACCTTACTGTTCTTCGCTCCAGATGGCGTGTAGC 100934
 Qy 181 AGTCCCTCAGAAACCTTAAGTCTCTTGAACCTCTCATGGAATAGAAATTTAAAGGAGA 240
 Db 100935 AGTCCCTCAGAAACCTTAAGTCTCTTGAACCTCTCATGGAATAGAAATTTAAAGGAGA 100994
 Qy 241 GAATGAGTCTTTACATGAATGGGAACAATTTCTTTGAAGTCAGTTCACCAAAATGGT 300
 Db 100995 GAATGAGTCTTTACATGAATGGGAACAATTTCTTTGAAGTCAGTTCACCAAAATGGT 101054
 Qy 301 CCACATGGCAGCCCTTTCAGAAAGAGACAAATTCAGTTTGAATATTTGAATGCGCAAT 360
 Db 101055 CCACATGGCAGCCCTTTCAGAAAGAGACAAATTCAGTTTGAATATTTGAATGCGCAAT 101114
 Qy 361 TGAAGACAGTGGAGATACAAATGTGAGCACCACCAAGTTTATGAGATGACCTGTCTA 420
 Db 101115 TGAAGACAGTGGAGATACAAATGTGAGCACCACCAAGTTTATGAGATGACCTGTCTA 101174
 Qy 421 CTTGGAAGTCTTTCAGTACTGGCTGCTCTTCAGAGCTCTCTGCTGAGGTGGTGTATGGAGG 480
 Db 101175 CTTGGAAGTCTTTCAGTACTGGCTGCTCTTCAGAGCTCTCTGCTGAGGTGGTGTATGGAGG 101234
 Qy 481 CAGGCCCTCTTCTCAGTGCCATGGTTGGAGGAACCTGGGATGTGTACAGGTGATCTA 540
 Db 101235 CAGGCCCTCTTCTCAGTGCCATGGTTGGAGGAACCTGGGATGTGTACAGGTGATCTA 101294
 Qy 541 TTATAGGATGGTGAAGCTCTCAAGTACTGTGATGAGAACCAACATCTCCATTACAAA 600
 Db 101295 TTATAGGATGGTGAAGCTCTCAAGTACTGTGATGAGAACCAACATCTCCATTACAAA 101354
 Qy 601 TGCCACAGTTGAAGACAGTGGAACTTACTGTGTACGGGCAAGTGTGGCAGCTGACTA 660
 Db 101355 TGCCACAGTTGAAGACAGTGGAACTTACTGTGTACGGGCAAGTGTGGCAGCTGACTA 101414
 Qy 661 TGAGTCTGAGCCCTCAACATTTACTGTATTAAGCTCGCGTGAGAGAGTACTGGCTACA 720
 Db 101415 TGAGTCTGAGCCCTCAACATTTACTGTATTAAGCTCGCGTGAGAGAGTACTGGCTACA 101474
 Qy 721 ATTTTATATCCCATTTGTTGGTGGTATTTCTGTTGCTGTGGACACAGGATTTATCTC 780
 Db 101475 ATTTTATATCCCATTTGTTGGTGGTATTTCTGTTGCTGTGGACACAGGATTTATCTC 101534
 Qy 781 AACTCAGCAGGAGTCAATTTCTTGAAGATTTAAGAACCCAGGAAGGCTTCAGACT 840
 Db 101535 AACTCAGCAGGAGTCAATTTCTTGAAGATTTAAGAACCCAGGAAGGCTTCAGACT 101594
 Qy 841 TCTGAACCCACATCTCTAAGGCCAAACCCCAAAACCACTGATATTAATTAACAAGAAAT 900
 Db 101595 TCTGAACCCACATCTCTAAGGCCAAACCCCAAAACCACTGATATTAATTAACAAGAAAT 101654

QY 901 TTGCAACATTAGTCTTTTTCAGCATCAGCAATGCTACTCAATGTCAAACACAGCTTG 960
Db 101655 TTGCAACATTAGTCTTTTTCAGCATCAGCAATGCTACTCAATGTCAAACACAGCTTG 101714
QY 961 CAATATACATGAACAGCTGTGCTCAAGGATTTATAGAAATGCTTCAATTAACCTGAGTG 1020
Db 101715 CAATATACATGAACAGCTGTGCTCAAGGATTTATAGAAATGCTTCAATTAACCTGAGTG 101774
QY 1021 AAATCGGTTAAAGTGCATGTAATAGTAAAGTCTCAATTAACATGTTGTAATAATGAGA 1080
Db 101775 AAATCGGTTAAAGTGCATGTAATAGTAAAGTCTCAATTAACATGTTGTAATAATGAGA 101834
QY 1081 GAATGAATAGATTCATTTATTAGCATTTTGTAAAGAGATGTTCAATTTCAATAAATAAA 1140
Db 101835 GAATGAATAGATTCATTTATTAGCATTTTGTAAAGAGATGTTCAATTTCAATAAATAAA 101894
QY 1141 TATAAACCAGTACAGCAATGCTCTGAGTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1198
Db 101895 TATAAACCAGTACAGCAATGCTCTGAGTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 101952

RESULT 14
AAF21435
ID AAF21435 standard; DNA; 117609 BP.
XX AAF21435;
AC AAF21435;
XX AAF21435;
DT 14-MAR-2001 (first entry)
XX Human receptor-related antisense polynucleotide #3002.
XX Low adenosine antisense oligonucleotide; phosphorothioate; allergy;
KW human; airway disorder; bronchoconstriction; lung inflammation;
KW surfactant depletion; respiratory; bronchodilator; anti-inflammatory;
KW immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatic;
KW respiratory obstruction; pulmonary obstruction; impeded respiration;
KW surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;
KW respiratory distress syndrome; pulmonary vasoconstriction; asthma; RDS;
KW pulmonary hypertension; emphysema; pain; cystic fibrosis; allergic rhinitis;
KW chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
KW cancer; ss.
XX Homo sapiens.
OS Homo sapiens.
XX WO2000062736-A2.
FN WO2000062736-A2.
XX 26-OCT-2000.
XX 24-MAR-2000; 2000WO-US008020.
XX 06-APR-1999; 99US-0127958P.
XX (UYEC-) UNIV EAST CAROLINA.
PA (NYCE/) NYCE J W.
XX Nyce JW;
XX WPI; 2000-679539/66.
XX Low adenosine (A) content antisense oligonucleotides which do not trigger
PT adenosine receptors during metabolism, useful e.g. for treating cancers
PT and respiratory obstructions.
XX Disclosure; Page 17-47; 1592pp; English.

XX The present invention describes low adenosine (A) content antisense
CC oligonucleotides and compositions (I) comprising them. In the antisense
CC oligonucleotides the A is replaced by a 'Universal' or alternative base.
CC (I) can have respiratory, bronchodilator, anti-inflammatory, analgesic,
CC immunosuppressive, antiasthmatic, hypotensive and cytostatic activities.
CC The antisense oligonucleotides and (I) can be used to down-regulate the
CC expression and or activity of target polypeptides associated with

CC lung/respiratory disorders and malignancies, such as stimulating and
CC activating peptide factors and transmitters, transcription factors,
CC immunoglobulins and antibodies, antibody receptors, cytokines and
CC chemokines, endogenously produced specific and non-specific enzymes,
CC binding proteins, adhesion molecules and their receptors, cytokine and
CC chemokine receptors, adenosine receptors, bradykinin receptors, central
CC nervous system (CNS) and peripheral nervous and non-nervous system
CC receptors, CNS and peripheral nervous and non-nervous system peptide
CC transmitters, defensins, growth factors, vasoactive peptides and
CC receptors, binding proteins and malignancy associated proteins. The
CC antisense oligonucleotides may be used in this way to treat disorders
CC including respiratory obstruction (especially pulmonary obstruction
CC and/or bronchoconstriction) and/or lung inflammation, allergy(ies) and/or
CC surfactant hypoproduction which are associated with a disease or
CC condition selected from pulmonary vasoconstriction, inflammation,
CC allergies, asthma, impeded respiration, respiratory distress syndrome
CC (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary
CC hypertension, emphysema, chronic obstructive pulmonary disease (COPD),
CC pulmonary transplantation rejection, pulmonary infections, bronchitis,
CC and/or cancer. AAF18434 to AAF21543 represent human polynucleotide
CC fragments and antisense oligonucleotides used in the exemplification of
CC the present invention
XX

SQ Sequence 117609 BP; 27530 A; 29942 C; 30320 G; 29441 T; 0 U; 376 Other;
Query Match 100.0%; Score 1198; DB 3; Length 117609;
Best Local Similarity 100.0%; Pred. No. 5e-230;
Matches 1198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TACTAAGAGTCTCCAGCATCTCCACCTGTCTTACCACCCAGCATGGCTTATTTGAAG 60
Db 100756 TACTAAGAGTCTCCAGCATCTCCACCTGTCTTACCACCCAGCATGGCTTATTTGAAG 100815
QY 61 CTTAGATCTCTCCAGCAGTAAGCACCAGGAGTCCATGAAGAGATGGCTCTGCCAT 120
Db 100816 CTTAGATCTCTCCAGCAGTAAGCACCAGGAGTCCATGAAGAGATGGCTCTGCCAT 100875
QY 121 GGAATCCCTACTCTACTGTGTAGCTTCTTTCGCTCCAGATGGCGTGTAGC 180
Db 100876 GGAATCCCTACTCTACTGTGTAGCTTCTTTCGCTCCAGATGGCGTGTAGC 100935
QY 181 AGTCCCTCAGAAACCTTAAGGTCTCTTGAACCTCCTCATGAATAGTAATTTAAAGGAGA 240
Db 100936 AGTCCCTCAGAAACCTTAAGGTCTCTTGAACCTCCTCATGAATAGTAATTTAAAGGAGA 100995
QY 241 GAATGTGACTCTTACATGTAATGGGAAACAATTTCTTTGAAGTCAGTTCACCAATGGTT 300
Db 100996 GAATGTGACTCTTACATGTAATGGGAAACAATTTCTTTGAAGTCAGTTCACCAATGGTT 101055
QY 301 CCACATGGCAGCCTTTTCAGAGAGACAAATTTCAAGTTTGAATATTGTGAATGCCAAAT 360
Db 101056 CCACATGGCAGCCTTTTCAGAGAGACAAATTTCAAGTTTGAATATTGTGAATGCCAAAT 101115
QY 361 TGAAGACAGTGGAGAAATCAAAATGTGAGCAACCAAGTTAATAGAGTGAACCTGTGTA 420
Db 101116 TGAAGACAGTGGAGAAATCAAAATGTGAGCAACCAAGTTAATAGAGTGAACCTGTGTA 101175
QY 421 CTTGGAAGTCTTCAGTACTGGCTGCTCCTTCAGGCTCTGCTGAGTGGTGTGAGGG 480
Db 101176 CTTGGAAGTCTTCAGTACTGGCTGCTCCTTCAGGCTCTGCTGAGTGGTGTGAGGG 101235
QY 481 CCAGCCCTCTTCTCCTCAGGTGCCATGGTTGGAGGAACCTGGGATGTGTACAAGTGATCTTA 540
Db 101236 CCAGCCCTCTTCTCCTCAGGTGCCATGGTTGGAGGAACCTGGGATGTGTACAAGTGATCTTA 101295
QY 541 TTATAGGATGGTGAAGCTCTCAAGTACTGGTATGAGACCAACATCTCCATTACAA 600
Db 101296 TTATAGGATGGTGAAGCTCTCAAGTACTGGTATGAGACCAACATCTCCATTACAA 101355
QY 601 TGCCACAGTGAAGACAGTGGAACTTACTACTGACGGGCAAGTGTGGCAGCTGAGCTA 660
Db 101356 TGCCACAGTGAAGACAGTGGAACTTACTACTGACGGGCAAGTGTGGCAGCTGAGCTA 101415

QY 661 TGAGTCTGAGCCCTCAACATTACTGTATATAAGCTCCGGTGAAGTACTGGCTACA 720
 Db 101416 TGAGTCTGAGCCCTCAACATTACTGTATATAAGCTCCGGTGAAGTACTGGCTACA 101475
 QY 721 ATTTTATCCATTGTTGGTGGTATCTGTTTCTGTGGACACAGGATTATTATCTC 780
 Db 101476 ATTTTATCCATTGTTGGTGGTATCTGTTTCTGTGGACACAGGATTATTATCTC 101535
 QY 781 AACTCAGCAGGCTCACATTTCTCTGAAGATTGAAGAAACCCAGAAAGCTTCAGACT 840
 Db 101536 AACTCAGCAGGCTCACATTTCTCTGAAGATTGAAGAAACCCAGAAAGCTTCAGACT 101595
 QY 841 TCTGAACCCACATCTCTAAGCCAAACCCCAAAACCACTGATATATTAATCTCAAGAAATAT 900
 Db 101596 TCTGAACCCACATCTCTAAGCCAAACCCCAAAACCACTGATATATTAATCTCAAGAAATAT 101655
 QY 901 TTGCAACATTAGTTTCTTCCAGCATCAGCAATCTCTCAATTTCAAAACACAGCTTG 960
 Db 101656 TTGCAACATTAGTTTCTTCCAGCATCAGCAATCTCTCAATTTCAAAACACAGCTTG 101715
 QY 961 CAATATACATAGAAAGCTGTGCTCAAGATTATAGAAATGCTTCATTAATTAATGAGT 1020
 Db 101716 CAATATACATAGAAAGCTGTGCTCAAGATTATAGAAATGCTTCATTAATTAATGAGT 101775
 QY 1021 AAAGTGGTTAAGTGCATGTAAGTGTCTCAATTAACATTGGTTGAATAATGAGA 1080
 Db 101776 AAAGTGGTTAAGTGCATGTAAGTGTCTCAATTAACATTGGTTGAATAATGAGA 101835
 QY 1081 GAATGAATAGATTCAATTTATAGCAATTTGTAAAGAGATGTTCAATTTCAATAAATAA 1140
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 QY 1141 TATAAACCATGTACAGAAATGCTTCTGAGTAAACCAACCAACCAACCAACCAACCA 1198
 Db 101896 TATAAACCATGTACAGAAATGCTTCTGAGTAAACCAACCAACCAACCAACCAACCA 101953

RESULT 15

AAQ14736
ID AAQ14736 standard; cDNA; 1199 BP.

AAQ14736;

25-MAR-2003 (revised)

17-DEC-2001 (revised)

03-FEB-1992 (first entry)

Human Fc(epsilon)RI alpha cDNA.

Immunoglobulin; receptor; high affinity receptor; ss.

Homo sapiens.

Key Location/Qualifiers

CDS 107..880

/*tag= a

/product= "alpha_subunit"

USN7626704-N.

15-OCT-1991.

14-DEC-1990; 90US-00626704.

14-DEC-1990; 90US-00626704.

(USSH) NAT INST OF HEALTH.

Kinet JP, Metzger H;

WPI; 1991-346755/47.

P-PSDB; AAR14772.

PT DNA coding alpha, beta and gamma-units of ige high affinity receptor -
 PT are used to prepare recombinant polypeptide(s) for treating allergy, drug
 PT screening or monitoring Ige level.
 XX

PS Disclosure; Fig 1; 58pp; English.

XX A lambda gtl1 library was prepared from poly-A RNA isolated from KUB12
 CC cells. Screening was by a cDNA fragment from the rat Fc(epsilon)RI alpha
 CC cDNA corresponding to nucleotides 119-781. Positive clones were subcloned
 CC and sequenced. (Note: Revised entry submitted to correct the patent
 CC number format of US Government-owned NTIS applications to prevent clashes
 CC with ongoing US granted patent numbers. For further information please
 CC visit the Derwent web site at www.derwent.com/dwpi/updates/ntis_us.html.)
 CC (Updated on 25-MAR-2003 to correct PF field.)
 XX

SQ Sequence 1199 BP; 390 A; 241 C; 247 G; 321 T; 0 U; 0 Other;

Query Match 99.3%; Score 1190; DB 2; Length 1199;

Best Local Similarity 99.6%; Pred. No. 9.4e-229;

Matches 1199; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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Db 1 TACTAAGAGTCTCCAGCATCTCCACCTGTCTACACCCAGCATGGCCCTATATTGAG 60

QY 61 CCTTAGATCTCTCCAGCACAGTAAGCACAGAGTCCATGAAGAGATGGCTCTGCCAT 120

Db 61 CCTTAGATCTCTCCAGCACAGTAAGCACAGAGTCCATGAAGAGATGGCTCTGCCAT 120

QY 121 GGAATCCCTTACTGTGTAGCTTACTGTCTTCTTCCAGTGGCGTGTAGC 180

Db 121 GGAATCCCTTACTGTGTAGCTTACTGTCTTCTTCCAGTGGCGTGTAGC 180

QY 181 AGTCCCTCAGAACTTAAGTCTCTTGAACCTCCATGGAATAGATAATTTAAAGGAGA 240

Db 181 AGTCCCTCAGAACTTAAGTCTCTTGAACCTCCATGGAATAGATAATTTAAAGGAGA 240

QY 241 GAATGTGACTCTTACATGTAATGGGAACAATTTCTTGAAGTCAGTTCACCAATGGTT 300

Db 241 GAATGTGACTCTTACATGTAATGGGAACAATTTCTTGAAGTCAGTTCACCAATGGTT 300

QY 301 CCACATGGCAGCTTTTCAAGAGAGACAATTCAGTTCAGTTCAGTTCAGTTCAGTTC 360

Db 301 CCACATGGCAGCTTTTCAAGAGAGACAATTCAGTTCAGTTCAGTTCAGTTCAGTTC 360

QY 361 TGAAGACAGTGGAGAAATACAAATGTGAGCACCACCAAGTTAATGAGAGTGAACCTGTGTA 420

Db 361 TGAAGACAGTGGAGAAATACAAATGTGAGCACCACCAAGTTAATGAGAGTGAACCTGTGTA 420

QY 421 CCTGGAAGTCTTCAGTGAATCTGCTGCTCTCTTCAAGCTCTGCTGAGTGGTGAAGGG 480

Db 421 CCTGGAAGTCTTCAGTGAATCTGCTGCTCTCTTCAAGCTCTGCTGAGTGGTGAAGGG 480

QY 481 CCAGCCCTCTCTCTCAGGTGCGATGTTGGAGAACTGGGATGTGTACAAGTGTATCTA 540

Db 481 CCAGCCCTCTCTCTCAGGTGCGATGTTGGAGAACTGGGATGTGTACAAGTGTATCTA 540

QY 541 TTATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCAACAATCTCCATTCACAA 600

Db 541 TTATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCAACAATCTCCATTCACAA 600

QY 601 TGCCACAGTTGAAGACAGTGGACCTTACTGTACGGCAAGTGTGGCAGCTGGACTA 660

Db 601 TGCCACAGTTGAAGACAGTGGACCTTACTGTACGGCAAGTGTGGCAGCTGGACTA 660

QY 661 TGAGTCTGAGCCCTCAACATTTACTGTATAAAGCTCCCGGTGAGAGTACTGGGTACA 720

Db 661 TGAGTCTGAGCCCTCAACATTTACTGTATAAAGCTCCCGGTGAGAGTACTGGGTACA 720

QY 721 ATTTTATCCCAATGTTGGTGGTATTCTGTTTGGTGGACACAGGATTTATATCTC 780

Db 721 ATTTTATCCCAATGTTGGTGGTATTCTGTTTGGTGGACACAGGATTTATATCTC 780

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Db      |||||
Qy 781 AACTCAGCAGCGGTGACATTTCTCTTGAAGATTAGAGAACCCAGGAAAGGCTTCAGACT 840
Db      |||||
Qy 841 TCTGAACCCACATCCTTAAGCCAAACCCCAAAACCACTGATATAATTACTCAAGAAATAT 900
Db      |||||
Qy 841 TCTGAACCCACATCCTTAAGCCAAACCCCAAAACCACTGATATAATTACTCAAGAAATAT 900
Db      |||||
Qy 901 TTGCAACATTAGTTTTTTTCCAGCATCAGCAATTGCTACTCAATTGTCAAAACACAGCTTG 960
Db      |||||
Qy 901 TTGCAACATTAGTTTTTTTCCAGCATCAGCAATTGCTACTCAATTGTCAAAACACAGCTTG 960
Db      |||||
Qy 961 CAATATACATAGAAACGCTGTGCTCAAGGATTTATAGAAATGCTTCATTAACTGAGTG 1020
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Qy 961 CAATATACATAGAAACGCTGTGCTCAAGGATTTATAGAAATGCTTCATTAACTGAGTG 1020
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Qy 1021 AAACCTGGTTAAGTGGCATGTAATAGTAAGTGCTCAATTAACTGGTTGAATAAATGAGA 1080
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Qy 1021 AAACCTGGTTAAGTGGCATGTAATAGTAAGTGCTCAATTAACTGGTTGAATAAATGAGA 1080
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Qy 1081 GAATGAATAGATTCAATTTATAGCAATTTGTAAGAGAGATGTTCAATTCAATAAATATA 1140
Db      |||||
Qy 1081 GAATGAATAGATTCAATTTATAGCAATTTGTAAGAGAGATGTTCAATTCAATAAATATA 1140
Db      |||||
Qy 1141 TATAAAACCATGTAAACAGAAATGCTTCTGAGTAAAAAAGAGAGAGAGAGAGAGAGAGAGAG 1198
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OM nucleic - nucleic search, using sw model

Run on: October 10, 2004, 11:14:29 ; Search time 105,911 seconds
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Searched: 682709 seqs, 277475446 residues

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Maximum DB seq length: 2000000000

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Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	1198	100.0	1198	4	US-09-285-873-1
4	1198	100.0	1198	4	US-09-285-873-3
5	1198	100.0	1198	4	US-09-944-277A-1
6	1198	100.0	1198	4	US-09-944-277A-3
7	1144.8	95.6	1174	1	US-07-869-933-10
8	1144.8	95.6	1174	3	US-09-103-663-10
9	774	64.6	774	2	US-08-756-387B-4
10	774	64.6	774	2	US-08-756-387B-5
11	774	64.6	774	4	US-09-285-873-4
12	774	64.6	774	4	US-09-285-873-5
13	774	64.6	774	4	US-09-944-277A-4
14	774	64.6	774	4	US-09-944-277A-5
15	773	64.5	773	4	US-08-897-956A-6
16	699	58.3	699	2	US-08-756-387B-7
17	699	58.3	699	4	US-09-285-873-7
18	699	58.3	699	4	US-09-944-277A-7
19	697	58.2	713	2	US-08-238-027-3
20	611	51.0	2955	4	US-08-897-956A-4
21	591	49.3	591	2	US-08-756-387B-10
22	591	49.3	591	4	US-09-285-873-10
23	591	49.3	591	4	US-09-944-277A-10
24	589.4	49.2	591	4	US-08-788-954-1
25	578.8	48.3	1015	3	US-09-015-734-1
26	578.8	48.3	1015	3	US-09-015-734-3
27	578.8	48.3	1015	4	US-09-515-311-1

C	28	578.8	48.3	1015	4	US-09-515-311-3	Sequence 3, Appl
	29	520.2	43.4	1069	2	US-08-768-964-1	Sequence 1, Appl
C	30	520.2	43.4	1069	2	US-08-768-964-3	Sequence 3, Appl
	31	520.2	43.4	1069	3	US-09-005-299-1	Sequence 1, Appl
C	32	520.2	43.4	1069	3	US-09-005-299-3	Sequence 3, Appl
	33	520.2	43.4	1069	3	US-09-515-431-1	Sequence 1, Appl
C	34	520.2	43.4	1069	3	US-09-515-431-3	Sequence 3, Appl
	35	516	43.1	516	2	US-08-756-387B-12	Sequence 12, Appl
	36	516	43.1	516	4	US-09-285-873-12	Sequence 12, Appl
	37	516	43.1	516	4	US-09-944-277A-12	Sequence 12, Appl
C	38	435	36.3	765	3	US-09-015-734-4	Sequence 4, Appl
	39	435	36.3	765	3	US-09-015-734-5	Sequence 5, Appl
	40	435	36.3	765	4	US-09-515-311-4	Sequence 4, Appl
C	41	435	36.3	765	4	US-09-515-311-5	Sequence 5, Appl
	42	433.8	36.2	991	3	US-08-833-488B-19	Sequence 19, Appl
C	43	433.8	36.2	991	3	US-08-833-488B-21	Sequence 21, Appl
	44	403.8	33.7	708	3	US-09-015-734-6	Sequence 6, Appl
C	45	403.8	33.7	708	3	US-09-015-734-8	Sequence 8, Appl

ALIGNMENTS

RESULT 1
US-08-756-387B-1
; Sequence 1, Application US/08756387B
; Patent No. 5945294
; GENERAL INFORMATION:
; APPLICANT: Frank, Glenn R.
; APPLICANT: Porter, James P.
; APPLICANT: Rushlow, Keith E.
; APPLICANT: Wassom, Donald L.
; TITLE OF INVENTION: Method to Detect IGB
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carol Talkington Verser, Ph.D.
; ADDRESSEE: Heska Corporation
; STREET: 1825 Sharp Point Drive
; CITY: Fort Collins
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80525
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: WordPerfect for Windows, Version 7.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/756.387B
; FILING DATE: No. 5945294ember 26, 1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Verser, Carol Talkington
; REGISTRATION NUMBER: 37,459
; REFERENCE/DOCKET NUMBER: DI-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 970/493-7272
; TELEFAX: 970/484-9505
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1198 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 107..877
US-08-756-387B-1

Query Match 100.0%; Score 1198; DB 2; Length 1198;
Best Local Similarity 100.0%; Pred. No. 2.5e-292;
Matches 1198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;


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QY 541 TTATAAGGATGGTGAAGTCTTCAAGTGAAGTCTGCTGCTGCTGCTGCTGCTGCTGCT 600
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Db 601 TGCCACAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 660
QY 661 TGAGTCTGAGCCCTCAACATTTCTGTAATATAAGTCTGCTGCTGCTGCTGCTGCTGCT 720
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Db 721 ATTTTATCCATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780
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Db 781 RACTCAGCAGAGTGCATTTCTGTAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 840
QY 841 TGTGAACCCACATCTTAAGCCAAACCCCAAAACCAACCTGATATAATTAATTAATTA 900
Db 841 TGTGAACCCACATCTTAAGCCAAACCCCAAAACCAACCTGATATAATTAATTAATTA 900
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Db 901 TTGCAACATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960
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QY 1021 AAATCTGTTAGTGCATGTAATAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1080
Db 1021 AAATCTGTTAGTGCATGTAATAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1080
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Db 1081 GAATGAATAGATTTCAATTTATAGCATTTGTAAGAGAGATGTTCAATTTCAATAA 1140
QY 1141 TATAAAACCATGTAACAGAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1198
Db 1141 TATAAAACCATGTAACAGAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1198
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RESULT 4

US-09-285-873-3/c

Sequence 3, Application US/09285873

Patent No. 6309832

GENERAL INFORMATION:

APPLICANT: Frank, Glenn R.

APPLICANT: Porter, James P.

APPLICANT: Rushlow, Keith E.

APPLICANT: Wasson, Donald L.

TITLE OF INVENTION: Method to Detect IGE

NUMBER OF SEQUENCES: 13

CORRESPONDENCE ADDRESS:

ADDRESSEE: Carol Talkington Verser, Ph.D.

STREET: 1825 Sharp Point Drive

CITY: Fort Collins

STATE: Colorado

COUNTRY: USA

ZIP: 80525

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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: WordPerfect for Windows, Version 7.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/285,873
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/756,387
FILING DATE: No. 630832ember 26, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Verser, Carol Talkington
REGISTRATION NUMBER: 37,459
REFERENCE/DOCKET NUMBER: DI-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 970/493-7272
TELEFAX: 970/484-9505
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1198 nucleotides
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cdna
US-09-285-873-3
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Query Match 100.0%; Score 1198; DB 4; Length 1198;

Best Local Similarity 100.0%; Pred. No. 2.5e-292; Indels 0; Gaps 0;

Matches 1198; Conservative 0; Mismatches 0;

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Db 1198 TACTAAGAGTCTCCAGCATCTCCACCTGTCTTACACCGAGCATGGGCTATTTTGAAG 1139
QY 61 CCTTAGATCTCTCCAGCAGTAAGCAGCAGAGTCCATGAGAGATGGCTCTCTGCCAT 120
Db 1138 CCTTAGATCTCTCCAGCAGTAAGCAGCAGAGTCCATGAGAGATGGCTCTCTGCCAT 1079
QY 121 GGAATCCCCTACTCTACTGTGTGTAGCCCTTACTGTTCTTCGCTCCAGATGGCGTTAGC 180
Db 1078 GGAATCCCCTACTCTACTGTGTGTAGCCCTTACTGTTCTTCGCTCCAGATGGCGTTAGC 1019
QY 181 AGTCCCTCAGAAACCTTAAGTCTCTTGAACCTCCATGGAATAGAAATATTTAAGGAGA 240
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Db 898 CCACAATGGCAGCCCTTTTCCAGAGAGACAAATTTCAAGTTTGAATATTTGAATGCCAAT 839
QY 361 TGAGACAGTGGAGATACAAATGTGAGCAGCAACCAAGTTAATGAGAGTGAACCTGTGTA 420
Db 838 TGAGACAGTGGAGATACAAATGTGAGCAGCAACCAAGTTAATGAGAGTGAACCTGTGTA 779
QY 421 CTTGGAAGTCTTTCAGTACTGCTCTCTTCCAGGCTCTCTGCTGAGGTGGTGAAGG 480
Db 778 CTTGGAAGTCTTTCAGTACTGCTCTCTTCCAGGCTCTCTGCTGAGGTGGTGAAGG 719
QY 481 CAGCCCCCTCTTCTCAGTGCCTGCTGCTGAGGAACTGGGATGTGACAGGCTCATCTA 540
Db 718 CAGCCCCCTCTTCTCAGTGCCTGCTGCTGAGGAACTGGGATGTGACAGGCTCATCTA 659
QY 541 TTATAAGGATGGTGAAGTCTTCAAGTACTGCTGATGAGAACCAACACATCTCCATTA 600
Db 658 TTATAAGGATGGTGAAGTCTTCAAGTACTGCTGATGAGAACCAACACATCTCCATTA 599
QY 601 TGGCAGAGTTGAAGACAGTGGAAACCTTACTGTTAGCGGCAAGTGTGGCAGCTGGACTA 660
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Db 598 TGCCACAGTTCAAGACAGTGAACCTACTACTGTACGGCAAGTGTGGCAGCTGGACTA 539
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Db 478 ATTTTATCCCAATTTGTTGGTGAATCTGTTTGTGTGGACACAGGATTTATTTATCTC 419
QY 781 AACTCAGCAGCAGTCAATTTCTTTGAAGATTAAGAGAACCCAGGAAAGCTTCAGACT 840
Db 418 AACTCAGCAGCAGTCAATTTCTTTGAAGATTAAGAGAACCCAGGAAAGCTTCAGACT 359
QY 841 TCTGAACCCCATCTTAAGCAACCCCAACCACTGATATAATTTACTCAAGAAATAT 900
Db 358 TCTGAACCCCATCTTAAGCAACCCCAACCACTGATATAATTTACTCAAGAAATAT 299
QY 901 TTGCAACATTAGTTTTTTCAGCATCAGCAATGTCTCAATTTGTTGAATAAATGAGA 960
Db 298 TTGCAACATTAGTTTTTTCAGCATCAGCAATGTCTCAATTTGTTGAATAAATGAGA 239
QY 961 CAATATACATAGAAACCTGTCTCAAGGATTTATAGAAATGCTTCATTAAGTCTGAGTG 1020
Db 238 CAATATACATAGAAACCTGTCTCAAGGATTTATAGAAATGCTTCATTAAGTCTGAGTG 179
QY 1021 AAACCTGTTAAGTGGCATGTAATAGTAGTAAAGTCTCAATTTGTTGAATAAATGAGA 1080
Db 178 AAACCTGTTAAGTGGCATGTAATAGTAGTAAAGTCTCAATTTGTTGAATAAATGAGA 119
QY 1081 GAATGAATAGATTCATTTATAGCATTTGTAAAGAGATTTCAATTTCAATTAATATAA 1140
Db 118 GAATGAATAGATTCATTTATAGCATTTGTAAAGAGATTTCAATTTCAATTAATATAA 59
QY 1141 TATAAAACCATGTAAACAGATGCTTCTGAGTAAAAAATTTTAAAAAATTTAAAAA 1198
Db 58 TATAAAACCATGTAAACAGATGCTTCTGAGTAAAAAATTTTAAAAAATTTAAAAA 1

RESULT 5

US-09-944-277A-1

Sequence 1, Application US/09944277A

Patent No. 6682894

GENERAL INFORMATION:

APPLICANT: Frank, Glenn R.

Porter, James P.

Rushlow, Keith E.

Wassom, Donald L.

TITLE OF INVENTION: Method to Detect IgE

NUMBER OF SEQUENCES: 13

CORRESPONDENCE ADDRESS:

ADDRESSEE: Carol Talkington Verser, Ph.D.

Heska Corporation

STREET: 1825 Sharp Point Drive

CITY: Fort Collins

STATE: Colorado

COUNTRY: USA

ZIP: 80525

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: Windows 95

SOFTWARE: WordPerfect for Windows, Version 7.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/944,277A

FILING DATE: 30-Aug-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/285,873

FILING DATE: 1999-03-31

ATTORNEY/AGENT INFORMATION:

NAME: Verser, Carol Talkington

REGISTRATION NUMBER: 37,459
REFERENCE/DOCKET NUMBER: DI-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 970/493-7272
TELEFAX: 970/484-3505
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1198 nucleotides
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 107..877
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-944-277A-1

Query Match 100.0%; Score 1198; DB 4; Length 1198;
Best Local Similarity 100.0%; Pred. No. 2.5e-292;
Matches 1198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TACTAAGAGTCTCCAGCATCTCCACCTGTCTACCAACGAGCATGGGCTATATTTGAAG 60
Db 1 TACTAAGAGTCTCCAGCATCTCCACCTGTCTACCAACGAGCATGGGCTATATTTGAAG 60
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QY 121 GGAATCCCTACTCTACTGTGTAGCCTTCTCTTCGCTCCAGATGGGCTGTAGC 180
Db 121 GGAATCCCTACTCTACTGTGTAGCCTTCTCTTCGCTCCAGATGGGCTGTAGC 180
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QY 361 TGAAGCAGTGGAGAAATACAAATGTGAGCAACCAACAAAGTTAATGAGAGTGAACCTGTGA 420
Db 361 TGAAGCAGTGGAGAAATACAAATGTGAGCAACCAACAAAGTTAATGAGAGTGAACCTGTGA 420
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Db 421 CCTGGAAGTCTTCAGTGAAGTCTCTTTCAGGCTCTCTGCTGAGGTGGTGTGGAGGG 480
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781 AACTCAGCAGGCTCACATTTCTCTTGAAGATTAGAGAACACAGGAAAGCTTCAGACT 840
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DB |||||
841 TCTGAACCCACATCTTAAGCCAAACCCCAAAACAACTGATATTAATTTACTCAGAAATAT 900
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DB |||||
961 CAATATACATAGAAACGCTGCTGCTCAAGGATTTATAGAAATGCTTCATTAACCTGAGTG 1020
QY |||||
1021 AAACCTGTTAGTGGCATGTAATAGTAGTCTCAATTAACATTTGTTGAATAAATGAGA 1080
DB |||||
1021 AAACCTGTTAGTGGCATGTAATAGTAGTCTCAATTAACATTTGTTGAATAAATGAGA 1080
QY |||||
1081 GAATGAATAGATTTCATTTATTAGCATTTGTAAAGAGATGTTCAATTTCAATAAATAA 1140
DB |||||
1081 GAATGAATAGATTTCATTTATTAGCATTTGTAAAGAGATGTTCAATTTCAATAAATAA 1140
QY |||||
1141 TATAAACCATGTAAACAGATGCTTCTGAGTAAACCAACCAACCAACCAACCAACCAAC 1198
DB |||||
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RESULT 6

US-09-944-277A-3/c
; Sequence 3, Application US/09944277A
; Patent No. 6682894
; GENERAL INFORMATION:
; APPLICANT: Frank, Glenn R.
; Porter, James P.
; Rushlow, Keith E.
; Wasson, Donald L.
; TITLE OF INVENTION: Method to Detect IGE
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carol Talkington Verser, Ph.D.
; Hesk Corporation
; STREET: 1825 Sharp Point Drive
; CITY: Fort Collins
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80525
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: WordPerfect for Windows, Version 7.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/944,277A
; FILING DATE: 30-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/285,873
; FILING DATE: 1999-03-31
; ATTORNEY/AGENT INFORMATION:
; NAME: Verser, Carol Talkington
; REGISTRATION NUMBER: 37,459
; REFERENCE/DOCKET NUMBER: DI-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 970/493-7272
; TELEFAX: 970/484-9505
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1198 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single

TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-944-277A-3
Query Match 100.0%; Score 1198; DB 4; Length 1198;
Best Local Similarity 100.0%; Pred. No. 2,5e-292;
Matches 1198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TACTAAGAGTCTCCAGCATCCTCCACCTGTCTACACCGAGCATGGGCTATATTGAG 60
DB 1198 TACTAAGAGTCTCCAGCATCCTCCACCTGTCTACACCGAGCATGGGCTATATTGAG 1199
QY 61 CTTTATAGTCTCCAGCAGCATAGCACCAGAGTCCATGAAGAGATGGCTCTCCGCAT 120
DB 1138 CTTTATAGTCTCCAGCAGCATAGCACCAGAGTCCATGAAGAGATGGCTCTCCGCAT 1079
QY 121 GGAATCCCTACTCTACTCTGCTGTAGTCTTACTGTCTTCTGCTCCAGATGGCTGTAGC 180
DB 1078 GGAATCCCTACTCTACTCTGCTGTAGTCTTACTGTCTTCTGCTCCAGATGGCTGTAGC 1019
QY 181 AGTCCCTCAGAAACCTTAAGTCTCTTGAACCTCCATGGAATAGATTAAGGAGA 240
DB 1018 AGTCCCTCAGAAACCTTAAGTCTCTTGAACCTCCATGGAATAGATTAAGGAGA 959
QY 241 GAATGTGACTCTTACATGTATATGGGAAACAATTTCTTGAAGTCAAGTCCACCAATGTT 300
DB 958 GAATGTGACTCTTACATGTATATGGGAAACAATTTCTTGAAGTCAAGTCCACCAATGTT 899
QY 301 CCACAATGGCAGCTTTCCAGAGAGACAAATTCAGTTTGAATTTGAATGCAATTT 360
DB 898 CCACAATGGCAGCTTTCCAGAGAGACAAATTCAGTTTGAATTTGAATGCAATTT 839
QY 361 TGAAGCAGTGGAGAAATACAAATGTACAGCAACCAAGTTAATGAGAGTGAACCTGTGTA 420
DB 838 TGAAGCAGTGGAGAAATACAAATGTACAGCAACCAAGTTAATGAGAGTGAACCTGTGTA 779
QY 421 CTTGGAAGTCTTTCAGTGTGCTCTCTTCAAGCCTCTCTGAGGCTCTCTGAGGCTGATGGAGG 480
DB 778 CTTGGAAGTCTTTCAGTGTGCTCTCTTCAAGCCTCTCTGAGGCTCTCTGAGGCTGATGGAGG 719
QY 481 CCAGCCCTCTTCTCCTCAGTGTCCATGTTGGAGGAACTGGGATGTGTAAGAGTGTATCTA 540
DB 718 CCAGCCCTCTTCTCCTCAGTGTCCATGTTGGAGGAACTGGGATGTGTAAGAGTGTATCTA 659
QY 541 TTATAAGGATGGTGAAGCTCTCAAGTACTGTGTATGAGAACCAACAACATCTCATTTACAAA 600
DB 658 TTATAAGGATGGTGAAGCTCTCAAGTACTGTGTATGAGAACCAACAACATCTCATTTACAAA 599
QY 601 TGCCACAGTTGAAGCAGTGGAACTTACTTCTGAGGAACTGGGCTGAGTGGAGTGGACTA 660
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QY 661 TGAGTCTGAGCCCTCAACATTTACTGTATATAAAGCTCCGCTGAGAAAGTCTGCTTACA 720
DB 538 TGAGTCTGAGCCCTCAACATTTACTGTATATAAAGCTCCGCTGAGAAAGTCTGCTTACA 479
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DB 478 ATTTTATATCCATTTGTTGGTGTGATTTGTTGCTGTGGACACAGATTTATTTATCTC 419
QY 781 AACTCAGCAGGCTCACATTTCTCTTGAAGATTAGAGAACACAGGAAAGCTTCAGACT 840
DB 418 AACTCAGCAGGCTCACATTTCTCTTGAAGATTAGAGAACACAGGAAAGCTTCAGACT 359
QY 841 TCTGAACCCACATCTTAAGCCAAACCCCAAAACAACTGATATTAATTTACTCAGAAATAT 900
DB 358 TCTGAACCCACATCTTAAGCCAAACCCCAAAACAACTGATATTAATTTACTCAGAAATAT 299
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DB 298 TTGCAACATTAGTTTTTTTCCAGCATCAGCAATTTGCTACTCAATTTGTCACACAGCTTG 239

QY 961 CAATATACATAGAAAGCTGTGCTCAAGGATTTATAGAAATGCTTCATTAAACTGAGTG 1020
Db
Db 238 CAATATACATAGAAAGCTGTGCTCAAGGATTTATAGAAATGCTTCATTAAACTGAGTG 179
QY 1021 AAATCTGGTTAAAGTGGCATGTAAATAGTAAAGTGTCAATTAACATTTGGTTGAATAAATGAGA 1080
Db 178 AAATCTGGTTAAAGTGGCATGTAAATAGTAAAGTGTCAATTAACATTTGGTTGAATAAATGAGA 119
QY 1081 GAATGAATAGATTCATTTATAGCATTTGTAAAGAGATGTTCAATTTCAATAAATAA 1140
Db 118 GAATGAATAGATTCATTTATAGCATTTGTAAAGAGATGTTCAATTTCAATAAATAA 59
QY 1141 TATAAAACCATGTAAACAGATGCTTCTGAGTAAAGAGATGTTCAATTTCAATAAATAA 1198
Db 58 TATAAAACCATGTAAACAGATGCTTCTGAGTAAAGAGATGTTCAATTTCAATAAATAA 1

RESULT 7

US-07-869-933-10
; Sequence 10, Application US/07869933
; Patent No. 5770396
; GENERAL INFORMATION:
; APPLICANT: KINET, Jean-Pierre
; TITLE OF INVENTION: ISOLATION, CHARACTERIZATION, AND USE OF
; TITLE OF INVENTION: THE HUMAN B SUBUNIT OF THE HIGH AFFINITY RECEPTOR FOR
; TITLE OF INVENTION: IMMUNOGLOBULIN
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 1800 Diagonal Road, Suite 500
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/869,933
; FILING DATE: 19920416
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 40399/154 NIHD
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)836-9300
; TELEFAX: (703)683-4109
; TELEX: 899149
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1174 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 107..880
US-07-869-933-10

Query Match 95.8%; Score 1144.8; DB 1; Length 1174;
Best Local Similarity 99.7%; Pred. No. 6.2e-279;
Matches 1157; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY 1 TACTAAGAGTCTCCAGATCCTCCACCTGCTACCAACCGAGCATGGGCTATATTGGAAG 60
Db 1 TACTAAGAGTCTCCAGATCCTCCACCTGCTACCAACCGAGCATGGGCTATATTGGAAG 60
QY 61 CCTTAGATCTCTCCAGACAGTAAAGCACCAGGAGTCCATGAAGAGATGCTCTGCGCAT 120

Db 61 CCTTAGATCTCTCCAGACAGTAAAGCACCAGGAGTCCATGAAGAGATGCTCTGCGCAT 120
QY 121 GGAATCCCTTACTCTACTGTGTGTAGCCTTACTCTTCTTCTGCTCCAGATGCGGTGTAGC 180
Db 121 GGAATCCCTTACTCTACTGTGTGTAGCCTTACTCTTCTTCTGCTCCAGATGCGGTGTAGC 180
QY 181 AGTCCCTCAGAAACCTTAAGGTCTCTTGAACCCCTCCATGGAATAGAATATTATTAAGGAGA 240
Db 181 AGTCCCTCAGAAACCTTAAGGTCTCTTGAACCCCTCCATGGAATAGAATATTATTAAGGAGA 240
QY 241 GAATGTGACTCTTACATGTAAATGGGAAACAATTTCTTTGAAAGTCAGTTCCACCAATGGTT 300
Db 241 GAATGTGACTCTTACATGTAAATGGGAAACAATTTCTTTGAAAGTCAGTTCCACCAATGGTT 300
QY 301 CCACAAATGGGAGCCTTTTCAGAGAGACAAATTCAGATTTGAATTTGAATGTCGAATGCCAAT 360
Db 301 CCACAAATGGGAGCCTTTTCAGAGAGACAAATTCAGATTTGAATTTGAATGTCGAATGCCAAT 360
QY 361 TGAAGACAGTGGAGATACAAATGTCAGCACCAACAAGTTAATGAGAGAGTGAACCTGTGTA 420
Db 361 TGAAGACAGTGGAGATACAAATGTCAGCACCAACAAGTTAATGAGAGAGTGAACCTGTGTA 420
QY 421 CCTGGAAGTCTTTCAGTGAATGCTGCTCCTTCAGGCTCTGCTGAGGTGGTGTGAGGG 480
Db 421 CCTGGAAGTCTTTCAGTGAATGCTGCTCCTTCAGGCTCTGCTGAGGTGGTGTGAGGG 480
QY 481 CCAGCCCTCTTCTCAGGTGCCATGCTGGAGAACTGGGATGTTCAAGGTGATCTA 540
Db 481 CCAGCCCTCTTCTCAGGTGCCATGCTGGAGAACTGGGATGTTCAAGGTGATCTA 540
QY 541 TTATAAGAGTGGTGAAGCTCTCAAGTACTGTATGAGAAACCAACATCTCCATTACAAA 600
Db 541 TTATAAGAGTGGTGAAGCTCTCAAGTACTGTATGAGAAACCAACATCTCCATTACAAA 600
QY 601 TGCCACAGTTCAGACAGTGGAACTACTACTGTACGGGCAAACTGTGGAGCTGGACTA 660
Db 601 TGCCACAGTTCAGACAGTGGAACTACTACTGTACGGGCAAACTGTGGAGCTGGACTA 660
QY 661 TGAGTCTGAGCCCTCAACATTTACTGTATAAAGCTCCGCGTGAGAAGTACTGGCTACA 720
Db 661 TGAGTCTGAGCCCTCAACATTTACTGTATAAAGCTCCGCGTGAGAAGTACTGGCTACA 720
QY 721 ATTTTATATCCATGTTGGTGTGATCTGTTGCTGTGACACAGATTTATTTATCTC 780
Db 721 ATTTTATATCCATGTTGGTGTGATCTGTTGCTGTGACACAGATTTATTTATCTC 780
QY 781 AACTCAGCAGCAGTGCATCTCTTGAAGATTAAAGAAACCAAGAAAGCTTCAGACT 840
Db 781 AACTCAGCAGCAGTGCATCTCTTGAAGATTAAAGAAACCAAGAAAGCTTCAGACT 840
QY 841 TCTGAACCCCATCCTAAGCCAAACCCCAAAACCAACTGATATATTAATCTCAAGAAATAT 900
Db 841 TCTGAACCCCATCCTAAGCCAAACCCCAAAACCAACTGATATATTAATCTCAAGAAATAT 900
QY 901 TTGCAACATTTAGTTTTTTTCCAGCATCAGCAATTTGCTACTCAATTTGTCAACACAGCTTG 960
Db 901 TTGCAACATTTAGTTTTTTTCCAGCATCAGCAATTTGCTACTCAATTTGTCAACACAGCTTG 960
QY 961 CAATATACATAGAAACCTGTGCTCAAGGATTTATAGAAATGCTTCATTAAACTGAGTG 1020
Db 961 CAATATACATAGAAACCTGTGCTCAAGGATTTATAGAAATGCTTCATTAAACTGAGTG 1020
QY 1021 AAACTGTTAAGTGGCATGTAATAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAG 1080
Db 1021 AAACTGTTAAGTGGCATGTAATAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAG 1080
QY 1081 GAATGAATAGATTCATTTATAGCA-TTGTAAAGAGATGTTCAATTTCAATAAATAA 1140
Db 1081 GAATGAATAGATTCATTTATAGCA-TTGTAAAGAGATGTTCAATTTCAATAAATAA 1159
QY 1141 TATAAAACCATGTAAACAGAA 1160
Db 1140 TATAAAACCATGTAAACAGAA 1159

RESULT 8
US-09-103-663-10
; Sequence 10, Application US/09103663D
; Patent No. 6171803
; GENERAL INFORMATION:
; APPLICANT: Kinst et al.
; TITLE OF INVENTION: Isolation, characterization, and use of the human beta
; TITLE OF INVENTION: subunit of the high affinity receptor for
; TITLE OF INVENTION: immunoglobulin E.
; FILE REFERENCE: 50490
; CURRENT APPLICATION NUMBER: US/09/103.663D
; CURRENT FILING DATE: 1998-06-23
; EARLIER APPLICATION NUMBER: 07/869.933
; EARLIER FILING DATE: 1992-04-16
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 10
; LENGTH: 1174
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (107)..(880)
US-09-103-663-10

Query Match 95.6%; Score 1144.8; DB 3; Length 1174;
Best Local Similarity 99.7%; Pred. No. 6.2e-279;
Matches 1157; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY 1 TACTAAGAGTCTCCAGCATCTCCACCTGCTACACCGAGCATGGCCCTATATTTGAAG 60
DB 1 TACTAAGAGTCTCCAGCATCTCCACCTGCTACACCGAGCATGGCCCTATATTTGAAG 60
QY 61 CCTTAGATCTCTCAGCAGCAGTAAAGCAGGAGTCCATGAAGAGATGGCTCTGSCCAT 120
DB 61 CCTTAGATCTCTCAGCAGCAGTAAAGCAGGAGTCCATGAAGAGATGGCTCTGSCCAT 120
QY 121 GGAATCCCTACTCTACTGTGTAGCTTACTGCTTCTGCTCCAGATGGCGTGTAGC 180
DB 121 GGAATCCCTACTCTACTGTGTAGCTTACTGCTTCTGCTCCAGATGGCGTGTAGC 180
QY 181 AGTCCTCAGAAACCTAAGTCTCTTGAACCCCTCCATGGAATAGATATTTAAAGAGA 240
DB 181 AGTCCTCAGAAACCTAAGTCTCTTGAACCCCTCCATGGAATAGATATTTAAAGAGA 240
QY 241 GAATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAAGTCCACCAATGGTT 300
DB 241 GAATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAAGTCCACCAATGGTT 300
QY 301 CCACAAATGGAGCCTTTTCCAGAGAGACAAATTCAGTTCAGTTCAGTTCAGTTCAGTTC 360
DB 301 CCACAAATGGAGCCTTTTCCAGAGAGACAAATTCAGTTCAGTTCAGTTCAGTTCAGTTC 360
QY 361 TGAAGAGAGTGGAGATCAATGTCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 420
DB 361 TGAAGAGAGTGGAGATCAATGTCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 420
QY 421 CCTGGAAGTCTTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCA 480
DB 421 CCTGGAAGTCTTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCA 480
QY 481 CCAGCCCTCTTCTCAGTCCAGTCCAGTCCAGTCCAGTCCAGTCCAGTCCAGTCCAGTCC 540
DB 481 CCAGCCCTCTTCTCAGTCCAGTCCAGTCCAGTCCAGTCCAGTCCAGTCCAGTCCAGTCC 540
QY 541 TTATAAGAGATGGTGAAGTCTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 600
DB 541 TTATAAGAGATGGTGAAGTCTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 600
QY 601 TGCCACAGTGAAGCAGTGAAGCAGTGAAGCAGTGAAGCAGTGAAGCAGTGAAGCAGTGA 660

DB 601 TGCCACAGTGAAGCAGTGAAGCAGTGAAGCAGTGAAGCAGTGAAGCAGTGAAGCAGTGA 660
QY 661 TGAGTCTGAGCCCTCAACATTAAGTCTGTAATTAAGTCTGTAATTAAGTCTGTAATTAAG 720
DB 661 TGAGTCTGAGCCCTCAACATTAAGTCTGTAATTAAGTCTGTAATTAAGTCTGTAATTAAG 720
QY 721 ATTTTATCCCATTTGTTGGTGGTCAATTTCTGTTGCTGTGGACACAGGATTTATTTCTC 780
DB 721 ATTTTATCCCATTTGTTGGTGGTCAATTTCTGTTGCTGTGGACACAGGATTTATTTCTC 780
QY 781 AACTCAGCAGGAGTCAATTTCTTGAAGATTAAGAGACCAAGGAAAGGCTTCAGACT 840
DB 781 AACTCAGCAGGAGTCAATTTCTTGAAGATTAAGAGACCAAGGAAAGGCTTCAGACT 840
QY 841 TCTGAACCCACATCTTAAGCCAAACCCCAACCAACCAACCAACCAACCAACCAACCAATAT 900
DB 841 TCTGAACCCACATCTTAAGCCAAACCCCAACCAACCAACCAACCAACCAACCAATAT 900
QY 901 TTGCAACATTTGTTTTCAGCATCAGCAATTTGCTTCAATTTGCTTCAACACAGCTTG 960
DB 901 TTGCAACATTTGTTTTCAGCATCAGCAATTTGCTTCAATTTGCTTCAACACAGCTTG 960
QY 961 CAATATACATGAAGACGCTGCTGCTCAAGGATTTATGAAGATTTATGAAGATTTATGA 1020
DB 961 CAATATACATGAAGACGCTGCTGCTCAAGGATTTATGAAGATTTATGAAGATTTATGA 1020
QY 1021 AAACCTGGTTAAGTGCATGTAATAGTAGTCTCAATTAAGTCTCAATTAAGTCTCAATTAAG 1080
DB 1021 AAACCTGGTTAAGTGCATGTAATAGTAGTCTCAATTAAGTCTCAATTAAGTCTCAATTAAG 1080
QY 1081 GAATCAATAGATTTCAATTTATGAGATTTGTAAGAGATTTGTAAGAGATTTGTAAGAGAT 1140
DB 1081 GAATCAATAGATTTCAATTTATGAGATTTGTAAGAGATTTGTAAGAGATTTGTAAGAGAT 1140
QY 1141 TATTAACCATGTAACAGAA 1160
DB 1140 TATTAACCATGTAACAGAA 1159

RESULT 9
US-08-756-387B-4
; Sequence 4, Application US/08756387B
; Patent No. 5945294
; GENERAL INFORMATION:
; APPLICANT: Frank, Glenn R.
; APPLICANT: Porter, James P.
; APPLICANT: Rushlow, Keith E.
; APPLICANT: Wasson, Donald L.
; TITLE OF INVENTION: Method to Detect IGB
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carol Talkington Verser, Ph.D.
; ADDRESS: Heskia Corporation
; STREET: 1825 Sharp Point Drive
; CITY: Fort Collins
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80525
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: WordPerfect for Windows, Version 7.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/756.387B
; FILING DATE: No. 5945294ember 26, 1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Verser, Carol Talkington
; REGISTRATION NUMBER: 37,459
; REFERENCE/DOCKET NUMBER: DI-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 970/493-7272

TELEFAX: 970/484-9505
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 774 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..774
US-08-756-387B-4

Query Match 64.6%; Score 774; DB 2; Length 774;
Best Local Similarity 100.0%; Pred. No. 1.3e-185;
Matches 774; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 107 ATGGCTCTCCATGGAAATCCCTACTCTACTGTGTAGCTTACTGTCTTCTCGCTCCA 166
Db 1 ATGGCTCTCCATGGAAATCCCTACTCTACTGTGTAGCTTACTGTCTTCTCGCTCCA 60

QY 167 GATGGCGTGTACAGTCCCTCAGAACCTAAGGTCTCCTTGAACCTCCATGGAAATAGA 226
Db 61 GATGGCGTGTAGCAGTCCCTCAGAACCTAAGGTCTCCTTGAACCTCCATGGAAATAGA 120

QY 227 ATATTTAAAGGAGAGAAATGTGACTCTTACATGTAATGGGAACAAATTTCTTTGAAGTCAGT 286
Db 121 ATATTTAAAGGAGAGAAATGTGACTCTTACATGTAATGGGAACAAATTTCTTTGAAGTCAGT 180

QY 287 TCACCAAAATGGTTCACAAATGGCAGCCTTTCAGAGAGACAAATTCAGATTTGAATATT 346
Db 181 TCACCAAAATGGTTCACAAATGGCAGCCTTTCAGAGAGACAAATTCAGATTTGAATATT 240

QY 347 GTGAATCCCAAAATTTGAAGACAGTGGAGAAATACAAATGTGAGCAACCAACAAATTAATAG 406
Db 241 GTGAATCCCAAAATTTGAAGACAGTGGAGAAATACAAATGTGAGCAACCAACAAATTAATAG 300

QY 407 AGTGAACCTGTGACCTGGGAAGTCTTCAGTGAATGGCTGTCTCTCAGGCTCTGCTGAG 466
Db 301 AGTGAACCTGTGACCTGGGAAGTCTTCAGTGAATGGCTGTCTCTCAGGCTCTGCTGAG 360

QY 467 GTGGTATGAGGGCCAGCCCTCTCTCAGGTGCCATGTTGGAGAACTCGGATGTG 526
Db 361 GTGGTATGAGGGCCAGCCCTCTCTCAGGTGCCATGTTGGAGAACTCGGATGTG 420

QY 527 TACAAGGTGATCTATTATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCAAC 586
Db 421 TACAAGGTGATCTATTATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCAAC 480

QY 587 ATCTCCAAATTAACAATGCCACAGTTGAAGACAGTGGAACTTACTACTGACGGGCAAGTG 646
Db 481 ATCTCCAAATTAACAATGCCACAGTTGAAGACAGTGGAACTTACTACTGACGGGCAAGTG 540

QY 647 TGGCAGCTGGACTATGAGTCTGAGCCCTCAACATTAATGTAATAAGCTCCGCGTGAG 706
Db 541 TGGCAGCTGGACTATGAGTCTGAGCCCTCAACATTAATGTAATAAGCTCCGCGTGAG 600

QY 707 AAGTACTGGGTACAAATTTTATCCCAATTTGTTGGTGTGATTTCTGTTTGTGTGGACACA 766
Db 601 AAGTACTGGGTACAAATTTTATCCCAATTTGTTGGTGTGATTTCTGTTTGTGTGGACACA 660

QY 767 GGATTATTATCTCAACTCAGCAGCAGTCAATTTCTTGAAGATTAAGAGAACCCAGG 826
Db 661 GGATTATTATCTCAACTCAGCAGCAGTCAATTTCTTGAAGATTAAGAGAACCCAGG 720

QY 827 AAAGGCTTCAGACTTCTGAACCCACATCTTAAGCCAAACCCCAAAACAACTGA 880
Db 721 AAAGGCTTCAGACTTCTGAACCCACATCTTAAGCCAAACCCCAAAACAACTGA 774

RESULT 10

US-08-756-387B-5/c

; Sequence 5, Application US/08756387B

; Patent No. 5945294
; GENERAL INFORMATION:
; APPLICANT: Frank, Glenn R.
; APPLICANT: Porter, James P.
; APPLICANT: Rushlow, Keith E.
; APPLICANT: Wassom, Donald L.
; TITLE OF INVENTION: Method to Detect i9E
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carol Talkington Verser, Ph.D.
; ADDRESSEE: Heska Corporation
; STREET: 1825 Sharp Point Drive
; CITY: Fort Collins
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80525
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: WordPerfect for Windows, Version 7.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/756.387B
; FILING DATE: No. 5945294ember 26, 1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Verser, Carol Talkington
; REGISTRATION NUMBER: 37,459
; REFERENCE/DOCKET NUMBER: DI-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 970/493-7272
; TELEFAX: 970/484-9505
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 774 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-756-387B-5

Query Match 64.6%; Score 774; DB 2; Length 774;
Best Local Similarity 100.0%; Pred. No. 1.3e-185;
Matches 774; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 107 ATGGCTCTCCATGGAAATCCCTACTCTACTGTGTAGCTTACTGTCTTCTCGCTCCA 166
Db 774 ATGGCTCTCCATGGAAATCCCTACTCTACTGTGTAGCTTACTGTCTTCTCGCTCCA 715

QY 167 GATGGCGTGTAGCAGTCCCTCAGAAACCTAAGGTCTCCTTGAACCTCCATGGAAATAGA 226
Db 714 GATGGCGTGTAGCAGTCCCTCAGAAACCTAAGGTCTCCTTGAACCTCCATGGAAATAGA 655

QY 227 ATATTTAAAGGAGAGAAATGTGACTCTTACATGTAATGGGAACAAATTTCTTTGAAGTCAGT 286
Db 654 ATATTTAAAGGAGAGAAATGTGACTCTTACATGTAATGGGAACAAATTTCTTTGAAGTCAGT 595

QY 287 TCACCAAAATGGTTCACAAATGGCAGCCTTTCAGAGAGACAAATTCAGATTTGAATATT 346
Db 594 TCACCAAAATGGTTCACAAATGGCAGCCTTTCAGAGAGACAAATTCAGATTTGAATATT 535

QY 347 GTGAATGCCAAATTTGAAGACAGTGGAGAAATACAAATGTGAGCAACCAACAAAGTTAATAG 406
Db 534 GTGAATGCCAAATTTGAAGACAGTGGAGAAATACAAATGTGAGCAACCAACAAAGTTAATAG 475

QY 407 AGTGAACCTGTGTACTGTGAAGTCTTCACTGACTGGCTCTCTTCAGGCTCTCTCAGGCTCTGCTGAG 466
Db 474 AGTGAACCTGTGTACTGTGAAGTCTTCACTGACTGGCTCTCTTCAGGCTCTCTCAGGCTCTGCTGAG 415

QY 467 GTGGTATGAGGGCCAGCCCTCTCTCAGGTGCCATGTTGGAGAACTCGGATGTG 526
Db 414 GTGGTATGAGGGCCAGCCCTCTCTCAGGTGCCATGTTGGAGAACTCGGATGTG 355


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STREET: 1825 Sharp Point Drive
CITY: Fort Collins
STATE: Colorado
COUNTRY: USA
ZIP: 80525
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: Wordperfect for Windows, Version 7.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/285,873
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
FILING DATE: US/08/756,387
APPLICATION NUMBER: 6309832ember 26, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Verser, Carol Talkington
REGISTRATION NUMBER: 37,459
REFERENCE/DOCKET NUMBER: DI-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 970/493-7272
TELEFAX: 970/484-9505
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 774 nucleotides
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-09-285-873-5

Query Match 64.6%; Score 774; DB 4; Length 774;
Best Local Similarity 100.0%; Pred. No. 1.3e-185;
Matches 774; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 107 ATGCTCTGTCATGGAATCCCTACTCTACTGTGTAGCTTACGTCTTCTCGTCCA 166
DB 774 ATGCTCTGTCATGGAATCCCTACTCTACTGTGTAGCTTACGTCTTCTCGTCCA 715
QY 167 GATGCGGTGTAGCAGTCCCTCAGAACCTTAAGTCTCCTGTGAACCTCCATGGAATAGA 226
DB 714 GATGCGGTGTAGCAGTCCCTCAGAACCTTAAGTCTCCTGTGAACCTCCATGGAATAGA 655
QY 227 ATATTAAAGGAGAGATGTGACTCTTACATGTATGGAACAAATTTCTTTGAAGTCAGT 286
DB 654 ATATTAAAGGAGAGATGTGACTCTTACATGTATGGAACAAATTTCTTTGAAGTCAGT 595
QY 287 TCCACCAATGGTTCCCAATGGCAGCTTTTCAAGAGAGACAAATTCAGTTTGAATATT 346
DB 594 TCCACCAATGGTTCCCAATGGCAGCTTTTCAAGAGAGACAAATTCAGTTTGAATATT 535
QY 347 GTGAATGCCAAATTTGAAGCAGTGGAGATACAAATGTGAGCACCACCAAGTTAATGAG 406
DB 534 GTGAATGCCAAATTTGAAGCAGTGGAGATACAAATGTGAGCACCACCAAGTTAATGAG 475
QY 407 AGTGAACCTGTGTACCTGGAAGTCTTCAAGTCACTGGCTGCTCCTCAGGCTCTGCTGAG 466
DB 474 AGTGAACCTGTGTACCTGGAAGTCTTCAAGTCACTGGCTGCTCCTCAGGCTCTGCTGAG 415
QY 467 GTGTGATGAGGGCCAGCCCTCTTCTCAGGTGCCATGTTGAGGAACCTGGATGTG 526
DB 414 GTGTGATGAGGGCCAGCCCTCTTCTCAGGTGCCATGTTGAGGAACCTGGATGTG 355
QY 527 TACAGGTGATCTATTATAGGATGGTGAAGCTCTCAAGTACTGTATGAGAACCAAC 586
DB 354 TACAGGTGATCTATTATAGGATGGTGAAGCTCTCAAGTACTGTATGAGAACCAAC 295
QY 587 ATCTCCATTACAAATGCCACAGTTGAAGACAGTGGAACTTACTACTGTACGGGCAAGTG 646
DB 294 ATCTCCATTACAAATGCCACAGTTGAAGACAGTGGAACTTACTACTGTACGGGCAAGTG 235

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647 TGGCAGCTGGACTATGAGTCTGAGCCCTCAACATTACTGTATAAAGCTCCGCTGAG 706
DB 234 TGGCAGCTGGACTATGAGTCTGAGCCCTCAACATTACTGTATAAAGCTCCGCTGAG 175
QY 707 AAGTACTGGCTACAAATTTTTTATCCATTGTTGGTGGTGAATCTCTTGTGTGACACA 766
DB 174 AAGTACTGGCTACAAATTTTTTATCCATTGTTGGTGGTGAATCTCTTGTGTGACACA 115
QY 767 GGAATTATTATCTCAACTCAGCAGAGTCAATTTCTTTGAAGATTAAAGAACCAAGG 826
DB 114 GGAATTATTATCTCAACTCAGCAGAGTCAATTTCTTTGAAGATTAAAGAACCAAGG 55
QY 827 AAAGGCTTCAGACTTCTTGAACCCATCTTAAGCCAAACCCCAAAACAACCTGA 880
DB 54 AAAGGCTTCAGACTTCTTGAACCCATCTTAAGCCAAACCCCAAAACAACCTGA 1

RESULT 13
US-09-944-277A-4
; Sequence 4, Application US/09944277A
; Patent No. 6682894
; GENERAL INFORMATION:
; APPLICANT: Frank, Glenn R.
; Porter, James P.
; Rushlow, Keith E.
; Wassom, Donald L.
; TITLE OF INVENTION: Method to Detect Ige
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carol Talkington Verser, Ph.D.
; Heska Corporation
; CITY: Fort Collins
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80525
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: Wordperfect for Windows, Version 7.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/944,277A
; FILING DATE: 30-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/285,873
; FILING DATE: 1999-03-31
; ATTORNEY/AGENT INFORMATION:
; NAME: Verser, Carol Talkington
; REGISTRATION NUMBER: 37,459
; REFERENCE/DOCKET NUMBER: DI-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 970/493-7272
; TELEFAX: 970/484-9505
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 774 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..774
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-944-277A-4

Query Match 64.6%; Score 774; DB 4; Length 774;
Best Local Similarity 100.0%; Pred. No. 1.3e-185;
Matches 774; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 107 ATGCTCTGTCATGGAATCCCTACTCTACTGTGTAGCTTACGTCTTCTCGTCCA 166

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Db 1 ATGGCTCTCCGATGGAATCCCTACTCTACTGTGTAGCTTACTGTCTCTGCTCCA 60
QY 167 GATGGCGTGTAGCAGTCCCTCAGAACTTAGGTCTCTTGAACCTCCATGGAATAGA 226
Db 61 GATGGCGTGTAGCAGTCCCTCAGAACTTAGGTCTCTTGAACCTCCATGGAATAGA 120
QY 227 ATATTAAAGGAGAGATGTACTCTTACATGTAATGGGAACAATTTCTTGAAGTCAGT 286
Db 121 ATATTAAAGGAGAGATGTACTCTTACATGTAATGGGAACAATTTCTTGAAGTCAGT 180
QY 287 TCCACCAATGTTCCACAACTGGAGCCCTTTCAGAGAGACAAATTCAGTTGAATATT 346
Db 181 TCCACCAATGTTCCACAACTGGAGCCCTTTCAGAGAGACAAATTCAGTTGAATATT 240
QY 347 GTCAATGCCAAATTTGAAGACAGTGGAGATACAAATGTGACACCAACAAGTTAATGAG 406
Db 241 GTGAATGCCAAATTTGAAGACAGTGGAGATACAAATGTGACACCAACAAGTTAATGAG 300
QY 407 AGTGAACCTGTACTGGAAGTCTTCAAGTGTAGTGGCTGCTCTTCAAGCTCTCTGCTGAG 466
Db 301 AGTGAACCTGTACTGGAAGTCTTCAAGTGTAGTGGCTGCTCTTCAAGCTCTCTGCTGAG 360
QY 467 GTGGTGTATGGAGGGCCAGCCCTCTTCTCAGGTGCCATGTTGGAGGAACCTGGATGTG 526
Db 361 GTGGTGTATGGAGGGCCAGCCCTCTTCTCAGGTGCCATGTTGGAGGAACCTGGATGTG 420
QY 527 TACAAGGTGATCTATTATAAGAGAGTGAAGTCTCAAGTACTGATGAGAACCAAC 586
Db 421 TACAAGGTGATCTATTATAAGAGATGGTGAAGTCTCAAGTACTGATGAGAACCAAC 480
QY 587 ATCTCCATACAAATGCCACAGTGTGAAGACAGTGGAACTACTACTGTACGGGCAAGTG 646
Db 481 ATCTCCATACAAATGCCACAGTGTGAAGACAGTGGAACTACTACTGTACGGGCAAGTG 540
QY 647 TGGCAGCTGGATGATGAGTCTGAGCCCTCAACATTTACTGTATAAAGTCTCCGCTGAG 706
Db 541 TGGCAGCTGGATGATGAGTCTGAGCCCTCAACATTTACTGTATAAAGTCTCCGCTGAG 600
QY 707 AGTACTGGCTACAAATTTTATCCATGTTGGTGGTATCTGTTGCTGGGACACA 766
Db 601 AGTACTGGCTACAAATTTTATCCATGTTGGTGGTATCTGTTGCTGGGACACA 660
QY 767 GGAATATTATCTCAACTCAGCAGCAGTGCATTTCTTGAAGATTTAAGAGAACCAAG 826
Db 661 GGAATATTATCTCAACTCAGCAGCAGTGCATTTCTTGAAGATTTAAGAGAACCAAG 720
QY 827 AAAGCTTTCAGACTTCTGAAACCCACATCCTTAAGCCAAACCCCAAAACAACTGA 880
Db 721 AAAGCTTTCAGACTTCTGAAACCCACATCCTTAAGCCAAACCCCAAAACAACTGA 774
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RESULT 14

US-09-944-277A-5/c

; Sequence 5, Application US/09944277A

; Patent No. 6682894

; GENERAL INFORMATION:

; APPLICANT: Frank, Glenn R.

; Porter, James P.

; Rushlow, Keith E.

; Wassom, Donald L.

; TITLE OF INVENTION: Method to Detect Ige

; NUMBER OF SEQUENCES: 13

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Carol Talkington Verser, Ph.D.

; STREET: 1825 Sharp Point Drive

; CITY: Fort Collins

; STATE: Colorado

; COUNTRY: USA

; ZIP: 80525

; MEDIUM TYPE: Floppy disk

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;
;
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: WordPerfect for Windows, Version 7.0
; CURRENT APPLICATION DATA: US/09/944,277A
; APPLICATION NUMBER: 09/944,277A
; FILING DATE: 30-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/285,873
; FILING DATE: 1999-03-31
; ATTORNEY/AGENT INFORMATION:
; NAME: Verser, Carol Talkington
; REGISTRATION NUMBER: 37,459
; REFERENCE/DOCKET NUMBER: DI-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 970/493-7272
; TELEFAX: 970/484-9505
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 774 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
; US-09-944-277A-5
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Query Match 64.6%; Score 774; DB 4; Length 774;

Best Local Similarity 100.0%; Pred. No. 1.3e-185;

Matches 774; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 167 GATGGCGTGTAGCAGTCCCTCAGAACTTAGGTCTCTTGAACCTCCATGGAATAGA 226
Db 714 GATGGCGTGTAGCAGTCCCTCAGAACTTAGGTCTCTTGAACCTCCATGGAATAGA 655
QY 227 ATATTAAAGGAGAGATGTACTCTTACATGTAATGGGAACAATTTCTTGAAGTCAGT 286
Db 654 ATATTAAAGGAGAGATGTACTCTTACATGTAATGGGAACAATTTCTTGAAGTCAGT 595
QY 287 TCCACCAATGTTCCACAACTGGAGCCCTTTCAGAGAGACAAATTCAGTTGAATATT 346
Db 594 TCCACCAATGTTCCACAACTGGAGCCCTTTCAGAGAGACAAATTCAGTTGAATATT 535
QY 347 GTGAATGCCAAATTTGAAGACAGTGGAGATACAAATGTGACACCAACAAGTTAATGAG 406
Db 534 GTGAATGCCAAATTTGAAGACAGTGGAGATACAAATGTGACACCAACAAGTTAATGAG 475
QY 407 AGTGAACCTGTACTGGAAGTCTTCAAGTGTAGTGGCTGCTCTTCAAGCTCTCTGCTGAG 466
Db 474 AGTGAACCTGTACTGGAAGTCTTCAAGTGTAGTGGCTGCTCTTCAAGCTCTCTGCTGAG 415
QY 467 GTGGTGTATGGAGGGCCAGCCCTCTTCTCAGGTGCCATGTTGGAGGAACCTGGATGTG 526
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QY 527 TACAAGGTGATCTATTATAAGAGATGGTGAAGTCTCAAGTCTCAAGTCTGATGAGAACCAAC 586
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QY 587 ATCTCCATACAAATGCCACAGTGTGAAGACAGTGGAACTACTACTGTACGGGCAAGTG 646
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QY 647 TGGCAGCTGGATGATGAGTCTGAGCCCTCAACATTTACTGTATAAAGTCTCCGCTGAG 706
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RESULT 15

US-08-897-956A-6
; Sequence 6, Application US/08897956A
; Patent No. 6423512
; GENERAL INFORMATION:
; APPLICANT: Mary Ellen Digan
; APPLICANT: Philip Lake
; APPLICANT: Hermann Gram
; TITLE OF INVENTION: Fusion Polypeptides
; FILE REFERENCE: 600-7244/CPA
; CURRENT APPLICATION NUMBER: US/08/897,956A
; CURRENT FILING DATE: 1997-07-21
; PRIOR APPLICATION NUMBER: 60/022,689
; PRIOR FILING DATE: 1996-07-26
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 773
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Fusion Polynucleotide
US-08-897-956A-6

Query Match 64.5%; Score 773; DB 4; Length 773;

Best Local Similarity 100.0%; Pred. No. 2,2e-185;

Matches 773; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 167 GATGGCGTGTAGCAGTCCCTCAGAAACCTTAAGTCTCTTGAACCCCTCCATGGAATAGA 226
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Qy 347 GTGAATGCCAAATTTGAAGACAGTGGAGAAATACAAATGTGAGCACCACCAAGTTAATGAG 406
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Qy 407 AGTGAACCTGTGTACCTGGAGTCTTCACTGACCTGGCTCTCTTCAAGGCTCTGCTGAG 466
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Qy 467 GTGGTGTAGGAGGCGCCGCCCTCTCTCTCAGGTGCCATGGTTGGAGGAACTGGGATGTG 526
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Db 481 ATCTCCATTACAAATGCCACAGTTTGAAGACAGTGGAACTACTACTGTACGGGCAAAAGTG 540
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Db 541 TGGCAGCTGGAGTACTATGAGTCTGTAGCCCTCTCAACATTTACTGTAAATAAAGCTCCCGCTGAG 600
Qy 707 AAGTACTGGCTACAAATTTTTTATCCCATTTGTTGGTGGTGAATTTCTGTTGCTGTGGACACA 766
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Qy 767 GGATTATTATCTCAACTCAGCAGCAGGTGCATTTCTCTTGAAGATTAAAGAAACCCAGG 826
Db 661 GGATTATTATCTCAACTCAGCAGCAGGTGCATTTCTCTTGAAGATTAAAGAAACCCAGG 720
Qy 827 AAAGGCTTCAGACTTCTGAACCCACATCTTAAGCCAAACCCCAAAACCAACTG 879
Db 721 AAAGGCTTCAGACTTCTGAACCCACATCTTAAGCCAAACCCCAAAACCAACTG 773

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OM nucleic - nucleic search, using sw model

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Gapop 10.0 , Gapext 1.0

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Total number of hits satisfying chosen parameters: 6681306

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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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4	1198	100.0	1198	17	US-10-775-163-141
5	882.8	73.7	898	13	US-10-236-392-27
6	774	64.6	774	9	US-09-944-277A-4
7	774	64.6	774	9	US-09-944-277A-5
8	699	58.3	699	9	US-09-944-277A-7
9	630	52.6	757	13	US-10-236-392-29
10	591	49.3	591	9	US-09-944-277A-10
11	578.8	48.3	1015	16	US-10-434-817-1
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Sequence 1306, Ap
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Sequence 13, Appli

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ALIGNMENTS

RESULT 1

US-09-944-277A-1
Sequence 1, Application US/09944277A
Patent No. US20020034771A1
GENERAL INFORMATION:
APPLICANT: Frank, Glenn R.
Porter, James P.
Rushlow, Keith E.
Wasson, Donald L.
TITLE OF INVENTION: Method to Detect Ige
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Carol Talkington Verser, Ph.D.
STREET: 1825 Sharp Point Drive
CITY: Fort Collins
STATE: Colorado
COUNTRY: USA
ZIP: 80525
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: WordPerfect for Windows, Version 7.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/944,277A
FILING DATE: 30-Aug-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/285,873
FILING DATE: 1999-03-31
ATTORNEY/AGENT INFORMATION:
NAME: Verser, Carol Talkington
REGISTRATION NUMBER: 37,459
REFERENCE/DOCKET NUMBER: DI-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 970/493-7272

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TELEFAX: 970/484-9505
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1198 nucleotides
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 107..877
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-944-277A-1

Query Match          100.0%; Score 1198; DB 9; Length 1198;
Best Local Similarity 100.0%; Pred. No. 1.9e-288;
Matches 1198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 CTTAGATCTCTCCAGCATGTAAGCAGGAGTCCATGAAGAAGATGGCTCTGCGCAT 120
DB 61 CTTAGATCTCTCCAGCATGTAAGCAGGAGTCCATGAAGAAGATGGCTCTGCGCAT 120
QY 121 GGAATCCCTCTACTGTGTGTAGCTTACTGTCTTCTGCTCCAGATGGCGTGTAGC 180
DB 121 GGAATCCCTCTACTGTGTGTAGCTTACTGTCTTCTGCTCCAGATGGCGTGTAGC 180
QY 181 AGTCCTCAGAAACCTAAGGCTCTCTTGAAACCTCCATGGAATAGATATTTAAAGAGA 240
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DB 721 ATTTTATCCATTGTTGGTGGTATTTCTGTTGCTGTGACACAGATTTATTTATCTC 780
QY 781 AACTCAGCAGAGGTTCATATTTCTTTGAAGATTAAGAGACCAAGGAGGCTTCAGACT 840
DB 781 AACTCAGCAGAGGTTCATATTTCTTTGAAGATTAAGAGACCAAGGAGGCTTCAGACT 840
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RESULT 2

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; Sequence 3, Application US/09944277A
; Patent No. US20020034771A1
; GENERAL INFORMATION:
; APPLICANT: Frank, Glenn R.
; Porter, James P.
; Rushlow, Keith E.
; Wassom, Donald L.
; TITLE OF INVENTION: Method to Detect Ige
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carol Talkington Verser, Ph.D.
; STREET: 1825 Sharp Point Drive
; CITY: Fort Collins
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80525
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: WordPerfect for Windows, Version 7.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/944,277A
; FILING DATE: 30-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/285,873
; FILING DATE: 1999-03-31
; ATTORNEY/AGENT INFORMATION:
; NAME: Verser, Carol Talkington
; REGISTRATION NUMBER: 37,459
; REFERENCE/DOCKET NUMBER: DI-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 970/493-7272
; TELEFAX: 970/484-9505
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1198 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-944-277A-3
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Query Match 100.0%; Score 1198; DB 9; Length 1198;
Best Local Similarity 100.0%; Pred. No. 1.9e-288;
Matches 1198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db CAATATACATAGAACCTCTGCTCAGGATTTATAGAAATGCTTCATTAAACTGAGTG 179

RESULT 3

US-09-962-832-244
; Sequence 244, Application US/09962832
; Patent No. US20020110821A1

GENERAL INFORMATION:

; APPLICANT: Elnor, Reinhard
; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signatu
; TITLE OF INVENTION: Sets
; FILE REFERENCE: 689290-74
; CURRENT APPLICATION NUMBER: US/09/962,832
; PRIORITY FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US/60/235,077
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: US/60/235,280
; PRIOR FILING DATE: 2000-09-25
; NUMBER OF SEQ ID NOS: 259
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 244
; LENGTH: 1198
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-962-832-244

Query Match 100.0%; Score 1198; DB 9; Length 1198;

Best Local Similarity 100.0%; Pred. No. 1.9e-288;

Matches 1198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TACTAAGAGTCTCCAGCATCCTCCACCTGTCTTACCCAGAGCATGGGCTATATTGAAG 60
Db 1 TACTAAGAGTCTCCAGCATCCTCCACCTGTCTTACCCAGAGCATGGGCTATATTGAAG 60

Qy 61 CCTTAGATCTCTCCAGCACAGTGAAGCAGGAGTCCATGAAGAAGATGGCTCCTGCCAT 120
Db 61 CCTTAGATCTCTCCAGCACAGTGAAGCAGGAGTCCATGAAGAAGATGGCTCCTGCCAT 120

Qy 121 GGAATCCCTACTCTACTGTGTGTAGCCTTACTGTCTTTCGCTCCAGATGGCGTGTAGC 180
Db 121 GGAATCCCTACTCTACTGTGTGTAGCCTTACTGTCTTTCGCTCCAGATGGCGTGTAGC 180

Qy 181 AGTCCTCAGAACCTAAGTCTCCTTGAAACCTCCATGGAATAGATATTTAAAGGAGA 240
Db 181 AGTCCTCAGAACCTAAGTCTCCTTGAAACCTCCATGGAATAGATATTTAAAGGAGA 240

Qy 241 GAATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGTTTCCACCAATGGTT 300
Db 241 GAATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGTTTCCACCAATGGTT 300

Qy 301 CCACATGGCAGCCTTTTCAAGAGAGACAATTTCAAGTTTGAATTTGAATGCCAAT 360
Db 301 CCACATGGCAGCCTTTTCAAGAGAGACAATTTCAAGTTTGAATTTGAATGCCAAT 360

Qy 361 TGAAGACAGTGGAGAAATACAAATCTCAGACCCACCAAGTTAATGAGAGTGAACCTGTGA 420
Db 361 TGAAGACAGTGGAGAAATACAAATCTCAGACCCACCAAGTTAATGAGAGTGAACCTGTGA 420

Qy 421 CCTGGAAGTCTTCAAGTACTGCTCCTTCCAGGCTCTGCTGAGGTGGTGTAGAGGG 480
Db 421 CCTGGAAGTCTTCAAGTACTGCTCCTTCCAGGCTCTGCTGAGGTGGTGTAGAGGG 480

Qy 481 CCAGCCCTCTTCTCAGGTGCCATGTTGGAGAACTGGGATGTGTACAGGTGATCTA 540

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Db 481 CCAGCCCTCTTCTCAGGTGCAATGGTGGAGAACTGGGATGTGTACAAGGTGACTA 540
Qy 541 TTATAAGGATGTTGAAGTCTCAAGTACTGTGTATGAGAACCAACATCTCCATTACAAA 600
Db 541 TTATAAGGATGTTGAAGTCTCAAGTACTGTGTATGAGAACCAACATCTCCATTACAAA 600
Qy 601 TCCACAGTTGAAGCAGTGGAACTTCTACTGTATGAGGCGAAAGTGTGGAGCTGGACTA 660
Db 601 TCCACAGTTGAAGCAGTGGAACTTCTACTGTATGAGGCGAAAGTGTGGAGCTGGACTA 660
Qy 661 TGAGTCTGAGCCCTCAACATTTCTGTAATAAAGCTCCGGTGAAGAGTACTGGCTACA 720
Db 661 TGAGTCTGAGCCCTCAACATTTCTGTAATAAAGCTCCGGTGAAGAGTACTGGCTACA 720
Qy 721 ATTTTATCCATTTGTTGGTGGTCAATTTCTGTCTGTGACACAGAGTTATTTATCTC 780
Db 721 ATTTTATCCATTTGTTGGTGGTCAATTTCTGTCTGTGACACAGAGTTATTTATCTC 780
Qy 781 RACTCAGCAGAGTGCATTTCTCTGAGATTAAGAGAACCCAGGAAGCTTCAGACT 840
Db 781 RACTCAGCAGAGTGCATTTCTCTGAGATTAAGAGAACCCAGGAAGCTTCAGACT 840
Qy 841 TCTGAACCCACATCTTAAGCCAAACCCCAAAACCACTGATATAATTTACTCAAGAAATAT 900
Db 841 TCTGAACCCACATCTTAAGCCAAACCCCAAAACCACTGATATAATTTACTCAAGAAATAT 900
Qy 901 TTGCAACATTTGTTTTCAGATCAGCAATTTCTCAATTTGTCACACAGCTTG 960
Db 901 TTGCAACATTTGTTTTCAGATCAGCAATTTCTCAATTTGTCACACAGCTTG 960
Qy 961 CAATATACATAGAAACGCTGTGCTCAAGGATTTATAGAAATGCTTCAATTAAGT 1020
Db 961 CAATATACATAGAAACGCTGTGCTCAAGGATTTATAGAAATGCTTCAATTAAGT 1020
Qy 1021 AAATGTTAGTGCATGTAATAGTAAAGTGCATTAATTAAGTGGTGAATTAATGAGA 1080
Db 1021 AAATGTTAGTGCATGTAATAGTAAAGTGCATTAATTAAGTGGTGAATTAATGAGA 1080
Qy 1081 GAATCAATAGATTTCAATTTATTAGCATTTGTAAGAGATGTTCAATTTCAATAAATAA 1140
Db 1081 GAATCAATAGATTTCAATTTATTAGCATTTGTAAGAGATGTTCAATTTCAATAAATAA 1140
Qy 1141 TATAAACCCTGTAACAGATGCTTCTGAGTAAATAAATAAATAAATAAATAA 1198
Db 1141 TATAAACCCTGTAACAGATGCTTCTGAGTAAATAAATAAATAAATAAATAA 1198

RESULT 4
US-10-775-169-141
; Sequence 141, Application US/10775169
; Publication No. US20040175743A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Burczynski, Michael
; APPLICANT: Twine, Natalie
; APPLICANT: Dorner, Andrew
; APPLICANT: Trepicchio, William
; TITLE OF INVENTION: Method for Monitoring Drug Activities In Vivo
; FILE REFERENCE: AM101080 (031896-013000)
; CURRENT APPLICATION NUMBER: US/10/775,169
; NUMBER OF SEQ ID NOS: 5278
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 141
; LENGTH: 1198
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-775-169-141
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Query Match 100.0%; Score 1198; DB 17; Length 1198;
Best Local Similarity 100.0%; Pred. No. 1.9e-288;
Matches 1198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 TACTAAGAGTCTCCAGCATCTCCACCTGTCTACACCGAGCATGGGCTATATTTGAAG 60
Db 1 TACTAAGAGTCTCCAGCATCTCCACCTGTCTACACCGAGCATGGGCTATATTTGAAG 60
Qy 61 CTTTACATCTCTCCAGCACAGTAAGCACAGGAGTCCATGAAGAAGATGGCTCTCGCCAT 120
Db 61 CTTTACATCTCTCCAGCACAGTAAGCACAGGAGTCCATGAAGAAGATGGCTCTCGCCAT 120
Qy 121 GGAATCCCTTACTCTACTGTGTAGCTTACTGTCTTCGCTCCAGATGGGCTGTAGC 180
Db 121 GGAATCCCTTACTCTACTGTGTAGCTTACTGTCTTCGCTCCAGATGGGCTGTAGC 180
Qy 181 AGTCCCTCAGAAACCTTAAGTCTCTCTGAAACCTCCATGGAATAGAATATTTAAAGGAGA 240
Db 181 AGTCCCTCAGAAACCTTAAGTCTCTCTGAAACCTCCATGGAATAGAATATTTAAAGGAGA 240
Qy 241 GAATGTGACTCTTACATGTAATGGGAACAATTTCTTGAAGTCAGTTCCACCAATGGTT 300
Db 241 GAATGTGACTCTTACATGTAATGGGAACAATTTCTTGAAGTCAGTTCCACCAATGGTT 300
Qy 301 CCACANTGCGAGCTTTTCAAGAGACAAATTTCAAGTTTGAATATTTGTAATGCCAAAT 360
Db 301 CCACANTGCGAGCTTTTCAAGAGACAAATTTCAAGTTTGAATATTTGTAATGCCAAAT 360
Qy 361 TGAAGACAGTGGAGATACAAATGTGAGCACCAACAAGTTAATGAGAGTGAACCTGTGTA 420
Db 361 TGAAGACAGTGGAGATACAAATGTGAGCACCAACAAGTTAATGAGAGTGAACCTGTGTA 420
Qy 421 CTTGGAAGTCTTCAAGTACTGCTGCTCTTCAAGGCTCTCTGAGGCTCTGCTGAGTGGT 480
Db 421 CTTGGAAGTCTTCAAGTACTGCTGCTCTTCAAGGCTCTCTGAGGCTCTGCTGAGTGGT 480
Qy 481 CCAGCCCTCTTCTCAGGTGCAATGTTGGAGAACTGGGATGTGTACAAGTGCATCTA 540
Db 481 CCAGCCCTCTTCTCAGGTGCAATGTTGGAGAACTGGGATGTGTACAAGTGCATCTA 540
Qy 541 TTATAAGGATGTTGAAGTCTCAAGTACTGTTGAGAACCAACAATCTCCATTACAAA 600
Db 541 TTATAAGGATGTTGAAGTCTCAAGTACTGTTGAGAACCAACAATCTCCATTACAAA 600
Qy 601 TCCACAGTGAAGCAGTGGAACTTCTACTGTACGGGCAAGTGTGGAGCTGGACTA 660
Db 601 TCCACAGTGAAGCAGTGGAACTTCTACTGTACGGGCAAGTGTGGAGCTGGACTA 660
Qy 661 TGAGTCTGAGCCCTCAACATTTCTGTAATAAAGCTCCGGTGAAGAGTACTGGCTACA 720
Db 661 TGAGTCTGAGCCCTCAACATTTCTGTAATAAAGCTCCGGTGAAGAGTACTGGCTACA 720
Qy 721 ATTTTATCCATTTGTTGGTGGTCAATTTCTGTCTGTGACACAGAGTTATTTATCTC 780
Db 721 ATTTTATCCATTTGTTGGTGGTCAATTTCTGTCTGTGACACAGAGTTATTTATCTC 780
Qy 781 AACTCAGCAGAGTGCATTTCTCTGAGATTAAGAGAACCCAGGAAGCTTCAGACT 840
Db 781 AACTCAGCAGAGTGCATTTCTCTGAGATTAAGAGAACCCAGGAAGCTTCAGACT 840
Qy 841 TCTGAACCCACATCTTAAGCCAAACCCCAAAACCACTGATATAATTTACTCAAGAAATAT 900
Db 841 TCTGAACCCACATCTTAAGCCAAACCCCAAAACCACTGATATAATTTACTCAAGAAATAT 900
Qy 901 TTGCAACATTTGTTTTCAGATCAGCAATTTCTCAATTTGTCACACAGCTTG 960
Db 901 TTGCAACATTTGTTTTCAGATCAGCAATTTCTCAATTTGTCACACAGCTTG 960
Qy 961 CAATATACATAGAAACGCTGTGCTCAAGGATTTTATAGAAATGCTTCAATTAAGT 1020
Db 961 CAATATACATAGAAACGCTGTGCTCAAGGATTTTATAGAAATGCTTCAATTAAGT 1020
Qy 1021 AAATGTTAGTGCATGTAATAGTAAAGTGCATTAATTAAGTGGTGAATTAATGAGA 1080
Db 1021 AAATGTTAGTGCATGTAATAGTAAAGTGCATTAATTAAGTGGTGAATTAATGAGA 1080
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QY 1081 GAATGATAGATTCATTATTAGCATTTGTAAGAGAGATTTCAATTTCAATAAAATAAA 1140
Db 1081 GAATGATAGATTCATTATTAGCATTTGTAAGAGAGATTTCAATTTCAATAAAATAAA 1140
QY 1141 TATAAACCCATGTAACAGATGCTTCTGAGTAAATATATATATATATATATATATAT 1198
Db 1141 TATAAACCCATGTAACAGATGCTTCTGAGTAAATATATATATATATATATATATAT 1198

RESULT 5
US-10-236-392-27
; Sequence 27, Application US/10236392
; Publication No. US20040067490A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, David W
; APPLICANT: Boldog, Ferenc L
; APPLICANT: Burgess, Catherine, E
; APPLICANT: Casman, Stacie J
; APPLICANT: Catterton, Elina
; APPLICANT: Chapoval, Andrei
; APPLICANT: Crabtree, Julie
; APPLICANT: Edinger, Shlomit, R
; APPLICANT: Ellertman, Karen
; APPLICANT: Gerlach, Valerie
; APPLICANT: Gorman, Linda
; APPLICANT: Grosse, William M
; APPLICANT: Gusev, Vladimir
; APPLICANT: Kekuda, Ramesh
; APPLICANT: LaRoche, William J
; APPLICANT: Li, Li
; APPLICANT: MacDougall, John R
; APPLICANT: Malvankar, Uriel M
; APPLICANT: Miller, Charles E
; APPLICANT: Millet, Isabelle
; APPLICANT: Padigaru, Muraidhara
; APPLICANT: Patturajan, Meera
; APPLICANT: Pena, Carol A
; APPLICANT: Peyman, John A
; APPLICANT: Rastelli, Luca
; APPLICANT: Reiger, Daniel K
; APPLICANT: Rothenberg, Mark E
; APPLICANT: Shenoy, Suresh
; APPLICANT: Shimkets, Richard A
; APPLICANT: Smithson, Glenna
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-442A
; CURRENT APPLICATION NUMBER: US/10/236,392
; CURRENT FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: US09/540,763
; PRIOR FILING DATE: 2000-03-30
; PRIOR APPLICATION NUMBER: US60/390,155
; PRIOR FILING DATE: 2002-06-19
; PRIOR APPLICATION NUMBER: US09/635,949
; PRIOR FILING DATE: 2000-08-10
; PRIOR APPLICATION NUMBER: US60/318,765
; PRIOR FILING DATE: 2001-09-12
; PRIOR APPLICATION NUMBER: US60/357,303
; PRIOR FILING DATE: 2002-02-15
; PRIOR APPLICATION NUMBER: US60/367,753
; PRIOR FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER: US60/369,479
; PRIOR FILING DATE: 2002-04-02
; PRIOR APPLICATION NUMBER: US09/659,634
; PRIOR FILING DATE: 2000-09-12
; PRIOR APPLICATION NUMBER: US60/318,120
; PRIOR FILING DATE: 2001-09-07
; PRIOR APPLICATION NUMBER: US60/318,130
; PRIOR FILING DATE: 2001-09-07
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 794
; SOFTWARE: Custom
; SEQ ID NO 27
; LENGTH: 898

; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (26)..(797)
US-10-236-392-27
Query Match 73.7%; Score 882.8; DB 13; Length 898;
Best Local Similarity 99.8%; Pred. No. 8.4e-210;
Matches 884; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 82 TAAGCACCAGGAGTCCATGAGAGATGGCTCCCTGCGCATGGAATCCCTTACTCTG 141
Db 1 TAAGCACCAGGAGTCCATGAGAGATGGCTCCCTGCGCATGGAATCCCTTACTCTG 60
QY 142 TGTAGCCTTACTGTTCTTCGCTCCAGATGGCGGTGTAGCAGTCCCTCAGAAACCTTAAGGT 201
Db 61 TGTAGCCTTACTGTTCTTCGCTCCAGATGGCGGTGTAGCAGTCCCTCAGAAACCTTAAGGT 120
QY 202 CTCCTTGAAACCTTCCATGGAATAGATATTTAAAGGAGAGATGTGACTCTTACATGTAA 261
Db 121 CTCCTTGAAACCTTCCATGGAATAGATATTTAAAGGAGAGATGTGACTCTTACATGTAA 180
QY 262 TGGGAACAAATTTCTTTGAAGTCAGTTCACCAAAATGGTTCCACAATGGCAGCCTTTCAGA 321
Db 181 TGGGAACAAATTTCTTTGAAGTCAGTTCACCAAAATGGTTCCACAATGGCAGCCTTTCAGA 240
QY 322 AGAGACAAATTCAGTTTGAATATTTGAATGCGCAATTTGGAACACAGTGGAGAAATACAA 381
Db 241 AGAGACAAATTCAGTTTGAATATTTGAATGCGCAATTTGGAACACAGTGGAGAAATACAA 300
QY 382 ATGTCAGCACCAACAAAGTTAATGAGAGTGAACCTGTGTACCTGGAAGTCTTTCAGTGACTG 441
Db 301 ATGTCAGCACCAACAAAGTTAATGAGAGTGAACCTGTGTACCTGGAAGTCTTTCAGTGACTG 360
QY 442 GCTGCTCTCTCAGGCTCTGCTGAGGTGGTGTATGAGAGGCCAGGCCCTCTTCTCAGGTG 501
Db 361 GCTGCTCTCTCAGGCTCTGCTGAGGTGGTGTATGAGAGGCCAGGCCCTCTTCTCAGGTG 420
QY 502 CCATGTTGGAGAACTGGGATGTACAAGTGATCTATTATAAGGATGTGAGCTCT 561
Db 421 CCATGTTGGAGAACTGGGATGTACAAGTGATCTATTATAAGGATGTGAGCTCT 480
QY 562 CAAGTACTGTTATGAGAACCAACATCTCCATTACAAATGCCAGTTGAAGACAGTGG 621
Db 481 CAAGTACTGTTATGAGAACCAACATCTCCATTACAAATGCCAGTTGAAGACAGTGG 540
QY 622 AACCTACTACTGTACGGCAAAAGTGTGCACTGTGCACTATGAGTCTGAGCCCTCAACAT 681
Db 541 AACCTACTACTGTACGGCAAAAGTGTGCACTGTGCACTATGAGTCTGAGCCCTCAACAT 600
QY 682 TACTGTATTAAGCTCCGCTGAGAGTACTGGTACAATTTTATCCCATTTGTTGTT 741
Db 601 TACTGTATTAAGCTCCGCTGAGAGTACTGGTACAATTTTATCCCATTTGTTGTT 660
QY 742 GGTGATTTCTGTTGCTGGACACAGGATTTATTTCTCAACTCAGCAGCAGGTACATTT 801
Db 661 GGTGATTTCTGTTGCTGGACACAGGATTTATTTATCTCAACCAGCAGCAGGTACATTT 720
QY 802 TCTCTTGAAGATTAAGAACCCAGAGAGGCTTCAGACTTCTGAGCCACACATCTTAAGCC 861
Db 721 TCTCTTGAAGATTAAGAACCCAGAGAGGCTTCAGACTTCTGAGCCACACATCTTAAGCC 780
QY 862 AAACCCCAAAACAACTGATATATTTACTCAAGAAATATTTGCAACATTTAGTTTTTCC 921
Db 781 AAACCCCAAAACAACTGATATATTTACTCAAGAAATATTTGCAACATTTAGTTTTTCC 840
QY 922 AGCATCAGCAATTTGCTACTCAATTTGCTCAAAACACAGCTTGCATATA 967
Db 841 AGCATCAGCAATTTGCTACTCAATTTGCTCAAAACACAGCTTGCATATA 886

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US-09-944-277A-4
; Sequence 4, Application US/09944277A
; Patent No. US20020034771A1
; GENERAL INFORMATION:
; APPLICANT: Frank, Glenn R.
; Porter, James P.
; Rushlow, Keith E.
; Wassom, Donald L.
; TITLE OF INVENTION: Method to Detect IGE
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carol Talkington Verser, Ph.D.
; STREET: 1825 Sharp Point Drive
; CITY: Fort Collins
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80525
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: WordPerfect for Windows, Version 7.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/944,277A
; FILING DATE: 30-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/285,873
; FILING DATE: 1999-03-31
; ATTORNEY/AGENT INFORMATION:
; NAME: Verser, Carol Talkington
; REGISTRATION NUMBER: 37,459
; REFERENCE/DOCKET NUMBER: DI-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 970/493-7272
; TELEFAX: 970/484-9505
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 774 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..774
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-944-277A-4
Query Match
Best Local Similarity 100.0%; Pred. No. 1.le-182; Gaps 0;
Matches 774; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 107 ATGGCTCTGCGATGGAATCCCTACTCTACTGTGTGTAGCCTTACTGTTCTTCGCTCCA 166
Db 1 ATGGCTCTGCGATGGAATCCCTACTCTACTGTGTGTAGCCTTACTGTTCTTCGCTCCA 60
QY 167 GATGCGGTGTAGCAGTCCCTCAGAACTTAAGTCTCTTGAACCTCCATGGAATAGA 226
Db 61 GATGCGGTGTAGCAGTCCCTCAGAACTTAAGTCTCTTGAACCTCCATGGAATAGA 120
QY 227 ATATTAAAGGAGAGAATGTGACTCTTACATGTAAATGGGAACAATTTCTTTGAAGTCAGT 286
Db 121 ATATTAAAGGAGAGAATGTGACTCTTACATGTAAATGGGAACAATTTCTTTGAAGTCAGT 180
QY 287 TCCACCAATGGTTCACAAATGGGAGCCTTTTCAGAGAGACAAATTCAGTTTGAATATT 346
Db 181 TCCACCAATGGTTCACAAATGGGAGCCTTTTCAGAGAGACAAATTCAGTTTGAATATT 240
QY 347 GTGAATGCCAAATTTGAAGACAGTGGAGAATACAAATGTTCAGCACCAACCAAGTTAATGAG 406
Db 241 GTGAATGCCAAATTTGAAGACAGTGGAGAATACAAATGTTCAGCACCAACCAAGTTAATGAG 300
407 ACTGAACCTGTGTACTCGAAGTCTTCAGTGAAGTGGCTGCTCTCTTCAGGCTCTGCTGAG 466
301 AGTGAACCTGTGTACTCGAAGTCTTCAGTGAAGTGGCTGCTCTCTTCAGGCTCTGCTGAG 360
467 GTGGGTGATGGAGGGCCAGCCCTCTTCCTCAGGTGCCATGGTGGAGGAACCTGGGATGTG 526
361 GTGGGTGATGGAGGGCCAGCCCTCTTCCTCAGGTGCCATGGTGGAGGAACCTGGGATGTG 420
527 TACAAGGTGATCTATTATAAGGATGGTGAAGCTCTCAAGTACTCTGATATGAGAACCAAC 586
421 TACAAGGTGATCTATTATAAGGATGGTGAAGCTCTCAAGTACTCTGATATGAGAACCAAC 480
587 ATCTCATTAACAATGCCACAGTTGAAGACAGTGAAGCTACTACTGTACGGGCAAGTG 646
481 ATCTCATTAACAATGCCACAGTTGAAGACAGTGAAGCTACTACTGTACGGGCAAGTG 540
647 TGGCAGCTGGACTATGAGTCTGAGCCCTCAACATTAAGTCTTAATAAAAGCTCCGCTGAG 706
541 TGGCAGCTGGACTATGAGTCTGAGCCCTCAACATTAAGTCTTAATAAAAGCTCCGCTGAG 600
707 AAGTACTGCTACAATTTTTATCCCATTTGTTGGTGGTGTCTCTTCTGCTGTGACACA 766
601 AAGTACTGCTACAATTTTTATCCCATTTGTTGGTGGTGTCTCTTCTGCTGTGACACA 660
767 GGATTATTATCTCAACTCAGCAGCAGGTCACTTCTTGAAGTAAAGAGAACCAAGG 826
661 GGATTATTATCTCACTCAGCAGCAGGTCACTTCTTGAAGTAAAGAGAACCAAGG 720
827 AAAGGCTTCAGACTTCTGAACCCCACTCTTAAGCCAAACCCCAAAACAACATGA 880
721 AAAGGCTTCAGACTTCTGAACCCCACTCTTAAGCCAAACCCCAAAACAACATGA 774
RESULT 7
US-09-944-277A-5/c
; Sequence 5, Application US/09944277A
; Patent No. US20020034771A1
; GENERAL INFORMATION:
; APPLICANT: Frank, Glenn R.
; Porter, James P.
; Rushlow, Keith E.
; Wassom, Donald L.
; TITLE OF INVENTION: Method to Detect IGE
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carol Talkington Verser, Ph.D.
; STREET: 1825 Sharp Point Drive
; CITY: Fort Collins
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80525
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: WordPerfect for Windows, Version 7.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/944,277A
; FILING DATE: 30-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/285,873
; FILING DATE: 1999-03-31
; ATTORNEY/AGENT INFORMATION:
; NAME: Verser, Carol Talkington
; REGISTRATION NUMBER: 37,459
; REFERENCE/DOCKET NUMBER: DI-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 970/493-7272
; TELEFAX: 970/484-9505
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 774 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..774
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-944-277A-4
Query Match
Best Local Similarity 100.0%; Pred. No. 1.le-182; Gaps 0;
Matches 774; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 107 ATGGCTCTGCGATGGAATCCCTACTCTACTGTGTGTAGCCTTACTGTTCTTCGCTCCA 166
Db 1 ATGGCTCTGCGATGGAATCCCTACTCTACTGTGTGTAGCCTTACTGTTCTTCGCTCCA 60
QY 167 GATGCGGTGTAGCAGTCCCTCAGAACTTAAGTCTCTTGAACCTCCATGGAATAGA 226
Db 61 GATGCGGTGTAGCAGTCCCTCAGAACTTAAGTCTCTTGAACCTCCATGGAATAGA 120
QY 227 ATATTAAAGGAGAGAATGTGACTCTTACATGTAAATGGGAACAATTTCTTTGAAGTCAGT 286
Db 121 ATATTAAAGGAGAGAATGTGACTCTTACATGTAAATGGGAACAATTTCTTTGAAGTCAGT 180
QY 287 TCCACCAATGGTTCACAAATGGGAGCCTTTTCAGAGAGACAAATTCAGTTTGAATATT 346
Db 181 TCCACCAATGGTTCACAAATGGGAGCCTTTTCAGAGAGACAAATTCAGTTTGAATATT 240
QY 347 GTGAATGCCAAATTTGAAGACAGTGGAGAATACAAATGTTCAGCACCAACCAAGTTAATGAG 406
Db 241 GTGAATGCCAAATTTGAAGACAGTGGAGAATACAAATGTTCAGCACCAACCAAGTTAATGAG 300
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SEQUENCE CHARACTERISTICS:
LENGTH: 774 nucleotides
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-944-277A-5

Query Match      64.6%; Score 774; DB 9; Length 774;
Best Local Similarity 100.0%; Pred. No. 1.1e-182;
Matches 774; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 107 ATGCTCTCCGATGGAATCCCTACTCTACTGTGTAGCTTCTTTCGCTCCA 166
Db 774 ATGCTCTCCGATGGAATCCCTACTCTACTGTGTAGCTTCTTTCGCTCCA 715
Qy 167 GATGGCGTGTAGCAGTCCCTCAGAAACCTTAAGTCTCTTGAACCCCTCATGGAATAGA 226
Db 714 GATGGCGTGTAGCAGTCCCTCAGAAACCTTAAGTCTCTTGAACCCCTCATGGAATAGA 655
Qy 227 ATATTTAAAGAGAGAAATGATCTTTACATGTAATGGGAACAATTTCTTTGAAGTCAGT 286
Db 654 ATATTTAAAGAGAGAAATGATCTTTACATGTAATGGGAACAATTTCTTTGAAGTCAGT 595
Qy 287 TCACACAAATGGTTCCAAATGGCAGCCTTTCAAGAGAGACAAATTCAGATTTGAATATT 346
Db 594 TCACACAAATGGTTCCAAATGGCAGCCTTTCAAGAGAGACAAATTCAGATTTGAATATT 535
Qy 347 GTGAATGCCAAATTTGAAGACAGTGGAGAAATCAAAATGTCAGACCAACAAGTTAATGAG 406
Db 534 GTGAATGCCAAATTTGAAGACAGTGGAGAAATCAAAATGTCAGACCAACAAGTTAATGAG 475
Qy 407 AGTGAACCTGTGTACCTGGAAGCTTTCAGTGAAGTGGCTGCTCTTCAGGCTCTGCTGAG 466
Db 474 AGTGAACCTGTGTACCTGGAAGCTTTCAGTGAAGTGGCTGCTCTTCAGGCTCTGCTGAG 415
Qy 467 GTGGTATGAGGGCCAGCCCTCTTCTCAGGTGCCANGSTTGGAGAACTGGGATGTG 526
Db 414 GTGGTATGAGGGCCAGCCCTCTTCTCAGGTGCCANGSTTGGAGAACTGGGATGTG 355
Qy 527 TACAGGTGATCTATTATAGGATGGTGAAGCTCTCAAGTACTCTGATGAGACCAAC 586
Db 354 TACAAGGTGATCTATTATAGGATGGTGAAGCTCTCAAGTACTCTGATGAGACCAAC 295
Qy 587 ATCTCCATTACAAATGCCAGTTGAAGACAGTGGAACTTACTGTACGGGCAAGTG 646
Db 294 ATCTCCATTACAAATGCCAGTTGAAGACAGTGGAACTTACTGTACGGGCAAGTG 235
Qy 647 TGGCAGCTGACATAGAGTCTGAGCCCTCAACATTAATTAATAAAGCTCCGCGTGAG 706
Db 234 TGGCAGCTGACATAGAGTCTGAGCCCTCAACATTAATTAATAAAGCTCCGCGTGAG 175
Qy 707 AAGTACTGGCTACAAATTTTATCCCATTTCTGGTGGTGAATCTGTTGCTGGACACA 766
Db 174 AAGTACTGGCTACAAATTTTATCCCATTTCTGGTGGTGAATCTGTTGCTGGACACA 115
Qy 767 GGATTTATTTATCTCAACTCAGCAGCAGGTCAATTTCTTCTTGAAGATTAAGAGAACAGG 826
Db 114 GGATTTATTTATCTCAACTCAGCAGCAGGTCAATTTCTTCTTGAAGATTAAGAGAACAGG 55
Qy 827 AAGGCTTCAGACTCTTGAACCCACATCTTAAGCCAAACCCCAAAACAACTGA 880
Db 54 AAGGCTTCAGACTCTTGAACCCACATCTTAAGCCAAACCCCAAAACAACTGA 1
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```
RESULT 8
US-09-944-277A-7
; Sequence 7, Application US/09944277A
; Patent No. US20020034771A1
; GENERAL INFORMATION:
; APPLICANT: Frank, Glenn R.
; Porter, James P.
```

```
;
; Rushlow, Keith E.
; Wasson, Donald L.
TITLE OF INVENTION: Method to Detect IGE
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Carol Talkington Verser, Ph.D.
Heska Corporation
STREET: 1825 Sharp Point Drive
CITY: Fort Collins
STATE: Colorado
COUNTRY: USA
ZIP: 80525
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: WordPerfect for Windows, Version 7.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/944,277A
FILING DATE: 30-Aug-2001
CLASSIFICATION: <unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/285,873
FILING DATE: 1999-03-31
ATTORNEY/AGENT INFORMATION:
NAME: Verser, Carol Talkington
REGISTRATION NUMBER: 37,459
REFERENCE/DOCKET NUMBER: DI-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 970/493-7272
TELEFAX: 970/484-9505
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 699 nucleotides
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..699
SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-09-944-277A-7

Query Match      58.3%; Score 699; DB 9; Length 699;
Best Local Similarity 100.0%; Pred. No. 5.7e-164;
Matches 699; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 182 GTCCCTCAGAAACCTTAAGTCTCTTGAACCCCTCCATGGAATAGAAATTTAAAGGAGAG 241
Db 1 GTCCCTCAGAAACCTTAAGTCTCTTGAACCCCTCCATGGAATAGAAATTTAAAGGAGAG 60
Qy 242 AATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGTTCCACCAAAATGGTTC 301
Db 61 AATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGTTCCACCAAAATGGTTC 120
Qy 302 CACAATGGCAGCTTTCAGAAAGACAAATTCAGTTTGAATATTTGTAATGCCAAATTT 361
Db 121 CACAATGGCAGCTTTCAGAAAGACAAATTCAGTTTGAATATTTGTAATGCCAAATTT 180
Qy 362 GAAGACAGTGGAGAAATACAAATGTGAGCAACAAAGTTAATGAGAGTGAACCTGTGTAC 421
Db 181 GAAGACAGTGGAGAAATACAAATGTGAGCAACAAAGTTAATGAGAGTGAACCTGTGTAC 240
Qy 422 CTGGAAGTCTTCAGTGAAGTGTGCTCTCTCAGGCTCTGCTGAGGCTGTGATGGAGGCG 481
Db 241 CTGGAAGTCTTCAGTGAAGTGTGCTCTCTCAGGCTCTGCTGAGGCTGTGATGGAGGCG 300
Qy 482 CAGCCCTCTTCTCAGGTGCTGCTGCTGAGGAGTGGATGTTGAGGAGTGTATCTAT 541
Db 301 CAGCCCTCTTCTCAGGTGCTGCTGCTGAGGAGTGGATGTTGAGGAGTGTATCTAT 360
Qy 542 TATAAGGATGGTGAAGCTCTCAAGTACTGTGATGAGAACCAACATCTCCATTACAAAT 601
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Db 361 TATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCAACAATCTCCATTACAAAT 420
QY 602 GCCACAGTTGAAGACAGTGAACCTACTACTGTACGGGCAAAAGTGTGGCAGCTGGACTAT 661
Db 421 GCCACAGTTGAAGACAGTGAACCTACTACTGTACGGGCAAAAGTGTGGCAGCTGGACTAT 480
QY 662 GAGCTGAGCCCTCAACATTAAGTCTATATTAAGCTCCGGTGAAGAGTACTGGCTACAA 721
Db 481 GAGCTGAGCCCTCAACATTAAGTCTATATAAAGCTCCGGTGAAGAGTACTGGCTACAA 540
QY 722 TTTTATATCCCATTTGCTGGTGGTATCTGTTTCTGTGGACACAGGATTTATCTCA 781
Db 541 TTTTATATCCCATTTGCTGGTGGTATCTGTTTCTGTGGACACAGGATTTATCTCA 600
QY 782 ACTGAGCAGCGGTACATTTCTCTTGAAGATTAAGAACCCAGGAAGGCTTCAGACTT 841
Db 601 ACTGAGCAGCGGTACATTTCTCTTGAAGATTAAGAACCCAGGAAGGCTTCAGACTT 660
QY 842 CTGAACCCACATCTCTAAGCCCAAAACCCCAAAACCAACTGA 880
Db 661 CTGAACCCACATCTCTAAGCCCAAAACCCCAAAACCAACTGA 699

RESULT 9

US-10-236-392-29
; Sequence 29, Application US/10236392
; Publication No. US20040067490A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, David W
; APPLICANT: Boldog, Ferenc L
; APPLICANT: Burgess, Catherine, E
; APPLICANT: Casman, Stacie J
; APPLICANT: Catterton, Elina
; APPLICANT: Chapoval, Andrei
; APPLICANT: Crabtree, Julie
; APPLICANT: Edinger, Shlomit, R
; APPLICANT: Ellerman, Karen
; APPLICANT: Gerlach, Valerie
; APPLICANT: Gorman, Linda
; APPLICANT: Grosse, William M
; APPLICANT: Gusev, Vladimir
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Laroche, William J
; APPLICANT: Li, Li
; APPLICANT: MacDougall, John R
; APPLICANT: Malyankar, Uriel M
; APPLICANT: Miller, Charles E
; APPLICANT: Millet, Isabelle
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Patturajan, Meera
; APPLICANT: Pena, Carol A
; APPLICANT: Peyman, John A
; APPLICANT: Rastelli, Luca
; APPLICANT: Reiger, Daniel K
; APPLICANT: Rothenberg, Mark E
; APPLICANT: Shenoy, Suresh
; APPLICANT: Shimkets, Richard A
; APPLICANT: Smithson, Glenda
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-442A
; CURRENT APPLICATION NUMBER: US/10/236,392
; CURRENT FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: US09/540,763
; PRIOR FILING DATE: 2000-03-30
; PRIOR APPLICATION NUMBER: US60/390,155
; PRIOR FILING DATE: 2002-06-19
; PRIOR APPLICATION NUMBER: US09/635,949
; PRIOR FILING DATE: 2000-08-10
; PRIOR APPLICATION NUMBER: US60/318,765
; PRIOR FILING DATE: 2001-09-12
; PRIOR APPLICATION NUMBER: US60/357,303
; PRIOR FILING DATE: 2002-02-15

; PRIOR APPLICATION NUMBER: US60/367,753
; PRIOR FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER: US60/369,479
; PRIOR FILING DATE: 2002-04-02
; PRIOR APPLICATION NUMBER: US09/659,634
; PRIOR FILING DATE: 2000-09-12
; PRIOR APPLICATION NUMBER: US60/318,120
; PRIOR FILING DATE: 2001-09-07
; PRIOR APPLICATION NUMBER: US60/318,130
; PRIOR FILING DATE: 2001-09-07
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 794
; SOFTWARE: Custom
; SEQ ID NO 29
; LENGTH: 757
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (26)..(680)
US-10-236-392-29
Query Match 52.6%; Score 630; DB 13; Length 757;
Best Local Similarity 86.6%; Pred. No. 1e-146; Indels 117; Gaps 1;
Matches 757; Conservative 0; Mismatches 0
QY 82 TAAGCACCAGGAGTCCATGAAGAGATGGCTCTCCATGGAATCCCTACTCTACTGTG 141
Db 1 TAAGCACCAGGAGTCCATGAAGAGATGGCTCTCCATGGAATCCCTACTCTACTGTG 60
QY 142 TGTAGCCTTACTGTCTTCGCTCCAGATGGCGTGTAGCAGTCCCTCGAAGACCTTAAGGT 201
Db 61 TGTAGCCTTACTGTCTTCGCTCCAGATGGCGTGTAGCAGTCCCTCGAAGACCTTAAGGT 120
QY 202 CTCCTTGAACCCCTCCATGGAATAGAAATATTTAAAGAGAGAGATGTGACTCTTACATGTAA 261
Db 121 CTCCTTGAACCCCTCCATGGAATAGAAATATTTAAAGAGAGAGATGTGACTCTTACATGTAA 180
QY 262 TCGGAACAATTTCTTTGAAGTCAGTTCACCAATGGTTCCCAATGGCAGCCCTTCAGA 321
Db 181 TCGGAACAATTTCTTTGAAGTCAGTTCACCAATGGTTCCCAATGGCAGCCCTTCAGA 240
QY 322 AGAGACAAATTCAGTTTGAATATTTGCAATGCCAAATTTGAAGACAGTGGAGATACAA 381
Db 241 AGAGACAAATTCAGTTTGAATATTTGCAATGCCAAATTTGAAGACAGTGGAGATACAA 300
QY 382 ATGTGAGCACCACCAAGTTAATGAGAGTGAACCTGTGTACCTGGAAGTCTTCAGTGACTG 441
Db 301 A-----TG 303
QY 442 GCTGTCTCTTCAAGGCTCTGCTGAGGTGGTATGAGGGCCAGCCCTCTTCTCCAGGTG 501
Db 302 -----TG 303
QY 502 CCATGTTTGGAGAACTGGGATGTGTACAAGGTGATCTATTATAGAGTGGTGAAGCTCT 561
Db 304 CCATGTTTGGAGAACTGGGATGTGTACAAGGTGATCTATTATAGAGTGGTGAAGCTCT 363
QY 562 CAACTACTGTTATGAGAACCAACAATCTCCATTAACAATGCCACAGTTGAAGACAGTGG 621
Db 364 CAACTACTGTTATGAGAACCAACAATCTCCATTAACAATGCCACAGTTGAAGACAGTGG 423
QY 622 AACCTACTACTGTACGGCAAGTGTGGCAGTGGACTATGAGTGTAGCCCTCAACAT 681
Db 424 AACCTACTACTGTACGGCAAGTGTGGCAGTGGACTATGAGTGTAGCCCTCAACAT 483
QY 682 TACTGTATAAAGCTCCGCGTGAAGATCTCTGGCTACAATTTTATCCCATTTGTTGGT 741
Db 484 TACTGTATAAAGCTCCGCGTGAAGATCTCTGGCTACAATTTTATCCCATTTGTTGGT 543
QY 742 GGTGATTTCTGTTTGTGGACACAGGATTTATTTATCTCAACTCAGCAGGAGTCAACAT 801
Db 544 GGTGATTTCTGTTTGTGGACACAGGATTTATTTATCTCAACTCAGCAGGAGTCAACAT 603

INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1015 nucleotides
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 12..776
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-434-817-1

Query Match 48.3%; Score 578.8; DB 16; Length 1015;
Best Local Similarity 75.5%; Pred. No. 7.4e-134;
Matches 764; Conservative 0; Mismatches 232; Indels 16; Gaps 3;

QY 96 CCATGAAGAAGTGGCTCCCTCCCATGGAATCCCTACTCTACTCTGTGTAGCCCTTACTGT 155
DB 1 CCACAGAGAGATGCTCTCCCATGGGAAGCCCTGCCCTGCTGTGATTAACCTTTCTGC 60
QY 156 TCTTGGCTCCAGATGGCGGTGTAGCAGTCCCTCAGAAACCTTAAGTCTCTTGAACCCCTC 215
DB 61 TCTTCTCTGTGATGGCGGTGCAGCAGCATCCGGAATCTACAGTGTCTTGAATCCCTC 120
QY 216 CATGGAATAGAAATATTAAAGGAGAGATGTGACTCTTACATGTAAATGGGAACAATTTCT 275
DB 121 CATGGAATAGAAATATTTCAGGAGAGAAATGTGACTCTTACATGTAAATGAAGAACAGCCCTC 180
QY 276 TTGAAGTCAGTTCACCAAAATGGTTCCACATGTCAGCGCTTTTCAGAAAGAGACAAATTCAA 335
DB 181 TTAAGGAACTCACTCAGTGGACCTACAACACACCACTTTAGAAGTGAACACTTCAA 240
QY 336 GTTTGAATATTGTGAATGCCAAATTTGAAGACAGTGGAGAAATACAAATGTGACACCAAC 395
DB 241 GTTTGAACATCACTAATGCCCTCACACCGGAGCAGTGGGGAATACAGATGTGCGGAACAATG 300
QY 396 AAGTTAATGAGATGAACCTGTGTACTGTGAAGTCTTCAGTGAAGTGTGCTCTCTTCAGG 455
DB 301 ACTTGAACCTGAGTGAAGCTGTGACCTGAGAGTTTCAGTGAAGTGTGCTCTCTTCAGG 360
QY 456 CCTCTGTGAGTGGTGTAGTGAAGGCGCAGCCCTCTTCTCAGTGTGCTGCTGTGAGGA 515
DB 361 CCTCTGTGAGGAGTGTAGTGAAGGCGTGAAGGCGCTCTCAGTGTGCTGCTGTGAGG 420
QY 516 ACTGGATGTGTAAAGTGTATCTATTATAAGGATGTGAGTCTCAAGTACTGTGTATG 575
DB 421 ATTGGGAGCTCTTCAAGGTGTATCTACTACAGGATGGCAACCCCTCGAGTACTGTGTATG 480
QY 576 AGAACCAACAATCTCCATTAACAATGCCAGTTGAAGACAGTGAACCTTACTACTGTA 635
DB 481 AGAACAAAACATCTCCATTTGAAGTGCACACAGAAAACAGTGGCACCTATTACTGG 540
QY 636 CGGG-----CAAAGTGTGGAGCTGGAGCTATGAGTCTGAGCCCTCAACATTA 683
DB 541 AGGTTGCTTTTAACTTTAAGCGAAACAAGTGAACCTATACCTCTGATTACCTCAACATTA 600
QY 684 CTGTAATAAAGCTCCGCG-----GTGAGAAGTACTGGCTACAAATTTTTATCCCATTTGG 740
DB 601 CTGTAATAAAGCTGTGAGCAAGCAACGCTACTGGCTACAAATTTATTTATTTCTG 660
QY 741 TGGTGAATCTTTTGTGTGGACACAGGATTTATTTATCTCAACTCAGCAGAGGTACAT 800
DB 661 TGGTGAATCTTTTGTGTGGACACAGGATTTTGTGTGTGTCGACCCAGCAGGTAAACAT 720
QY 801 TTCTCTTGAAGATTAAAGACACAGGAAGCTTTCAGACTTCTGAACCCACATCC--TAAG 859
DB 721 TTCTCTTGAAGATTAAAGAGCCAGGAGAGCAAACTTATGAGCCCCCTCTTTAAG 780
QY 860 CCAAAACCCCAAAACAACTGTATATAATTTACTTCAAGAAATATTGTCAACATTTATTTT 919
DB 781 TGAGACCCGAGAAAGAACTGTATGTCACTGTCTCAAGAAACCTTTTGAACAGCAATTTCTTC 840

RESULT 12
US-10-434-817-3/c
; Sequence 3, Application US/10434817
; Publication No. US20030235579A1
; GENERAL INFORMATION:
; APPLICANT: Weber, Eric R.
; TITLE OF INVENTION: NOVEL EQUINE PC EPSILON RECEPTOR ALPHA
; CHAIN NUCLEIC ACID MOLECULES, PROTEINS AND USES THEREOF
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Heska Corporation
; STREET: 1825 Sharp Point Drive
; CITY: Fort Collins
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80525
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect for Windows, Version 7.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/434,817
; FILING DATE: 08-May-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/015,734
; FILING DATE: 29-JAN-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Verser, Carol Talkington
; REGISTRATION NUMBER: 37,459
; REFERENCE/DOCKET NUMBER: DI-4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 970/493-7272
; TELEFAX: 970/484-9505
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1015 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-10-434-817-3

Query Match 48.3%; Score 578.8; DB 16; Length 1015;
Best Local Similarity 75.5%; Pred. No. 7.4e-134;
Matches 764; Conservative 0; Mismatches 232; Indels 16; Gaps 3;

QY 96 CCATGAAGAAGTGGCTCCCTCCCATGGAATCCCTACTCTACTGTGTAGCCCTTACTGT 155
DB 1015 CCACAGAGAGATGCTCTCCCATGGGAAGCCCTGCCCTGCTGTGATTAACCTTTCTGC 956
QY 156 TCTTGGCTCCAGATGGCGGTGTAGCAGTCCCTCAGAAACCTTAAGTCTCTTGAACCCCTC 215
DB 955 TCTTCTCTGTGATGGCGGTGCAGCAGCATCCGGAATCTACAGTGTCTTGAATCCCC 896
QY 216 CATGGAATAGAAATATTAAAGGAGAGAAATGTGACTCTTACATGTAAATGGGAACAATTTCT 275

Db 895 CATGGAATAGATATTTTCGAGGAGAGAAATGTGACTCTTACATGTAATTAAGAACAGGCC 836
Qy 276 TTGAAGTCAGTTCCACCAATAGTTCCACATGGGAGCCTTTTCAGAGAGAGACAAATTCAA 335
Db 835 TTAAGGCACTCCACTGAGTGGACCTACACACACACCACTTTAGAAAGTGAACATTCAA 776
Qy 336 GTTTGAATATTTGAATGCCAAATTTGAAGACAGTGGAGAAATACAAATGTCAAGCCAC 395
Db 775 GTTTGACATCACTAATGCTCACACGGAGCAGTGGGAATACAGATGTCGGAACAATG 716
Qy 396 AAGTTAATAGAGTGAACCTGTGTACTGGAAGTCTTTCAGTGAAGTGGCTGCTCTTCAGG 455
Db 715 ACTTGAACCTGAGTGAAGCTGTGACCTAGAAAGTTTTCAGTGAAGTGGCTGCTCTTCAGG 656
Qy 456 CCTCTGCTGAGGTTGTGATGAGGGGCGAGCCCTCTTCTCAGGTCCATGTTGGAGGA 515
Db 655 CCTCTGCTGAGGAGGTCATAGAGGTAAGGCCCTCGTTCTCAGGTCGCTGGCTGGAAG 596
Qy 516 ACTGGATGTGTAACAAGGTGATCTATTATAAGGATGGTGAAGTCTCAAGTACTGTATG 575
Db 595 ATTGGGACGCTTCAAGGTGATCTACTACAAGGATGGCAACCCCTCGAGTACTGTATG 536
Qy 576 AGAACGACATCTCCATTAACAATGCCACAGTTGAAGACAGTGGAACTACTACTGTA 635
Db 535 AGAACAAAACATCTCCATTTGAAGTGGCCACACAGAAACAGTGGCACCCTATTCTGCG 476
Qy 636 CCGG-----CAAGTGTGCGAGCTGAGCTATGAGTCTGAGCCCTCAACATTA 683
Db 475 AGGTGCTTTTAACTTTAAGCGAACAGTGAACGCTATACCTCTGATTACCTCAACATTA 416
Qy 684 CTGTAATAAAGCTCCG-----GTGAGAAGTACTGGGTACAAATTTTATCCCATTTG 740
Db 415 CTGTAAAAAAGCTGAGCAAGCAAGCAAGCTACTGGCTACAAATTTATTTCATTTG 356
Qy 741 TGGTATCTGTTGCTGCGACACAGGATTTATTTCTCAACTCAGCAGCAGGTCAACAT 800
Db 355 TGGTATCTGTTGCTGCGACACAGGATTTATTTCTCGACCCAGCAGGTAAACAT 296
Qy 801 TTCTTTGAAGATTAAGAGAACAGCAAGCTTTCAGACTCTGAACCCACATCC-TAAG 859
Db 295 TTCTTTGAAGATTAAGAGAACAGCAAGCTTTCAGACTCTGAACCCACATCC-TAAG 236
Qy 860 CCAACCCCAAAACACTATATATTAATCTCAAGAAATTTTTCAGACTCTGTTT 919
Db 235 TGAGACCCGAGAAGAACTGATGCTCTCAAGAAACCTTTGCAACAGCAATTTCTTC 176
Qy 920 CCAGCATCAGCAATTTGCTACTCAATTTGCAACACAGCTTGCATATATACATGAAGCGTC 979
Db 175 CTGGCATCAGCAATTTGCTACTCAATTTGCAACACAGCTTGCATATATACATGAAGCGTC 116
Qy 980 TGTGCTCAAGATTTAAGAAATGCTTTCATTAACCTGAGTGAACCTGGTTAAGTGGCATG 1039
Db 115 TATGCCACCGCTTTGCAAGATTTGCATCATTAACCTAACTAGAACTGGTTAAGTGGCATG 56
Qy 1040 TAATAGTAAGTCTCAATTAACATTTGTTGTAATAAATGAGAGATGAATAGA 1091
Db 55 TAATAGTAAGTCTCAATTAACATTTTAAATAAATATATAAAAAA 4

RESULT 13
US-09-809-715-1
; Sequence 1, Application US/09809715
; Publication No. US20030003502A1
; GENERAL INFORMATION:
; APPLICANT: Jaretzky, Theodore S.
; APPLICANT: Garman, Scott Clayton
; APPLICANT: Wurzburg, Beth A.
; APPLICANT: Kinet, Jean-Pierre
; TITLE OF INVENTION: THREE-DIMENSIONAL MODEL OF A COMPLEX BETWEEN A PC
; TITLE OF INVENTION: EPSILON RECEPTOR ALPHA CHAIN AND A PC REGION OF AN IGE
; TITLE OF INVENTION: ANTIBODY AND USES THEREOF
; FILE REFERENCE: AL-8
; CURRENT APPLICATION NUMBER: US/09/809,715

; CURRENT FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: 60/189,853
; PRIOR FILING DATE: 2000-03-15
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 1
; LENGTH: 528
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(528)
US-09-809-715-1

Query Match 44.1%; Score 528; DB 10; Length 528;
Best Local Similarity 100.0%; Pred.No. 2.4e-121;
Matches 528; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 182 GTCCCTCAGAAACCTAAGGTCTCTTGAACCCCTCCATGGAATAGAAATTTTAAAGGAGAG 241
Db 1 GTCCCTCAGAAACCTAAGGTCTCTTGAACCCCTCCATGGAATAGAAATTTTAAAGGAGAG 60
Qy 242 AATGTGACTCTTACATGTAATGGGAAACAATTTCTTGAAGTCAGTTCACCAAAATGGTTC 301
Db 61 AATGTGACTCTTACATGTAATGGGAAACAATTTCTTGAAGTCAGTTCACCAAAATGGTTC 120
Qy 302 CACAATGCCACCTTTTCAGAAAGACAAATTCAGATTTGAATATTTGGAATGCCAAATTT 361
Db 121 CACAATGCCACCTTTTCAGAAAGACAAATTCAGATTTGAATATTTGGAATGCCAAATTT 180
Qy 362 GAAGACAGTGGAGATACAAATGTGAGCAACCAAGTAAATGAGTGAACCTGTGTAC 421
Db 181 GAAGACAGTGGAGATACAAATGTGAGCAACCAAGTAAATGAGTGAACCTGTGTAC 240
Qy 422 CTGGAAGTCTTTCAGTGAAGTGGCTCTCTTCAGGCTCTGCTGAGGTGGTGAAGGAGGC 481
Db 241 CTGGAAGTCTTTCAGTGAAGTGGCTCTCTTCAGGCTCTGCTGAGGTGGTGAAGGAGGC 300
Qy 482 CAGCCCTCTTCTCAGTGGCCATGGTTGGAGGAACCTGGATGTGACAGGTGATCTAT 541
Db 301 CAGCCCTCTTCTCAGTGGCCATGGTTGGAGGAACCTGGATGTGACAGGTGATCTAT 360
Qy 542 TATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCAACACATCTCCATTACAAAT 601
Db 361 TATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCAACACATCTCCATTACAAAT 420
Qy 602 GCCACAGTTGAAGACAGTGGAACTTACTGTCAGGGCAAGTGTGACAGTGGACTAT 661
Db 421 GCCACAGTTGAAGACAGTGGAACTTACTGTCAGGGCAAGTGTGACAGTGGACTAT 480
Qy 662 GAGTCTGAGCCCTCAACATTAACCTGTAATAAAGCTCCGCTGAGAG 709
Db 481 GAGTCTGAGCCCTCAACATTAACCTGTAATAAAGCTCCGCTGAGAG 528

RESULT 14
US-10-293-992-1
; Sequence 1, Application US/10293992
; Publication No. US20040003527A1
; GENERAL INFORMATION:
; APPLICANT: Jaretzky, Theodore S.
; APPLICANT: Garman, Scott Clayton
; APPLICANT: Kinet, Jean-Pierre
; TITLE OF INVENTION: METHODS OF USING A THREE-DIMENSIONAL MODEL OF A PC
; TITLE OF INVENTION: CHAIN
; FILE REFERENCE: AL-3-CI-1
; CURRENT APPLICATION NUMBER: US/10/293,992
; CURRENT FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: 09/434,193
; PRIOR FILING DATE: 1999-11-04
; PRIOR APPLICATION NUMBER: 60/107,219
; PRIOR FILING DATE: 1998-11-05
; NUMBER OF SEQ ID NOS: 6

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; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 528
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(528)
; OTHER INFORMATION:
US-10-293-992-1

Query Match
Best Local Similarity 44.1%; Score 528; DB 13; Length 528;
Matches 528; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 182 GTCCCTCAGAACCTTAAGTCTCCTTGAACCTTCATGGAATAGAAATATTTAAAGGAGAG 241
Db 1 GTCCCTCAGAACCTTAAGTCTCCTTGAACCTTCATGGAATAGAAATATTTAAAGGAGAG 60

QY 242 AATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGTTCACCAAAATGGTTC 301
Db 61 AATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGTTCACCAAAATGGTTC 120

QY 302 CACAATGGCAGCCTTTTCAGAGAGACAAATTCAGTTTGAATATTTGAATGCAATGCAAAATTT 361
Db 121 CACAATGGCAGCCTTTTCAGAGAGACAAATTCAGTTTGAATATTTGAATGCAATGCAAAATTT 180

QY 362 GAAGACAGTGGAGATACAAATGTGACCAACAAGTTAATGAGAGTGAACCTGTGTAC 421
Db 181 GAAGACAGTGGAGATACAAATGTGACCAACAAGTTAATGAGAGTGAACCTGTGTAC 240

QY 422 CTGGAAGTCTTTCAGTGAAGTGGTCTCTTTCAGGCTCTCTGTCAGGCTGGTGGTGGAGGC 481
Db 241 CTGGAAGTCTTTCAGTGAAGTGGTCTCTTTCAGGCTCTCTGTCAGGCTGGTGGTGGAGGC 300

QY 482 CAGCCCTCTTCTCAGTGCATGTTGGAGGAACCTGGGATGTGTACAAGGTGATCTAT 541
Db 301 CAGCCCTCTTCTCAGTGCATGTTGGAGGAACCTGGGATGTGTACAAGGTGATCTAT 360

QY 542 TATAAGGATGGTGAAGCTCTCAAGTACTGTTGAGAACCAACAACATCTCCATTACAAAT 601
Db 361 TATAAGGATGGTGAAGCTCTCAAGTACTGTTGAGAACCAACAACATCTCCATTACAAAT 420

QY 602 GCCACAGTTGAAGACAGTGAAGTCTTCTGTTACGGGCAAAAGTGGGAGCTGGACTAT 661
Db 421 GCCACAGTTGAAGACAGTGAAGTCTTCTGTTACGGGCAAAAGTGGGAGCTGGACTAT 480

QY 662 GAGTCTGAGCCCTCAACATTACTGTAATAAAGCTCCGGTGAAGAAG 709
Db 481 GAGTCTGAGCCCTCAACATTACTGTAATAAAGCTCCGGTGAAGAAG 528
```

RESULT 15

```
US-09-944-277A-12
; Sequence 12, Application US/09944277A
; Patent No. US20020034771A1
; GENERAL INFORMATION:
; APPLICANT: Frank, Glenn R.
; Porter, James P.
; Rushlow, Keith E.
; Wassom, Donald L.
; TITLE OF INVENTION: Method to Detect IgE
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carol Talkington Verser, Ph.D.
; Heska Corporation
; STREET: 1825 Sharp Point Drive
; CITY: Fort Collins
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80525
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
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; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: WordPerfect for Windows, Version 7.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/944,277A
; FILING DATE: 30-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/285,873
; FILING DATE: 1999-03-31
; ATTORNEY/AGENT INFORMATION:
; NAME: Verser, Carol Talkington
; REGISTRATION NUMBER: 37,459
; REFERENCE/DOCKET NUMBER: DI-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 970/493-7272
; TELEFAX: 970/484-9505
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 516 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..516
; SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-09-944-277A-12

Query Match
Best Local Similarity 43.1%; Score 516; DB 9; Length 516;
Matches 516; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 182 GTCCCTCAGAACCTTAAGTCTCCTTGAACCTTCATGGAATAGAAATATTTAAAGGAGAG 241
Db 1 GTCCCTCAGAACCTTAAGTCTCCTTGAACCTTCATGGAATAGAAATATTTAAAGGAGAG 60

QY 242 AATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGTTCACCAAAATGGTTC 301
Db 61 AATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGTTCACCAAAATGGTTC 120

QY 302 CACAATGGCAGCCTTTTCAGAGAGACAAATTCAGTTTGAATATTTGAATGCAATGCAAAATTT 361
Db 121 CACAATGGCAGCCTTTTCAGAGAGACAAATTCAGTTTGAATATTTGAATGCAATGCAAAATTT 180

QY 362 GAAGACAGTGGAGATACAAATGTGACCAACAAGTTAATGAGAGTGAACCTGTGTAC 421
Db 181 GAAGACAGTGGAGATACAAATGTGACCAACAAGTTAATGAGAGTGAACCTGTGTAC 240

QY 422 CTGGAAGTCTTTCAGTGAAGTGGTCTCTTTCAGGCTCTCTGTCAGGCTGGTGGTGGAGGC 481
Db 241 CTGGAAGTCTTTCAGTGAAGTGGTCTCTTTCAGGCTCTCTGTCAGGCTGGTGGTGGAGGC 300

QY 482 CAGCCCTCTTCTCAGTGCATGTTGGAGGAACCTGGGATGTGTACAAGGTGATCTAT 541
Db 301 CAGCCCTCTTCTCAGTGCATGTTGGAGGAACCTGGGATGTGTACAAGGTGATCTAT 360

QY 542 TATAAGGATGGTGAAGCTCTCAAGTACTGTTGAGAACCAACAACATCTCCATTACAAAT 601
Db 361 TATAAGGATGGTGAAGCTCTCAAGTACTGTTGAGAACCAACAACATCTCCATTACAAAT 420

QY 602 GCCACAGTTGAAGACAGTGAAGTCTTCTGTTACGGGCAAAAGTGGGAGCTGGACTAT 661
Db 421 GCCACAGTTGAAGACAGTGAAGTCTTCTGTTACGGGCAAAAGTGGGAGCTGGACTAT 480

QY 662 GAGTCTGAGCCCTCAACATTACTGTAATAAAGCT 697
Db 481 GAGTCTGAGCCCTCAACATTACTGTAATAAAGCT 516
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Search completed: October 11, 2004, 01:41:39
Job time : 700.935 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 10, 2004, 11:14:29 ; Search time 4042.38 Seconds
(without alignments)

8849.962 Million cell updates/sec

Title: US-10-763-400-1

Perfect score: 1198
Sequence: 1 tactaagagtcctccagcatc.....aaaaaaaaaaaaaaaaaaaaa 1198

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST:*

1: em_estba:*

2: em_esthum:*

3: em_estin:*

4: em_estmu:*

5: em_estov:*

6: em_estpl:*

7: em_estro:*

8: em_hic:*

9: gb_est1:*

10: gb_est2:*

11: gb_est3:*

12: gb_est4:*

13: gb_est5:*

14: gb_est6:*

15: em_estin:*

16: em_estom:*

17: em_gss_hum:*

18: em_gss_inv:*

19: em_gss_pln:*

20: em_gss_vrt:*

21: em_gss_fun:*

22: em_gss_mam:*

23: em_gss_mus:*

24: em_gss_pro:*

25: em_gss_rod:*

26: em_gss_phg:*

27: em_gss_vrl:*

28: gb_gss1:*

29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
c 1	750.6	62.7	768	13	BQ573778
c 2	719.8	60.1	810	12	BG542554
c 3	690.6	57.6	707	14	CA448745
c 4	688.4	57.5	712	14	CA419024

c 5	640	53.4	669	10	AW612525
c 6	637	53.2	834	10	BF679057
c 7	596.8	49.8	615	12	BM991911
c 8	586.6	49.0	840	12	BG548515
c 9	577	48.2	760	12	BG542157
c 10	523.6	43.7	846	10	BF678252
c 11	494.6	41.3	540	9	AI685796
c 12	484.8	40.5	488	13	EX110472
c 13	478.8	40.0	570	9	AI676114
c 14	464	38.7	478	12	BQ005218
c 15	455	38.0	479	10	BF593204
c 16	441.2	36.8	446	9	AI676097
c 17	438.4	36.6	618	10	BF677190
c 18	342.8	28.8	641	14	CB429248
c 19	342.8	28.6	660	14	CF362072
c 20	311.4	26.0	651	14	CF363368
c 21	289.6	24.2	500	9	AV757598
c 22	286.6	23.9	757	14	CA508723
c 23	272.6	22.8	652	13	BY752906
c 24	224	18.7	264	9	AI765235
c 25	222.8	18.6	394	10	AW357271
c 26	218.8	18.3	422	10	BF603113
c 27	201.8	16.8	255	12	BM966772
c 28	199.2	16.6	483	13	BY593556
c 29	175.8	14.7	403	14	CB768694
c 30	174.4	14.6	1201	9	AL514096
c 31	172.8	14.4	438	13	BY585428
c 32	172.4	14.4	429	13	BY228345
c 33	169.8	14.2	848	14	CB958187
c 34	169.4	14.1	1033	9	AL549464
c 35	169.4	14.1	1201	9	AL531122
c 36	167.8	14.0	874	14	CD244068
c 37	167.8	14.0	1201	13	BY399366
c 38	164.8	13.8	528	14	CB152997
c 39	163.8	13.7	823	12	BI768140
c 40	163	13.6	1201	13	EX402696
c 41	162.6	13.6	403	13	BY228552
c 42	162.6	13.6	404	13	BY227642
c 43	162.6	13.6	1201	9	AL558081
c 44	162.2	13.5	664	14	CB555672
c 45	162.2	13.5	987	13	EX345202

ALIGNMENTS

RESULT 1
BQ573778/c

LOCUS BQ573778 768 bp mRNA linear EST 19-JUN-2002
DEFINITION UI-H-EZO-bav-1-04-0-UI-s1 NCI CGAP Ch1 Homo sapiens cDNA clone
UI-H-EZO-bav-1-04-0-UI 3', mRNA sequence.

ACCESSION BQ573778.1 GI:21477095
VERSION BQ573778.1
KEYWORDS EST.

SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 768)
AUTHORS NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index

JOURNAL Unpublished (1997)

COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaps@mail.nih.gov
Tissue Procurement: Dr. Steven Gitelis/ Rush Presbyterian, Dept. of
Orthopedics

cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
cDNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be obtained
from Dr. M. Bento Soares, bento-soares@uiowa.edu
The following repetitive elements were found in this cDNA

sequence: 1-41, >AT rich#Low complexity (matched complement)
 93-129, >LINE2 (matched complement)
 Seq primer: M13 FORWARD
 POLA=yes.

FEATURES

source
 1. .768
 Location/Qualifiers
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="UI-H-EZ0-Bav-1-04-0-UI"
 /tissue_type="Chondrosarcoma Grade II"
 /dev_stages="Adult"
 /lab_host="DH10B (Life Technologies)"
 /clone_lib="NCI CGAP Ch1"
 /note="Organ: Left Pelvis; Vector: p773-Pac (Pharmacia) with a modified polylinker; Site_1: EcoR I; Site_2: Not I; NCI CGAP Ch1 is a cDNA library containing the following tissue(s): Chondrosarcoma Grade II. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor digested with Not I, and cloned directionally into p773-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is TCATCACGCT.
 TAG TISSUE=grade-2-chondrosarcoma
 TAG LIB=UI-H-EZ0
 TAG_SEQ=ATCTAATATG"

ORIGIN

Query Match 62.7%; Score 750.6; DB 13; Length 768;
 Best Local Similarity 99.3%; Pred. No. 6e-107;
 Matches 753; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 403 TGAGAGTGAACCTGTGACCTGGAGCTTTCAGTGAAGTCTCTTCTGAGTGGAGTGGGCTCTGC 462
 Db 768 TGAGAGTGAACCTGTGACCTGGAGCTTTCAGTGAAGTCTCTTCTGAGTGGAGTGGGCTCTGC 709
 QY 463 TGAGTGTGTGATGAGGCGCCAGCCCTCTTCTCAGTGCCATGCTGGTGGAGTGGGCTGGGA 522
 Db 708 TGAGTGTGTGATGAGGCGCCAGCCCTCTTCTCAGTGCCATGCTGGTGGAGTGGGCTGGGA 649
 QY 523 TGTGTCAAGGTGATCTATTATTAAGGATGGTGAAGCTCTCAAGTACTGTTATGAGAACCA 582
 Db 648 TGTGTCAAGGTGATCTATTATTAAGGATGGTGAAGCTCTCAAGTACTGTTATGAGAACCA 589
 QY 583 CAACATCTCCATTACAATGCCAGTTGAAGCAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAG 642
 Db 588 CAACATCTCCATTACAATGCCAGTTGAAGCAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAG 529
 QY 643 AGTGTGGCAGTGGAGTACTGAGTGTGAGCCCTCAACATTAATCTGTTATTAAGGCTCCGGG 702
 Db 528 AGTGTGGCAGTGGAGTACTGAGTGTGAGCCCTCAACATTAATCTGTTATTAAGGCTCCGGG 469
 QY 703 TGAGAGTACTGGCTACAATTTTATCCCATTTGTTGGTGGTGAATCTGTTCTGCTGGA 762
 Db 468 TGAGAGTACTGGCTACAATTTTATCCCATTTGTTGGTGGTGAATCTGTTCTGCTGGA 409
 QY 763 CACAGGATTAATTAATCTCAATCAGCAGCAGGTCACATTTCTCTTGAAGATTAAGGAAC 822
 Db 408 CACAGGATTAATTAATCTCAATCAGCAGCAGGTCACATTTCTCTTGAAGATTAAGGAAC 349
 QY 823 CAGGAAGGCTTCAGATCTTCGAACCCACATCTCTAAGCCAAACCCCAAAACCAACTGATA 882
 Db 348 CAGGAAGGCTTCAGATCTTCGAACCCACATCTCTAAGCCAAACCCCAAAACCAACTGATA 289
 QY 883 TAATTAATCAAGAAATATTTGCAACATTAAGTATTTTTCAGCATCAGCAATTCCTACTCA 942
 Db 288 TAATTAATCAAGAAATATTTGCAACATTAAGTATTTTTCAGCATCAGCAATTCCTACTCA 229

QY 943 ATTGTCAACACAGCTTGCATATATACATAGAAACGCTCTGCTCAAGGATTTATAGAAAT 1002
 Db 228 ATTGTCAACACAGCTTGCATATATACATAGAAACGCTCTGCTCAAGGATTTATAGAAAT 169
 QY 1003 GCTTCAATTAACCTGAGTGAACCTGGTTAAGTGGCATGTAATAGTAGTCTCAATTAACA 1062
 Db 168 GCTTCAATTAACCTGAGTGAACCTGGTTAAGTGGCATGTAATAGTAGTCTCAATTAACA 109
 QY 1063 TTGGTTGAATAATGAGAGATGAATAGATTCAATTTATTAGCATTTGTTAAAGAGATGTT 1122
 Db 108 TTGGTTGAATAATGAGAGATGAATAGATTCAATTTATTAGCATTTGTTAAAGAGATGTT 49
 QY 1123 CAATTTCAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 1160
 Db 48 CAATTTCAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 11

RESULT 2
 BG542554 810 bp mRNA linear EST 03-APR-2001
 LOCUS 602572052F1 NIH_MGC_77 Homo sapiens cDNA clone IMAGE:4696381 5',
 DEFINITION mRNA sequence.
 ACCESSION BG542554
 VERSION BG542554.1 GI:13534787
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 810)
 AUTHORS NIH-MGC http://mgi.nci.nih.gov/
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: CLONTECH Laboratories, Inc.
 cDNA Library Preparation: CLONTECH Laboratories, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone Distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LCM1523 row: h column: 14
 High quality sequence stop: 667.
 Location/Qualifiers
 1. .810
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:4696381"
 /lab_host="DH10B (TI phage-resistant)"
 /clone_lib="NIH_MGC_77"
 /note="Organ: lung; Vector: pDNR-LIB (Clontech); Site 1: SfiI (ggccattcgcc); Site 2: SfiI (ggccattcgcc); 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CAGGGCCATATGCCC-3', and 3' adaptor sequence: 5'-ATTCTAGAGCGGAGCGCGGACATG-dt(30)BN-3', (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.9 kb (range 0.5-4.0 kb). 12/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH_MGC Library."

ORIGIN

Query Match 60.1%; Score 719.8; DB 12; Length 810;
 Best Local Similarity 97.1%; Pred. No. 3.4e-102;
 Matches 776; Conservative 0; Mismatches 17; Indels 6; Gaps 4;

QY 78 ACAGTAGACCCAGAGTCCCATGAAGAGATGGCTCTCGCATGGATCCCTACTCTAC 137
 Db 2 ACAGTAGACCCAGAGTCCCATGAAGAGATGGCTCTCGCATGGATCCCTACTCTAC 61
 QY 138 TGTGTAGCTTACTGTCTTCTGCTCCAGATGGCGTGTAGCAGTCCCTCAGAAACCTA 197

CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be obtained
from Dr. M. Bento Soares, bento-soares@uiowa.edu
The following repetitive elements were found in this cDNA
sequence: 93-129, >LINE2 (matched complement)
Seq primer: M13 FORWARD
POLYA=Yes.

FEATURES
source
Location/Qualifiers
1..707
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-H-E10-ayo-p-24-0-UI"
/tissue="Chondrosarcoma"
/dev_stage="Adult"
/lab_hosts="DH10B (Life Technologies)"
/clone_lib="NCI-CGAP_E10"
/note="Organ: Left Pelvis; Vector: p773-Pac (Pharmacia)
with a modified polylinker; Site 1: EcoR I; Site 2: Not I;
NCI CGAP E10 is a cDNA library containing the following
tissue(s): Chondrosarcoma. The library was constructed
according to Bonaldo, Lennon and Soares, Genome Research,
6:791-806, 1996. First strand cDNA synthesis was primed
with an oligo-dT primer containing a Not I site. Double
stranded cDNA was ligated to an EcoR I adaptor, digested
with Not I, and cloned directionally into p773-Pac
vector. The oligonucleotide used to prime the synthesis of
first-strand cDNA contains a library tag sequence that is
located between the Not I site and the (dT)18 tail. The
sequence tag for this library is ACATTGAC.
TAG_TISSUE=chondrosarcoma
TAG_LIB=UI-H-E10
TAG_SEQ=ACACTTGCAC"

ORIGIN
Query Match 57.6%; Score 690.6; DB 14; Length 707;
Best Local Similarity 99.4%; Pred. No. 1.2e-97; Indels 0; Gaps 0;
Matches 693; Conservative 0; Mismatches 4;
QY 464 GAGGTGGTGTATGAGGGGCGAGCCCTCTCTCAGGTGCCATGTTGGAGGAACCTGGAT 523
DB 707 GAGGTGGTGTATGAGGGGCGAGCCCTCTCTCAGGTGCCATGTTGGAGGAACCTGGAT 648
QY 524 GTGTACAAGGTGATCTATTATAGGATGGTGAAGCTCTCAAGTACTGTGTATGAGAACCC 583
DB 647 GTGTACAAGGTGATCTATTATAAGGATGGTGAAGCTCTCAAGTACTGTGTATGAGAACCC 588
QY 584 AACATCTCCATTACAAATGCCACAGTTGAAGACAGTGAACCTACTACTGTACGGGCAAA 643
DB 587 AACATCTCCATTACAAATGCCACAGTTGAAGACAGTGAACCTACTACTGTACGGGCAAA 528
QY 644 GTGTGGCAGCTGGACTATGAGTCTGAGCCCTCTCAACATTACTGTATTAAGAGCTCGGCT 703
DB 527 GTGTGGCAGCTGGACTATGAGTCTGAGCCCTCTCAACATTACTGTATTAAGAGCTCGGCT 468
QY 704 GAGAGTACTGGCTACAAATTTTATCCCATGTTGGTGTGATCTGTCTCTGTGGAC 763
DB 467 GAGAGTACTGGCTACAAATTTTATCCCATGTTGGTGTGATCTGTCTCTGTGGAC 408
QY 764 ACAGGATTTATTTATCTCAACTCAGCAGCAGGTCAATTTCTCTTGAAGATTGAAGAAC 823
DB 407 ACAGGATTTATTTATCTCAACTCAGCAGCAGGTCAATTTCTTGAAGATTGAAGAAC 348
QY 824 AGAAGAGGTTCAGACTTCTGAACCCACATCTTAGCCAAACCCCAAAACAACTGATAT 883
DB 347 AGAAGAGGTTCAGACTTCTGAACCCACATCTTAGCCAAACCCCAAAACAACTGATAT 288
QY 884 AATTACTCAAGAAATATTTTGAACATTTAGTTTTTCCAGCATCAGCAATTTCTACTCAA 943
DB 287 AATTACTCAAGAAATATTTTGAACATTTAGTTTTTCCAGCATCAGCAATTTCTACTCAA 228
QY 944 TTGTCAACACACAGCTTGCATATATACAGAAACAGTCTGTGCTCAAGGATTTATAGAAATG 1003

DB 62 TGTGTAGCTTACTGTTCTTTCGCTCCAGATGGCGTGTAGAGTCCCTCAGAAACCTA 121
QY 198 AGGTCTCTTGAACCTCCATGAAATAGAAATATTTAAAGGAGAGATGTGACTCTTACAT 257
DB 122 AGGTCTCTTGAACCTCCATGAAATAGAAATATTTAAAGGAGAGATGTGACTCTTACAT 181
QY 258 GTAATGGGAACAATTTCTTTGAAGTCAAGTCTCAACCAATGGTTCACAAATGGCAGCTTT 317
DB 182 GTAATGGGAACAATTTCTTTGAAGTCAAGTCTCAACCAATGGTTCACAAATGGCAGCTTT 241
QY 318 CAGAAGAGACAAATTTCAAGTTTCAATATTGTGAATGCCAAATTTGAAGACAGTGGAGAT 377
DB 242 CAGAAGAGACAAATTTCAAGTTTCAATATTGTGAATGCCAAATTTGAAGACAGTGGAGAT 301
QY 378 ACAAATGTCTAGCACCACCAAGTTTAATCAGAGTGAACCTGTGTACCTGGAAAGTCTTCAGTG 437
DB 302 ACAAATGTCTAGCACCACCAAGTTTAATCAGAGTGAACCTGTGTACCTGGAAAGTCTTCAGTG 361
QY 438 ACTGGTCTCTCTTCAAGGCTCTGCTGAGTGGTGTGATGGAGGCCAGCCCTCTTCTCA 497
DB 362 ACTGGTCTCTCTTCAAGGCTCTGCTGAGTGGTGTGATGGAGGCCAGCCCTCTTCTCA 421
QY 498 GGTGCCATGTTGGAGGAATGGGATGTGTACAAAGTGTATCTTATTAAGGATGGTGAAG 557
DB 422 GGTGCCATGTTGGAGGAATGGGATGTGTACAAAGTGTATCTTATTAAGGATGGTGAAG 481
QY 558 CTCTCAAGTACTGTATGAGAACACAAATCTCCATTACAAATGCCACAGTTGAAGACA 617
DB 482 CTCTCAAGTACTGTATGAGAACACAAATCTCCATTACAAATGCCACAGTTGAAGACA 541
QY 618 GTGGAACCTACTACTGTACGGGCAAAAGTGTGGCAGTGGACTGTAGTCTGAGCCCTCA 677
DB 542 GTGGAACCTACTACTGTACGGGCAAAAGTGTGGCAGTGGACTGTAGTCTGAGCCCTCA 601
QY 678 ACATTACTGTATTAAGAGCTCCGGTGTGAGAACTGTGGTGTACAAATTTTATCCCATTTGT 737
DB 602 ACATTACTGT-ATAAGAGCTCCGGTGTGACAACTGTGGTGTACAAATTTTATCCCATTTGT 650
QY 738 TGGTGGTATCTGTTCTGTGGACAC--AGGATTTATTTATCT-CAACTCAGCAGCAGG 794
DB 661 TGGTGGTATCTGTTGGTGTGGACACACAGGAGTATTTATCTCCAACTCAGCAGCAGG 720
QY 795 TCATATTTCTC--TTGAAGATTGAAGAACACAGAAAGGCTTCAGACTTCTGAACCCACA 852
DB 721 TCATATTTCTCCTTTGACGATTAGAAAGACCCGGAAGGCTCAGACTCTCTGAACCCAA 780
QY 853 TCCTAAGCCAAACCCCAA 871
DB 781 TCCTAAGACAAACCCCAA 799

RESULT 3
CA448745/c
LOCUS
DEFINITION
UI-H-E10-ayo-p-24-0-UI.s1 NCI CGAP E10 Homo sapiens cDNA clone
UI-H-E10-ayo-p-24-0-UI 3', mRNA sequence.
CA448745
VERSION
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 707)
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
JOURNAL
AUTHORS
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-re@mail.nih.gov
Tissue Procurement: Dr. Jose Mercuende
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa

Db	227	TTGTCAAAACAGCTTGCCAATATACATAGAAACGCTGTGCTCAAGGATTTATAGAAATG	168
Qy	1004	CTTCATTAAACTGAGTGAAACTGGTTAAGTGGCATGTAAATAGTAAGTGCTCAATTAAACAT	1063
Db	167	CTTCATTAAACTGAGTGAAACTGGTTAAGTGGCATGTAAATAGTAAGTGCTCAATTAAACAT	108
Qy	1064	TGGTTGAATAAANTGAGGAATGAATGATTCATTATTATACANTTGTAAAGAGATGTTTC	1123
Db	107	TGGTTGAATAAATGAGGAATGAATGATTCATTATTATACANTTGTAAAGAGATGTTTC	48
Qy	1124	AATTTCAATAAAATAAATATATAAAACCAGTGTAAACAGAA	1160
Db	47	AATTTCAATAAAATAAATATATAAAACCCTGAAAAAAA	11

RESULT 4	CA419024/c	712 bp	mRNA	linear	EST 07-NOV-2002
LOCUS	CA419024				
DEFINITION	UI-H-EZ1-bbj-e-19-0-UI.s1	NCI CGAP Ch2	Homo sapiens	CDNA clone	
	UI-H-EZ1-bbj-e-19-0-UI 3'	mRNA sequence.			
ACCESSION	CA419024				
VERSION	CA419024.1	GI:24781675			
KEYWORDS	EST.				
SOURCE	Homo sapiens				
ORGANISM	Homo sapiens (human)				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
REFERENCE	1 (bases 1 to 712)				
AUTHORS	NCI-CGAP	http://www.ncbi.nlm.nih.gov/ncicgap.			
TITLE	National Cancer Institute, Cancer Genome Anatomy Project (CGAP),				
	Tumor Gene Index				
JOURNAL	Unpublished (1997)				
COMMENT	Contact: Robert Strausberg, Ph.D.				
	Email: cgabsr@mail.nih.gov				
	Tissue Procurement: Dr. Steven Gitelis/ Rush Presbyterian, Dept. of				
	Orthopedics				
	CDNA Library preparation: Dr. M. Bento Soares, University of Iowa				
	CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa				
	DNA Sequencing by: Dr. M. Bento Soares, University of Iowa				
	Clone Distribution: Clone distribution information can be obtained				
	from Dr. M. Bento Soares, bent-soares@uiowa.edu				
	The following repetitive elements were found in this cDNA				
	sequence: 1-42, >(TAAAA)n#Simple_repeat (matched complement)				
	94-130, >LINE2 (matched complement)				
	Seq primer: M13 FORWARD				
	POLYA=Yes.				

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QY	1000 AATGCTTCATTAACTCAGTGAACCTGGTTAAGTGCATGTAATAGTAAGTGTCTCAATTA 1059
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ACCESSION	AW612525
VERSION	AW612525.1
KEYWORDS	GI:7317711
SOURCE	EST.
ORGANISM	Homo sapiens (human)
REFERENCE	Homo sapiens
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE	Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.
	1 (bases 1 to 669)
	NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap .
	National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
	Tumor Gene Index

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Email: cgapbs-remail.nih.gov							
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.							
CDNA Library Preparation: M. Bento Soares, Ph.D.							
CDNA Library Arrayed by: Greg Lennon, Ph.D.							
DNA Sequencing by: Washington University Genome Sequencing Center							
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov/image/html/iresources.shtml							
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Patima Bonaldo."							
ORIGIN							
Query Match							
Best Local Similarity							
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Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.							
CDNA Library Preparation: M. Bento Soares, Ph.D.							
CDNA Library Arrayed by: Greg Lennon, Ph.D.							
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Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.							
CDNA Library Preparation: M. Bento Soares, Ph.D.							
CDNA Library Arrayed by: Greg Lennon, Ph.D.							
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Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov/image/html/iresources.shtml							
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Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.							
CDNA Library Preparation: M. Bento Soares, Ph.D.							
CDNA Library Arrayed by: Greg Lennon, Ph.D.							
DNA Sequencing by: Washington University Genome Sequencing Center							
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Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.							
CDNA Library Preparation: M. Bento Soares, Ph.D.							
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DNA Sequencing by: Washington University Genome Sequencing Center							
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	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.	
QY	NIH-MGC http://mgi.nci.nih.gov/		National Institutes of Health, Mammalian Gene Collection (MGC)	Unpublished (1999)	
	Contact: Robert Strausberg, Ph.D.			Email: cgapbs-remail.nih.gov	
QY	Tissue Procurement: CLONETECH Laboratories, Inc.		CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)	DNA Sequencing by: Inyte Genomics, Inc.	
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Db 122 AGGCTCTCTTGAACCTCCATCGAATAGAAATATTTAAAGAGAGAAATGTGACTCTTACAT 181
QY 258 GTAATGGGAACAATTTCTTTGAAGTCAGTTCACCAAAATGGTTCCACAAATGGCAGCCTTT 317
Db 182 GTAATGGGAACAATTTCTTTGAAGTCAGTTCACCAAAATGGTTCCACAAATGGCAGCCTTT 241
QY 318 CAGAAGAGACAAATTTCAAGTTTGAATATTTGTAATGCCAAATTTGAAGACAGTGGAGAAAT 377
Db 242 CAGAAGAGACAAATTTCAAGTTTGAATATTTGTAATGCCAAATTTGAAGACAGTGGAGAAAT 301
QY 378 ACAAAATGTCAGCACCAACAAAGTAATGAGAGTGAACCTGTGTACCTGGAAGTCTTCAGTG 437
Db 302 ACAAAATGTCAGCACCAACAAAGTAATGAGAGTGAACCTGTGTACCTGGAAGTCTTCAGTG 361
QY 438 ACTGGTGTCTCTCTCAGGCTCTGTGAGGTGGTGTGATGAGGGCCAGGCCCTCTTCCTCA 497
Db 362 ACTGGTGTCTCTCAGGCTCTGTGAGGTGGTGTGATGAGGGCCAGGCCCTCTTCCTCA 421
QY 498 GGTGCCATGGTTGGAGGAACCTGGGATGTGTACAGGTGATCTATTATAAGGATGGTGAAG 557
Db 422 GGTGCCATGGTTGGAGGAACCTGGGATGTGTACAGGTGATCTATTATAAGGATGGTGAAG 481
QY 558 CTCTCAAGTACTGGTATGAGAACCAACAATCTCCATTACAAATGCCACAGTTGAAGACA 617
Db 482 CTCTCAAGTACTGGTATGAGAACCAACA-ATCTCCATTACAAATGCCACAGTTGAAGACA 540
QY 618 GTGGAACCTACTACTGTACGGCAAAAGTGTGGCAGCTGGACTATGAGTCTGAGCCCTCA 677
Db 541 GTGGAACCTACTACTGTACGGCAAAAGTGTGGCAGCTGGACTATGAGTCTGAG-CCCTCA 599
QY 678 ACATTACTGTATATAAAGCTCGCGTGAGAGTACTGGCTACAAATTTTATCCCAT-- 735
Db 600 ACATTACTGTATATAAAGCTCGCGTGAGAGTACTGGCTACAAATTTTATCCCATGG 659
QY 736 GTTGGTGTGATTTCTGTGTGGACACAGGATTTATTTCTCAACTCAGCAG 790
Db 660 GTTGGCGGTGAATTTCTGGTGGCGTGGACACAGGCTTATTTCTCACTCAGCG 714

RESULT 7
BM991911/c
LOCUS
DEFINITION
IMAGE:5870747 3', mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 615)
NCI-CCGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. Jose Mercuende
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
The following repetitive elements were found in this cDNA
sequence: 90-126, LINE2 (matched complement)
Seq primer: M13 FORWARD
POLYA=yes.
Location/Qualifiers
1. .615
/organism="Homo sapiens"
FEATURES
source

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/clone="IMAGE:5870747"
/tissue_type="Subchondral Bone"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
/clone_lib="NCI_CGAP_Df1"
/notes="Organ: Bone; Vector: pT7T3-Pac (Pharmacia) with a
modified polylinker; Site 1: EcoR I; Site 2: Not I;
NCI CGAP Df1 is a normalized cDNA library containing the
following tissue(s): Subchondral Bone. The library was
constructed according to Bonaldo, Lennon and Soares,
Genome Research, 6:791-806, 1996. First strand cDNA
synthesis was primed with an oligo-dT primer containing a
Not I site. Double stranded cDNA was ligated to an EcoR I
adaptor, digested with Not I, and cloned directionally
into pT7T3-Pac vector. The oligonucleotide used to prime
the synthesis of first-strand cDNA contains a library tag
sequence that is located between the Not I site and the
(gt)18 tail. The sequence tag for this library is
GTAAAGCGTC.
TAG_TISSUE=Subchondral bone
TAG_LIB=UI-H-Df1
TAG_SEQ=GTAAAGCGTC"

```

ORIGIN

```

Query Match 49.8%; Score 596.8; DB 12; Length 615;
Best Local Similarity 98.8%; Pred. No. 4.4e-83;
Matches 601; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 553 TGAAGCTCTCAAGTACTGTGTATGAGAACCAACAATCTCCATTACAAATGCCACAGTTGA 612
Db 615 TGAAGCTCTCAAGTACTGTGTATGAGAACCAACAATCTCCATTACAAATGCCACAGTTGA 556
QY 613 AGACAGTGGAACTACTACTGTACGGGCAAAAGTGTGGCAGCTGGACTATGAGTCTGAGCC 672
Db 555 AGACAGTGGAACTACTACTGTACGGGCAAAAGTGTGGCAGCTGGACTATGAGTCTGAGCC 496
QY 673 CCTCAACATTACTGTAAATAAAGCTCCGCGTGAGAGTACTGGCTACAAATTTTATCC 732
Db 495 CCTCAACATTACTGTAAATAAAGCTCCGCGTGAGAGTACTGGCTACAAATTTTATCC 436
QY 733 ATTGTTGGTGTGATTTCTGTTGTGGACACAGGATTTATTTATCTCAACTCAGCAGCA 792
Db 435 ATTGTTGGTGTGATTTCTGTTGTGGACACAGGATTTATTTATCTCAACTCAGCAGCA 376
QY 793 GGTCACTATTTCTTGAAGATTTAAGAACCCAGGAAGCTTCAGACTTCTGAACCCACA 852
Db 375 GGTCACTATTTCTTGAAGATTTAAGAACCCAGGAAGCTTCAGACTTCTGAACCCACA 316
QY 853 TCCTAAGCCAAACCCCAAAACAACCTGATATAATTTACTCAAGAAATATTTGCAACATTAG 912
Db 315 TCCTAAGCCAAACCCCAAAACAACCTGATATAATTTACTCAAGAAATATTTGCAACATTAG 256
QY 913 TTTTTCAGCATCAGCAATGCTACTCAATTTGCAACACAGCTTCGAATATACATAG 972
Db 255 TTTTTCAGCATCAGCAATGCTACTCAATTTGCAACACAGCTTCGAATATACATAG 196
QY 973 AAACGCTGTGCTCAAGGATTTATAGAAATGCTTCATTATAACTAGTCAAACTGGTTAAG 1032
Db 195 AAACGCTGTGCTCAAGGATTTATAGAAATGCTTCATTATAACTAGTCAAACTGGTTAAG 136
QY 1033 TGGCATGTAATAGTAGTGTCTCAATTTAACTGGTTGAATAAATGAGAGAAATGAATAGAT 1092
Db 135 TGGCATGTAATAGTAGTGTCTCAATTTAACTGGTTGAATAAATGAGAGAAATGAATAGAT 76
QY 1093 TCATTATATACATTTGTAAAGAGAGTGTTCAAATTTCAATAAATAAATAAACCAGT 1152
Db 75 TCATTATATAGCATTTGTAAAGAGAGTGTTCAAATTTCAATAAATAAATAAACCAGT 16

1153 TAACAGAA 1160
15 AAAAAAAAA 8

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SfiI (ggcgcttggcc); Site 2: SfiI (ggcattatggcc); 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CAGCGCATATGCGC-3' and 3' adaptor sequence: 5'-ATTCTAGAGCGCGCGCGCATATG-dt(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.9 kb (range 0.5-4.0 kb). 12/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH_MGC Library."

ORIGIN

```

Query Match      48.2%; Score 577; DB 12; Length 760;
Best Local Similarity 96.3%; Pred. No. 4.6e-80;
Matches 533; Conservative 0; Mismatches 20; Indels 4; Gaps 4;

QY 273 TCTTTGAAGTCAGTTCACCAAAATGGTTCCAAATGGCAGCCTTTTCAGAGAGACAAATT 332
DB 98 TGTTAGCAGTCAGTTCACCAAAATGGTTCCAAATGGCAGCCTTTTCAGAGAGACAAATT 157
QY 333 CAAGTTTGAATATGTGATGCCAAATTTGAAGACAGTGGAGATACAAATGTGACGACC 392
DB 158 CAAGTTTGAATATGTGATGCCAAATTTGAAGACAGTGGAGATACAAATGTGACGACC 217
QY 393 AACAAAGTTAATGAGAGTGAACCTGTGTACTTGGAAAGTCTTCAGTACTGGCTGCTCTTC 452
DB 218 AACAAAGTTAATGAGAGTGAACCTGTGTACTTGGAAAGTCTTCAGTACTGGCTGCTCTTC 277
QY 453 AGGCTCTGCTGAGTGGTGTGATGAGCGCCAGCCCTCTTCTCAGTGGCCATGGTTGA 512
DB 278 AGGCTCTGCTGAGTGGTGTGATGAGCGCCAGCCCTCTTCTCAGTGGCCATGGTTGA 337
QY 513 GGAAGTGGATGTGTACAAGGTGATCTATTATAGGATGTGTGAAGCTCTCAAGTACTGGT 572
DB 338 GGAAGTGGATGTGTACAAGGTGATCTATTATAGGATGTGTGAAGCTCTCAAGTACTGGT 397
QY 573 ATGAGAACCAACATCTCCATTAACAATGCCAGTTGAAGACAGTGGAAACCTACTACT 632
DB 398 ATGAGAACCAACATCTCCATTAACAATGCCAGTTGAAGACAGTGGAAACCTACTACT 457
QY 633 GTACGGGCAAGTGTGGCAGTGGACTATGAGTCTGAGCCCTCAACATTACTGTATTA 692
DB 458 GTACGGGCAAGTGTGGCAGTGGACTATGAGTCTGAGCCCTCAACATTACTGTATTA 517
QY 693 AAGTCCGCGTGAAGATCTGGCTACAATTTTATCCCATTTGGTGGTGAATCTGT 752
DB 518 AAGTCCGCGTGAAGATCTGGCTACAATTTTATCCCATTTGGTGGTGAATCTGT- 576
QY 753 TTGCTGTGGACACAGGATTTATCTCAACTCAGCAGAGTCAATTTCTCTTGAAGA 812
DB 577 TTGCTGTGGACACAGGATTTATCTCAACTCAGCAGAGTCAATTTCTCTTGAAGA 636
QY 813 TTAAGAGAACCAAGAAA-GGCTTCAGACTTCTGAACCCACATCTTAAGCCAAACCCCAA 871
DB 637 TTAAGAGAACCAAGAAAAGGCTTCAGACTTCTGAACCCA-ATCCTAAGCCAAACCCGAA 695
QY 872 AACAACTGATATATTACTCAAGAAATTTTGAACATTTAGTTTTCAGCATCA 928
DB 696 AA-AAATGATATAATTACTCCAGACATTTTGCACATTAGTTTTCAGCATCAGCA 751

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RESULT 10

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BF678252
LOCUS      BF678252
DEFINITION 602086161F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4250222 5',
            mRNA sequence.
ACCESSION  BF678252
VERSION    BF678252.1
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 846)

```

AUTHORS

National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs@mail.nih.gov
 Tissue Procurement: CLONETECH Laboratories, Inc.
 cDNA Library Preparation: CLONETECH Laboratories, Inc.
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LLCM1071 row: j column: 15
 High quality sequence stop: 609.

FEATURES

source

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1..846
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  /mol_type="mRNA"
  /db_xref="taxon:9606"
  /clone="IMAGE:4250222"
  /lab_host="DH10B (TI phage-resistant)"
  /clone_lib="NIH_MGC_83"
  /note="Organ: prostate; Vector: pDNR-LIB (Clontech);
  Site 1: SfiI (ggcgcttggcc); Site 2: SfiI
  (ggcattatggcc); 5' and 3' adaptors were used in cloning
  as follows: 5' adaptor sequence: 5'-CAGCGCATATGCGC-3'
  and 3' adaptor sequence:
  5'-ATTCTAGAGCGCGCGCGCATATG-dt(30)BN-3' (where B = A,
  C, or G and N = A, C, G, or T). Average insert size 1.4
  kb (range 0.5-4.0 kb). 14/15 colonies contained inserts
  by PCR. This library was enriched for full-length clones
  and was constructed by Clontech Laboratories (Palo Alto,
  CA)."
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ORIGIN

```

Query Match      43.7%; Score 523.6; DB 10; Length 846;
Best Local Similarity 93.1%; Pred. No. 8.2e-72;
Matches 670; Conservative 0; Mismatches 34; Indels 16; Gaps 11;

QY 83 AAGCACCAAGAGTCATGAAGAAGTGGCTCCTGCCATGGAAATCCCTACTTACTGTGT 142
DB 2 AAGCACCAAGAGTCATGAAGAAGTGGCTCCTG-CATGGATCCCTACTTACTGTGT 60
QY 143 GTAGCTTACTGTCTTCGCTCCAGATGGCGGTGTAGCAGTCCCTCAGAAACCTAAGGTC 202
DB 61 GTAGCTTACTGTCTTCGCTCCAGATGGCGGTGTAGCAGTCCCTCAGAAACCTAAGGTC 120
QY 203 TCCTTGAACCTCCATGGAATAGAAATATTTAA-AGGAGAGATGTGACTCTTACATGTAA 261
DB 121 TCCTTGAACCTCCATGGAATAGAAATATTTAAAGAGAGATGTGACTCTTACATGTAA 180
QY 262 TGGGAACAATTTCTTTGAAGTCAGTTCCACCAATGGTTCCCAATGGCAGCCCTTTCAGA 321
DB 181 TGGGAACAATTTCTTTGAAGTCAGTTCCACCAATGGTTCCCAATGGCAGCCCTTTCAGA 240
QY 322 AGAGACAAATTCAGATTTGATATTTGAATGCCAAATTTGAACACAGTGGAGATCAAA 381
DB 241 AGAGACAAATTCAGATTTGATATTTGAATGCCAAATTTGAACACAGTGGAGATCAAA 298
QY 382 ATGTGAGACCAACAAGTTAATGAGAGTGAACCTGTGTACTGGAAGTCTTTCAGTACTG 441
DB 299 ATGTGAGACCAACAAGTTAATGAGAGTGAACCTGTGTACTGGAAGTCTTTCAGTACTG 357
QY 442 GCTGCTCTTTCAGGCTCTGCTGAGTGGTGTGATGAGGCGCCAGCCCTCTTTCCTCAGGTG 501
DB 358 GCTGCTCTTTCAGGCTCTGCTGAGTGGTGTGATGAGGCGCCAGCCCTCTTTCCTCAGGTG 417
QY 502 CCATGGTTGGAGGAACCTGGGATGTGACAAAGTGTCTATTATTAAGGATGGTGAAGTCT 561
DB 418 CCATGGTTGGAGGAACCTGGGATGTGACAAAGTGTCTATTATTAAGGATGGTGAAGTCT 476
QY 562 CAAGTACTGGTATGAGAACCAACATCTCCATTAACAAATGCCACAGTGGCAAGACAGTGG 621

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NIH-MGC http://mgc.nci.nih.gov/.

Db 477 CAAGTACT-GTATGAGAACCAAA-ATCTCCATTACAAATGCCAG-TGAAGACAGTGG 533
 QY 622 AACCTACTACTGACGGCAAAAGTGTGGCAGCTGGAAGTATGAGTCTGAGCCCTCAACAT 681
 Db 534 AACCTACTACTGACGGGCAAGTGTGGCAGCT-GACTATGAGTCTGAGCCCTCAAAAT 592
 QY 682 TACTGTAAATAAAGCTCCGCGTGAAGTACTGGCTACAAATTTTATCCCATTTGTTGT 741
 Db 593 AACTGTAAATAAAGCTCCGCGTGAAGTACTGGCTACCACTTTTATCCCATTTGTTGT 652
 QY 742 GGTGATTCTGTTGCTGTGGACACAGGATTATTTATCTCAACTCAGCAGCAGTCAACAT 801
 Db 653 GAT-----TCTGTGGCTGGACACAGGATTA-TTATCTCAACTCAGCAGCAGTCCCAT 706

RESULT 11
 AI685796/c
 LOCUS
 DEFINITION
 540 bp mRNA linear EST 27-MAY-1999
 tu20g08.x1 NCI CGAP Pr28 Homo sapiens cDNA clone IMAGE:2251646 3'
 similar to gb:X06948 HIGH AFFINITY IMMUNOGLOBULIN EPSILON RECEPTOR
 ALPHA-SUBUNIT (HUMAN); mRNA sequence.

ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Homo sapiens (human)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 540)
 NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 Unpublished (1997)
 Contact: Robert Straube, Ph.D.
 Email: cgaps@email.nih.gov
 Tissue Procurement: Michael J. Brownstein, M.D., Ph.D., Michael R.
 Emmert-Buck, M.D., Ph.D.
 cDNA Library Preparation: M. Bento Soares, Ph.D.
 cDNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality
 Seq primer: -40UP from Gibco
 High quality sequence stop: 1.
 Location/Qualifiers

FEATURES
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 /clone="IMAGE:2251646"
 /sex="male"
 /dev_stage="adult"
 /lab_host="DH10B"
 /clone_lib="NCI CGAP Pr28"
 /note="Organ: prostate; Vector: pT7T3D-Pac (Pharmacia)
 with a modified polylinker; plasmid DNA from the
 normalized library NCI CGAP Pr22 was prepared, and ss
 circles were made in vitro. Following HAP purification,
 this DNA was used as tracer in a subtractive hybridization
 reaction. The driver was PCR-amplified cDNAs from a pool
 of 5,000 clones made from the same library (clonids
 985608-986759, 110192-110199, and 1217928-1220615).
 Subtraction by Bento Soares and M. Fatima Bonaldo."

ORIGIN

Query Match 41.3%; Score 494.6; DB 9; Length 540;
 Best Local Similarity 95.5%; Pred. No. 3.2e-67;
 Matches 509; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

QY 616 CAGTGGAACTACTACTGTCGGGCAAAAGTGTGGCAGCTGGATGAGTCTGAGCCCT 675

Db 533 CAATGACCATACTACTGTACGGCAAAAGTGTGGCAGCTGGCTAAGAGTCAACCCCT 474
 QY 676 CAACATTACTGTATAAAAGCTCCGCGTGAAGTACTGGCTACAAATTTTATCCCAT 735
 Db 473 CCACAATACTGTATAAAGCTCCGCGTGAAGTACTGGCTACAAATTTTATCCCAT 414
 QY 736 GTTGTGTGATCTGTTTGTGTGGACACAGGATTATTTATCTCAACTCAGCAGCAGGT 795
 Db 413 GTTGTGTGATCTGTTTGTGTGGACACAGGATTATTTATCTCAACTCAGCAGCAGGT 354
 QY 796 CACATTTCTCTTTGAAGATTAAAGAACCCAGGAAAGGTTTCAGACTTCGAAACCCACATCC 855
 Db 353 CACATTTCTCTTTGAAGATTAAAGAACCCAGGAAAGGTTTCAGACTTCGAAACCCACATCC 294
 QY 856 TAAGCCAAACCCAAACACACTGATATAATTAATCTCAGAAATATTTTGAACATTAGTTT 915
 Db 293 TAAGCCAAACCCAAACACACTGATATAATTAATCTCAGAAATATTTTGAACATTAGTTT 234
 QY 916 TTTTCCAGCATCAGCAATTTGCTACTCAATTTGTCAACACACAGCTTGCATATACATAGAAA 975
 Db 233 TTTTCCAGCATCAGCAATTTGCTACTCAATTTGTCAACACCCAGCTTGCATATACATAGAAA 174
 QY 976 CGTCTGTCTCAAGGATTATAGAAATGCTTCATTAACCTGAGTGAACCTGGTTAAGTGG 1035
 Db 173 CGTCTGTCTCAAGGATTATAGAAATGCTTCATTAACCTGAGTGAACCTGGTTAAGTGG 114
 QY 1036 CATGTAATAGTAAGTGTCTCAATTAACCTGCTTGTGTAATAATGAGAGATGAATAGATTCA 1095
 Db 113 CATGTAATAGTAAGTGTCTCGATTAAACATTGTTGTAATCAATGAGAGATGAATAGATTCA 54
 QY 1096 TTTTATGACATTTGTAAAGAGATGTTCAATTTCAATAAATAAATAATAAAC 1148
 Db 53 TTTTATGACATTTGTAAAGAGATGTTCACTTCAATTAATAATAATAAAC 1

RESULT 12

EX110472

LOCUS

DEFINITION

EX110472

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

EX110472 488 bp mRNA linear EST 07-FEB-2003
 IMAGE:2314294, mRNA sequence.

EX110472
 EX110472.1 GI:27836404

EST.
 Homo sapiens (human)
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 488)
 Ebert, L., Heil, O., Hennig, S., Neubert, P., Partsch, E., Peters, M.,
 Radelef, U., Schneider, B. and Korn, B.
 Human Unigeneset - RZPD3
 Unpublished (2003)
 Contact: Ina Rolfs

RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
 Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany
 RZPD; IMAGP998B35736.
 RZPDLIB; I.M.A.G.E. cDNA clone collection;
 Human Unigeneset - RZPD3 (RZPDLIB No.972)
[http://www.rzpd.de/CloneCards/cgi-](http://www.rzpd.de/CloneCards/cgi-bin/showLib.pl.cgi?response?libNo=972)
 bin/showLib.pl.cgi?response?libNo=972 Contact: Ina Rolfs
 RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
 Heubnerweg 6 D-14059 Berlin, Germany
 Tel: +49 30 32639 101
 Fax: +49 30 32639 111
www.rzpd.de
 This clone is available royalty-free from RZPD;
 contact RZPD (clone@rzpd.de) for further information. Seq primer:
 M13r, Primer sequence: TTTCCACAGGAAACAGCTATGAC.

FEATURES

source

1..488

/organism="Homo sapiens"

/mol_type="mRNA"

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/db_xref="taxon:9606"
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/sex="male"
/dev_stages="adult"
/clone_lib="DH10B"
/clone_lib="NCI CGAP pr28"
/notes="Organ: prostate; Vector: pT7T3D-Pac (Pharmacia)
with a modified polylinker; Plasmid DNA from the
normalized library NCI CGAP_P22 was prepared, and ss
circles were made in vitro. Following HAP purification,
this DNA was used as tracer in a subtractive hybridization
reaction. The driver was PCR-amplified cDNAs from a pool
of 5,000 clones made from the same library (clones 1
985608-986759, 1101192-1101959, and 1217928-1220615).
Subtraction by Bento Soares and M. Fatima Bonaldo."

ORIGIN
Query Match 40.5%; Score 484.8; DB 13; Length 488;
Best Local Similarity 99.6%; Pred. No. 1.1e-65;
Matches 486; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 571 GTATGAGAACACACATCTCCATTACAAATGCCACAGTTGACACAGTGGAACTACTA 630
Db 1 GTATGAGAACACACATCTCCATTACAAATGCCACAGTTGACACAGTGGAACTACTA 60

QY 631 CTGTACGGGCAAGTGTGGCAGCTGGACTATGAGTCTGAGCCCTCAACATTACTGTAAT 690
Db 61 CTGTACGGGCAAGTGTGGCAGCTGGACTATGAGTCTGAGCCCTCAACATTACTGTAAT 120

QY 691 AAAAGCTCCGGTGTGAGAGTACTGGCTACAAATTTTATCCCATTTGTGGTGATCT 750
Db 121 AAAAGCTCCGGTGTGAGAGTACTGGCTACAAATTTTATCCCATTTGTGGTGATCT 180

QY 751 GTTGTCTGTGACACAGGATTTATCTCAACTCAGCAGCAGTGCACATTTCTTTGAA 810
Db 181 GTTGTCTGTGACACAGGATTTATCTCAACTCAGCAGCAGTGCACATTTCTTTGAA 240

QY 811 GATTAAGAGAACACAGGCTTCAGACTTCTGAACCCACATCTTAAGCCCAACCCCAA 870
Db 241 GATTAAGAGAACACAGGCTTCAGACTTCTGAACCCACATCTTAAGCCCAACCCCAA 300

QY 871 AAACAACCTGATATTAATCTCAAGAAATATTTGCAACATAGTTTTCACGATCAGC 930
Db 301 AAACAACCTGATATTAATCTCAAGAAATATTTGCAACATAGTTTTCACGATCAGC 360

QY 931 AATTGCTACTCAATTGTCAACACAGCTTGCAATATACATAGAAAGCTGTGCTCAAG 990
Db 361 AATTGCTACTCAATTGTCAACACAGCTTGCAATATACATAGAAAGCTGTGCTCAAG 420

QY 991 ATTTATGAAGTCTTCATTAACCTGAGTGAAGTGAAGTGAAGTGAAGTGAAGT 1050
Db 421 ATTTATGAAGTCTTCATTAACCTGAGTGAAGTGAAGTGAAGTGAAGTGAAGT 480

QY 1051 GCTCAATT 1058
Db 481 GCTCAATT 488

RESULT 13
AI676114/c
LOCUS
DEFINITION wc05e12.x1 NCI CGAP P28 Homo sapiens cDNA clone IMAGE:2314318 3'
similar to cb:X06948 HIGH AFFINITY IMMUNOGLOBULIN EPSILON RECEPTOR
ALPHA-SUBUNIT (HUMAN); mRNA sequence.
ACCESSION AI676114
VERSION AI676114.1 GI:4876594
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 570)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

```

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue Procurement: Michael J. Brownstein, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality
Insert Length: 625 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 1.
Location/Qualifiers
1..570
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2314318"
/sex="male"
/dev_stages="adult"
/lab_host="DH10B"
/clone_lib="NCI CGAP pr28"
/notes="Organ: prostate; Vector: pT7T3D-Pac (Pharmacia)
with a modified polylinker; Plasmid DNA from the
normalized library NCI CGAP_P22 was prepared, and ss
circles were made in vitro. Following HAP purification,
this DNA was used as tracer in a subtractive hybridization
reaction. The driver was PCR-amplified cDNAs from a pool
of 5,000 clones made from the same library (clones 1
985608-986759, 1101192-1101959, and 1217928-1220615).
Subtraction by Bento Soares and M. Fatima Bonaldo."

ORIGIN

Query Match 40.0%; Score 478.8; DB 9; Length 570;
Best Local Similarity 90.0%; Pred. No. 8.6e-65;
Matches 513; Conservative 0; Mismatches 57; Indels 0; Gaps 0;

QY 571 GTATGAGAACACACATCTCCATTACAAATGCCACAGTTGAACACAGTGAACCTACTA 630
Db 570 GTATGAGAACACATCTCTGTGCCATAGCAATGCCAGGTGATACAGTAGGGCTATTG 511
QY 631 CTGTACGGGCAAGTGTGGCAGCTGGACTATGAGTCTGAGCCCTCAACATTACTGTAAT 690
Db 510 CTGTACGGGCAAGTGTGGCAGCTGGACTATGAGTCTGAGCCCTCAACATTACTGTAAT 451
QY 691 AAAAGCTCCGGTGTGAGAGTACTGGCTACAAATTTTATCCCATTTGTGGTGATCT 750
Db 450 AAAAGCTCCGGTGTGAGAGTACTGGCTACAAATTTTATCCCATTTGTGGTGATCT 391
QY 751 GTTGTCTGTGACACAGGATTTATCTCAACTCAGCAGCAGTGCACATTTCTTTGAA 810
Db 390 GTTGTCTGTGACACAGGATTTATCTCAACTCAGCAGCAGTGCACATTTCTTTGAA 331
QY 811 GATTAAGAGAACACAGGAGCTTCAGACTTCTGAACCCACATCTTAAGCCCAACCCCAA 870
Db 330 GATTAAGAGAACACAGGAGCTTCAGACTTCTGAACCCACATCTTAAGCCCAACCCCAA 271
QY 871 AAACAACCTGATATTAATCTCAAGAAATATTTGCAACATAGTTTTCACGATCAGC 930
Db 270 AAACAACCTGATATTAATCTCAAGAAATATTTGCAACATAGTTTTCACGATCAGC 211
QY 931 AATTGCTACTCAATTGTCAACACAGCTTGCAATATACATAGAAAGCTGTGCTCAAG 990
Db 210 AATTGCTACTCAATTGTCAACACAGCTTGCAATATACATAGAAAGCTGTGCTCAAG 151
QY 991 ATTTATGAAGTCTTCATTAACCTGAGTGAAGTGAAGTGAAGTGAAGTGAAGT 1050
Db 151 ATTTATGAAGTCTTCATTAACCTGAGTGAAGTGAAGTGAAGTGAAGTGAAGT 1050

Plasmid DNA from the normalized library NCI CGAP Kid3 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (clones 132376-132391, 145607-145677, and 150052-150285). Subtraction by Bento Soares and M. Fatima Bonaldo. "

ORIGIN

```
Query Match      38.0%; Score 455; DB 10; Length 479;
Best Local Similarity 96.9%; Pred. No. 4.6e-61;
Matches 464; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 671 CCCCTCAACATTACTGTATATAAGCTCCGGCTGAGAGTACTGGCTACAAATTTTTTATC 730
Db      |||||
QY 479 CCCCTCAACATTATTGTAAAAAGCTCCGGCTAAGAGGTACGGATACATTTTTTATC 420
Db      |||||
QY 731 CCATTGTTGGTGGTATTCTGTTGCTGTGACACAGGATTATTATCTCACTCAGCAG 790
Db      |||||
QY 419 CCATTGTTGGTGGTATTCTGTTGCTGTGACACAGGATTATTATCTCACTCAGCAG 360
Db      |||||
QY 791 CAGGTCACATTTCTCTGAAGATTAAAGAACACAGGAAGGCTTCAGACTTCTGAACCCA 850
Db      |||||
QY 359 CAGGTCACATTTCTCTGAAGATTAAAGAACACAGGAAGGCTTCAGACTTCTGAACCCA 300
Db      |||||
QY 851 CATCTAAGCCAAACCCCAAAACAACATGATATAATTAATCAAGAAATATTGCAACATT 910
Db      |||||
QY 299 CATCTAAGCCAAACCCCAAAACAACATGATATAATTAATCAAGAAATATTGCAACATT 240
Db      |||||
QY 911 AGTTTTTTCCAGCATCAGCAATTGCTACTCAATTGTCAAAACACAGCTTGCAATATACAT 970
Db      |||||
QY 239 AGTTTTTTCCAGCATCAGCAATTGCTACTCAATGTCAAAACACAGCTTGCAATATACAT 180
Db      |||||
QY 971 AGAAACGTCCTGCTCAAGGATTTATAGAAATGCTTCATTAAACTGAGTGAAACTGGTTA 1030
Db      |||||
QY 1031 AGTGCATGTAATAGTAGTCTCAATTAACATTGGTTGAATAAATGAGAGATGATAG 1090
Db      |||||
QY 119 AGTGCATGTAATAGTAGTCTCAATTAACATTGGTTGAATAAATGAGAGATGATAG 60
Db      |||||
QY 1091 ATTCATTATTAGCATTGTGAAAAGAGATGTTCAATTTCAATATAAATAATAAAACC 1149
Db      |||||
QY 59 ATTCATTATTAGCATTGTGAAAAGAGATGTTCAATTTCAATATAAATAATAAAACC 1
```

Search completed: October 10, 2004, 19:44:35
Job time : 4048.38 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 6, 2004, 08:59:39 ; Search time 8.68648 Seconds
(without alignments)
1540.558 Million cell updates/sec

Title: US-10-763-400-2

Perfect score: 1390

Sequence: 1 MAPAVESPTLLCVALLFPAP.....RTRKGFRLNPHKPNKNN 257

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1390	100.0	257	1 FCEA_HUMAN	P12319 homo sapien
2	626.5	45.1	250	1 FCEA_MOUSE	P20489 mus musculus
3	597.5	43.0	245	1 FCEI_RAT	P12371 rattus norv
4	419	30.1	257	1 FCGI_PIG	Q28942 sus scrofa
5	418	30.1	254	1 FC3A_HUMAN	F08637 homo sapien
6	417	30.0	250	1 FC3B_BOVIN	F79107 bos taurus
7	406	29.2	233	1 FC3B_HUMAN	Q75015 homo sapien
8	405	29.1	296	1 FCG2_BOVIN	Q28110 bos taurus
9	401.5	28.9	261	1 FCG3_MOUSE	P08308 mus musculus
10	400	28.8	267	1 FCG3_RAT	P27645 rattus norv
11	395	28.4	341	1 FCG3_CAVPO	Q60313 cavia porce
12	379	27.3	374	1 FCG1_HUMAN	P12314 homo sapien
13	379	27.3	404	1 FCG1_MOUSE	P26151 mus musculus
14	371.5	26.7	310	1 FCGB_HUMAN	P31994 homo sapien
15	371.5	26.7	323	1 FCGC_HUMAN	P31995 homo sapien
16	368	26.5	285	1 FCG2_RAT	Q63203 rattus norv
17	367	26.4	330	1 FCG3_MOUSE	P08101 mus musculus
18	351	25.3	316	1 FCGA_PANTR	Q89pvs pan troglod
19	348	25.0	157	1 FCE2_RAT	P12840 rattus norv
20	347	25.0	317	1 FCGA_HUMAN	P12318 homo sapien
21	175.5	12.6	1709	1 SN_HUMAN	Q9b222 homo sapien
22	166	11.9	1694	1 SN_MOUSE	P62230 mus musculus
23	154	11.1	422	1 K3L1_RAT	P83556 rattus norv
24	144	10.4	432	1 K3L1_MOUSE	P83555 mus musculus
25	137.5	9.9	521	1 CEAL_MOUSE	P31809 mus musculus
26	137.5	9.9	837	1 NCM2_MOUSE	Q35136 mus musculus
27	136.5	9.8	519	1 ECTO_RAT	P16573 rattus norv
28	129.5	9.3	1302	1 NRG_DROME	P20241 drosophila
29	128.5	9.2	344	1 CEAF5_HUMAN	P40199 homo sapien
30	126	9.1	1240	1 NFAS_HUMAN	Q94856 homo sapien
31	125.5	9.0	978	1 KFMS_RAT	Q00435 rattus norv
32	125	9.0	458	1 CD4_MACNE	Q08340 macaca mela
33	124.5	9.0	977	1 KFMS_MOUSE	P09581 mus musculus

34	123	8.8	1240	1 NFAS_MOUSE	Q810u3 mus musculu
35	123	8.8	1240	1 NFAS_RAT	P97685 rattus norv
36	122	8.8	458	1 CD4_CERAS	Q08338 cercopithe
37	121.5	8.7	739	1 VCAI_RAT	P29534 rattus norv
38	120	8.6	458	1 CD4_MACFU	P79184 macaca fusc
39	120	8.6	702	1 CEAS_HUMAN	P06731 homo sapien
40	120	8.6	837	1 NCM2_HUMAN	Q35394 homo sapien
41	120	8.6	847	1 CD22_HUMAN	P20273 homo sapien
42	120	8.6	862	1 CD22_MOUSE	P35329 mus musculu
43	120	8.6	6632	1 UN89_CABEL	O01761 caenorhabdi
44	119	8.6	458	1 CD4_MACVU	P16003 macaca mula
45	119	8.6	739	1 VCAI_HUMAN	P19320 homo sapien

ALIGNMENTS

RESULT 1

FCEA_HUMAN					
ID FCEA_HUMAN	STANDARD;	PRT;	257 AA.		
AC P12319;					
DT 01-OCT-1989 (Rel. 12, Created)					
DT 01-OCT-1989 (Rel. 12, Last sequence update)					
DT 10-OCT-2003 (Rel. 42, Last annotation update)					
DE High affinity immunoglobulin epsilon receptor alpha-subunit precursor					
DE (FCERI) (IgE Fc receptor, alpha-subunit) (FC-epsilon RI-alpha).					
GN FCERI OR FCE1A.					
OS Homo sapiens (Human).					
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.					
OX NCBI_TaxID=9606;					
RN [1]					
SEQUENCE FROM N.A.					
RP MEDLINE=88233953; PubMed=2967464;					
RA Kochan J., Pettine L.F., Hakimi J., Kishi K., Kinet J.-P.;					
RT "Isolation of the gene coding for the alpha subunit of the human high					
RT affinity IgE receptor."					
RL Nucleic Acids Res. 16:3584-3584(1988).					
[2]					
SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.					
RP TISSUE=Mast cells;					
RX MEDLINE=88158102; PubMed=2964640;					
RA Shimizu A., Tepler I., Benfey P.N., Berenstein E.H., Siraganian R.P.,					
Leder P.;					
RT "Human and rat mast cell high-affinity immunoglobulin E receptors:					
RT characterization of putative alpha-chain gene products."					
RL Proc. Natl. Acad. Sci. U.S.A. 85:1907-1911(1988).					
[3]					
3D-STRUCTURE MODELING OF 26-197.					
RX MEDLINE=93111350; PubMed=1472946;					
RA Padlan E.A., Helm B.A.;					
RT "A modeling study of the alpha-subunit of human high-affinity					
RT receptor for immunoglobulin-E."					
RL Receptor 2:129-144(1992).					
CC -!- FUNCTION: BINDS TO THE FC REGION OF IMMUNOGLOBULINS EPSILON. HIGH					
CC AFFINITY RECEPTOR. RESPONSIBLE FOR INITIATING THE ALLERGIC					
CC RESPONSE. BINDING OF ALLERGEN TO RECEPTOR-BOUND ICE LEADS TO CELL					
CC ACTIVATION AND THE RELEASE OF MEDIATORS (SUCH AS HISTAMINE)					
CC RESPONSIBLE FOR THE MANIFESTATIONS OF ALLERGY. THE SAME RECEPTOR					
CC ALSO INDUCES THE SECRETION OF IMPORTANT LIPHOKINES.					
CC -!- SUBUNIT: TETRAMER OF AN ALPHA CHAIN, A BETA CHAIN, AND TWO					
CC DISULFIDE LINKED GAMMA CHAINS.					
CC -!- SUBCELLULAR LOCATION: Type 1 membrane protein.					
CC -!- SIMILARITY: Contains 2 immunoglobulin-like domains.					
CC					
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CC					

DR EMBL; X06948; CAA30025.1; -;
 DR EMBL; J03605; AAA36204.1; -;
 DR EMBL; A21606; CAA01564.1; -;
 DR PIR; S00682; S00682.
 DR PDB; 1ALS; 27-FEB-95.
 DR PDB; 1ALT; 27-FEB-95.
 DR PDB; 1F2Q; 08-JUN-00.
 DR PDB; 1J86; 29-AUG-01.
 DR PDB; 1J87; 29-AUG-01.
 DR PDB; 1J88; 29-AUG-01.
 DR PDB; 1J89; 05-SEP-01.
 DR PDB; 1J89; 05-SEP-01.
 DR MIM; 147140; -;
 DR GO; GO:0005887; C:integral to plasma membrane; TAS.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003598; IG_c2.
 DR Pfam; PF00047; Ig; 2.
 DR SMART; SM00408; IGC2; 1.
 DR PROSITE; PS00835; IG_LIKE; 2.
 KW Ig-binding protein; Receptor; Transmembrane; Glycoprotein; Signal;
 KW Immunoglobulin domain; Repeat; 3D-structure.
 FT SIGNAL 1 25
 FT CHAIN 26 257
 FT DOMAIN 26 205
 FT TRANSMEM 206 224
 FT DOMAIN 225 257
 FT DOMAIN 30 110
 FT DOMAIN 111 193
 FT DISULFID 51 93
 FT DISULFID 132 176
 FT CARBOHYD 46 46
 FT CARBOHYD 67 67
 FT CARBOHYD 75 75
 FT CARBOHYD 99 99
 FT CARBOHYD 160 160
 FT CARBOHYD 165 165
 FT CARBOHYD 191 191
 FT STRAND 31 35
 FT HELIX 39 42
 FT TURN 43 43
 FT STRAND 48 54
 FT STRAND 61 66
 FT TURN 67 68
 FT STRAND 69 71
 FT STRAND 74 74
 FT TURN 75 76
 FT STRAND 77 79
 FT HELIX 82 87
 FT STRAND 91 96
 FT TURN 101 101
 FT TURN 104 107
 FT STRAND 114 116
 FT STRAND 120 124
 FT STRAND 128 133
 FT STRAND 143 145
 FT HELIX 146 148
 FT TURN 149 149
 FT STRAND 150 150
 FT TURN 152 153
 FT STRAND 154 155
 FT TURN 156 159
 FT STRAND 160 163
 FT HELIX 165 170
 FT STRAND 175 178
 FT STRAND 181 182
 FT TURN 183 185
 FT STRAND 186 187
 FT STRAND 190 193
 SQ SEQUENCE 257 AA; 29596 MW; F183BB2357DDAD58 CRC64;
 100.0%; Score 1390; DB 1; Length 257;

Best Local Similarity 100.0%; Pred. No. 1.9e-107;
 Matches 257; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MAPAMESPTLLCVALLFPAPDGLAVPQPKVSLNPPNRRIFKGNVTLTCGNFFFEVS 60
 DB 1 MAPAMESPTLLCVALLFPAPDGLAVPQPKVSLNPPNRRIFKGNVTLTCGNFFFEVS 60
 QY 61 STKWFHNGSLSEETNSLNINNAKPEDSGEYKCOHQVNESEPVYLEVFSWLLLOASAE 120
 DB 61 STKWFHNGSLSEETNSLNINNAKPEDSGEYKCOHQVNESEPVYLEVFSWLLLOASAE 120
 QY 121 VVMEGQPLFLRCHGWRNWDVYKVIYKDGKALKYWYENHNISITNATVEDSGTYCTGKV 180
 DB 121 VVMEGQPLFLRCHGWRNWDVYKVIYKDGKALKYWYENHNISITNATVEDSGTYCTGKV 180
 QY 181 WOLDYSEPLNITVIKAPREKYWLOFFIPLLVILFAVDTGLFISTQQQVTFLLKIKETR 240
 DB 181 WOLDYSEPLNITVIKAPREKYWLOFFIPLLVILFAVDTGLFISTQQQVTFLLKIKETR 240
 QY 241 KGFRLNHPKPNKNN 257
 DB 241 KGFRLNHPKPNKNN 257
 RESULT 2
 FCEA MOUSE STANDARD; PRT; 250 AA.
 ID FCEA MOUSE
 AC F20489;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE High affinity immunoglobulin epsilon receptor alpha-subunit precursor
 DE (FCRI) (IGE FC receptor, alpha-subunit) (FC-epsilon RI-alpha).
 GN FCER1A OR FCEA.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 OX NCBI_TaxID=10090;
 OX [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89359361; PubMed=2527850;
 RA Ra C.; Jouvin M.H.E.; Kinet J.-P.;
 RT "Complete structure of the mouse mast cell receptor for IgE (Fc
 epsilon RI) and surface expression of chimeric receptors
 (rat-mouse-human) on transfected cells";
 RL J. Biol. Chem. 264:15323-15327(1989).
 CC -|- FUNCTION: BINDS TO THE FC REGION OF IMMUNOGLOBULIN EPSILON. HIGH
 CC AFFINITY RECEPTOR. RESPONSIBLE FOR INITIATING THE ALLERGIC
 CC RESPONSE. BINDING OF ALLERGEN TO RECEPTOR-BOUND IGE LEADS TO CELL
 CC ACTIVATION AND THE RELEASE OF MEDIATORS (SUCH AS HISTAMINE) RECEPTOR
 CC RESPONSIBLE FOR THE MANIFESTATIONS OF ALLERGY. THE SAME RECEPTOR
 CC ALSO INDUCES THE SECRETION OF IMPORTANT LYMPHOKINES.
 CC -|- SUBUNIT: TETRAMER OF AN ALPHA CHAIN, A BETA CHAIN, AND TWO
 CC DISULFIDE LINKED GAMMA CHAINS.
 CC -|- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -|- SIMILARITY: Contains 2 immunoglobulin-like domains.
 CC
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 CC EMBL; J05018; AAA37600.1; -;
 DR PIR; A34342; A34342.
 DR HSP; P12319; 1ALS.
 DR MGD; MGI:95494; Fcer1a.
 DR GO; GO:0007185; P:signal transduction; IDA.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003599; Ig.
 DR Pfam; PF00047; Ig; 2.


```

QY 131 RCHGWRNDVYKVIYKDGALKYWYENHNISITNATVEDSGTYCTKWQWLDYSEPL 190
Db 129 RCRSKWKVHKVYIKDYDIAFKYSNNSIRKATPNDSGSHCTGYLNKVECKSDKF 188
QY 191 NITVIKAPREKY-WIQFFIPLVILFAVDTGTLFISTQQOQVTLKIKRTRKG 242
Db 189 SIADVVDYIEVWMLQIFPSLAVILFAVDTGTLFISTQQOQVTLKIKRTRKG 241

RESULT 4
FCG3_PIG STANDARD; PRT; 257 AA.
AC Q28942; Q28940; Q28941;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Low affinity immunoglobulin gamma Fc region receptor III precursor
DE (IgG Fc receptor III) (Fc-gamma RIII) (FCRIII) (Cytolytic trigger
DE molecule G7).
GN FCGR3.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 27-47; 92-107 AND 179-188.
RC STRAIN=Minnesota miniature swine;
RX MEDLINE=94358430; PubMed=8077673;
RA Halloran P.J., Sweeney S.E., Strichmeier C.M., Kim Y.B.;
RT "Molecular cloning and identification of the porcine cytolytic
RT trigger molecule G7 as a Fc gamma RIII alpha (CD16) homologue.";
RL J. Immunol. 153:2631-2641(1994).
CC -!- FUNCTION: Receptor for the Fc region of complexed immunoglobulins
CC gamma. Low affinity receptor.
CC -!- SUBUNIT: FORMS A COMPLEX WITH NK-E.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
CC -!- TISSUE SPECIFICITY: FOUND IN POLYMORPHONUCLEAR CELLS (PMN), PBMC,
CC MACROPHAGES, SPLEEN, AND AT LOW LEVELS IN LYMPH NODES BUT NOT IN
CC THYMUS OR LIVER.
CC -!- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
CC -----
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CC -----
DR EMBL; U08993; AAA57190.1; -;
DR EMBL; U08991; AAA57188.1; -;
DR EMBL; U08992; AAA57189.1; -;
DR HSSP; P12319; IALS.
DR InterPro; IPR007110; Ig-like.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00409; Ig; 2.
DR PROSITE; PS00835; IG-LIKE; 2.
KW Ig-binding protein; Receptor; Transmembrane; Glycoprotein; Signal;
KW Immunoglobulin domain; Repeat.
FT SIGNAL 1 19
FT CHAIN 20 257
FT FT LOW AFFINITY IMMUNOGLOBULIN GAMMA FC
FT FT REGION RECEPTOR III.
FT FT EXTRACELLULAR (POTENTIAL).
FT FT POTENTIAL.
FT FT DOMAIN 20 209
FT FT TRANSMEM 210 230
FT FT DOMAIN 231 257
FT FT CYTOPLASMIC (POTENTIAL).
FT FT DOMAIN 25 104
FT FT IG-LIKE C2-TYPE 1.
FT FT DOMAIN 108 190
FT FT IG-LIKE C2-TYPE 2.
FT FT BY SIMILARITY.
FT FT DISULFID 48 90
FT FT BY SIMILARITY.
FT FT DISULFID 129 173
FT FT CARBOHYD 64 64
FT FT CARBOHYD 134 134
FT FT N-LINKED (GLCNAC. . .) (POTENTIAL).
FT FT N-LINKED (GLCNAC. . .) (POTENTIAL).
FT FT N-LINKED (GLCNAC. . .) (POTENTIAL).
FT FT CARBOHYD 162 162

```

```

FT CARBOHYD 181 181 N-LINKED (GLCNAC. . .) (IN CLONE 334.8)
FT VARIANT 55 55 (POTENTIAL).
FT VARIANT 149 149 R -> G (IN CLONE 284.4).
FT VARIANT 181 181 K -> M (IN CLONE 334.8).
FT VARIANT 181 181 D -> N (IN CLONE 334.8).
FT VARIANT 186 186 P -> A (IN CLONE 334.8).
SQ SEQUENCE 257 AA; 29062 MW; 1D038CC1552B97CB CRC64;

Query Match 30.1%; Score 419; DB 1; Length 257;
Best Local Similarity 38.8%; Pred. No. 1.7e-27;
Matches 94; Conservative 41; Mismatches 91; Indels 16; Gaps 3;

QY 7 SPTLLCVALLFPAPDGVLAPOKPVSLNPPWNRIFKGNVTLTCNGNFFEVSGTKWFH 66
Db 6 SPTAL--LLLSVPGTHAEDPKSVVILDPPADRLLKXDSVTLKCGAYPRDSDTEWRW 63
QY 67 NGSLSSEETNSSLNIVNAKPEDSGEYKCOHQQVNESEPVYLFVSDWLLQLQASAEVWMEGQ 126
Db 64 NGTLISNKASSYSITDATVGNSEGYTCKTGLSAQSDPLRLVYKGLWLLQLQAPRWVQGE 123
QY 127 PLFLRCHGWRNDVYKVIYKDGALKYWYENHNISITNATVEDSGTYCTKWQWLDYE 186
Db 124 SRLRCHTWKNTITQKVQYFQNGMKFQSHQNFYHPNATLKDGSGYFCRGIKNYDLS 183
QY 187 SEPLNITVIKAPREKYWLOFFIP-----LLVILFAVDTGTLFISTQQOQVTLKIKR 239
Db 184 SEPVKVTYQGSKSPSIFLFWHQLIFCLVWGFLFAVDTLGLYFSVR-----KVLRS 236
QY 240 RK 241
Db 237 SK 238

RESULT 5
FCG3A_HUMAN STANDARD; PRT; 254 AA.
ID FC3A_HUMAN
AC P08637;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Low affinity immunoglobulin gamma Fc region receptor III-A precursor
DE (IGG Fc receptor III-2) (Fc-gamma RIII-alpha) (Fc-gamma RIIIA)
DE (FCRIIIA) (Fc-gamma RIII) (FCRIII) (CD16-A) (FCR-10).
GN FCGR3A OR FCG3 OR FCGR3 OR IGRF3 OR CD16A.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89328325; PubMed=2526846;
RA Ravetch J.V., Perussia B.;
RT "Alternative membrane forms of Fc gamma RIII(CD16) on human natural
RT killer cells and neutrophils. Cell type-specific expression of two
RT genes that differ in single nucleotide substitutions.";
RL J. Exp. Med. 170:481-497(1989).
RN [2]
RP SEQUENCE OF 1-39 FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=95138131; PubMed=7836402;
RA Gessner J.E., Grussemeyer T., Kolanus W., Schmidt R.E.;
RT "The human low affinity immunoglobulin G Fc receptor III-A and III-B
RT genes. Molecular characterization of the promoter regions.";
RL J. Biol. Chem. 270:1350-1361(1995).
RN [3]
RP VARIANTS ARG-66 AND HIS-66.
RX MEDLINE=96183251; PubMed=8609432;
RA de Haas M., Koene H.R., Kleijer M., de Vries E., Simsek S.,
RA van Tol M.J.D., Roos D., von dem Borne A.E.G.K.;
RT "A triallelic Fc gamma receptor type IIIA polymorphism influences the
RT binding of human IGG by NK cell Fc gamma RIIIA.";
RL J. Immunol. 156:3948-3955(1996).
RN [4]

```


VARIANT VAL-157.
MEDLINE=97385047; PubMed=9242542;
Koene H.R., Kleijer M., Algra J., Roos D., von dem Borne A.E.G.K.,
de Haas M.;
"Fc gammaRIIIa-156V/F polymorphism influences the binding of IgG by
natural killer cell Fc gammaRIIIa, independently of the Fc
gammaRIIIa-48L/R/H phenotypes";
Blood 90:1109-1114(1997).
[5]
VARIANT VAL-176.
MEDLINE=97426467; PubMed=9276722;
Wu J., Edberg J.C., Redecha P.B., Bansal V., Guyre P.M., Coleman K.,
Salmon J.E., Kimberly R.P.;
"A novel polymorphism of Fc gammaRIIIa (CD16) alters receptor function
and predisposes to autoimmune disease.";
J. Clin. Invest. 100:1059-1070(1997).
CC -!- FUNCTION: RECEPTOR FOR THE FC REGION OF IGG. BINDS COMPLEXED OR
AGGREGATED IGG AND ALSO MONOMERIC IGG. MEDIATES ANTIBODY-DEPENDENT
CELLULAR CYTOTOXICITY (ADCC) AND OTHER ANTIBODY-DEPENDENT
RESPONSES, SUCH AS PHAGOCYTOSIS.
CC -!- SUBUNIT: EXISTS AS A HETERO-OLIGOMERIC RECEPTOR COMPLEX WITH FC
EPSILON RECEPTOR I GAMMA SUBUNIT AND / OR THE CD3 ZETA SUBUNIT.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (Potential). Exists
also as a soluble receptor.
CC -!- TISSUE SPECIFICITY: Expressed on natural killer cells,
macrophages, subpopulation of T cells, immature thymocytes and
placental trophoblasts.
CC -!- PTM: Glycosylated. Contains high mannose-and complex-type
oligosaccharides.
CC -!- PTM: The soluble form is produced by a proteolytic cleavage.
CC -!- POLYMORPHISM: Isoform Val-157 shows a higher binding capacity of
IgG1, IgG3 and IgG4 compared with isoform Phe-157. Alleles Leu-66
and Phe-157, and alleles His-66 / Arg-66 and Val-157 are in
linkage disequilibrium.
CC -!- MISCELLANEOUS: ENCODED BY ONE OF TWO NEARLY IDENTICAL GENES:
FCGR3A (SHOWN HERE) AND FCGR3B WHICH ARE EXPRESSED IN A TISSUE-
SPECIFIC MANNER. THE PHE-203 IN III-A DETERMINES THE TRANSMEMBRANE
DOMAINS WHEREAS THE SER-203 IN III-B DETERMINES THE GPI-ANCHORING.
CC -!- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
CC -!- DATABASES: NAME=PROW; NOTE=CD guide CD16A entry;
WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cdl6a.htm".

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entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).

EMBL; X52645; CAA86870.1; -.
DR DR EMBL; Z46222; CAA86295.1; -.
DR DR PIR; JL0107; JLO107.
DR DR HSSP; P42319; IALS.
DR DR Gnew; HGNC:3619; FCGR3A.
DR DR MIM; 146740; -.
DR DR GO; GO:0005886; Cytoplasma membrane; TAS.
DR DR GO; GO:0006955; P:Immune response; TAS.
DR DR InterPro; IPR007110; Ig-Like.
DR DR InterPro; IPR003599; Ig.
DR DR Pfam; PF000047; ig; 2.
DR DR SMART; SM00409; IG_2.
DR DR PROSITE; PS50835; IG_LIKE; 2.
KW IgG-binding protein; Receptor; Transmembrane; Glycoprotein; Signal;
KW Immunoglobulin domain; Repeat; Multigene family; Polymorphism.
FT SIGNAL 1 16
FT CHAIN 17 254 LOW AFFINITY IMMUNOGLOBULIN GAMMA FC
FT FT REGION RECEPTOR III-A.
FT FT EXTRACELLULAR (POTENTIAL).
FT DOMAIN 17 209 POTENTIAL.
FT TRANSMEM 209 229 POTENTIAL.
FT DOMAIN 230 254 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 24 105 IG-LIKE C2-TYPE 1.
FT DOMAIN 107 189 IG-LIKE C2-TYPE 2.

FT	DISULFID	47	89		BY SIMILARITY.
FT	DYSULFID	128	172		BY SIMILARITY.
FT	CARBHYD	56	56		N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBHYD	63	63		N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBHYD	92	92		N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBHYD	180	180		N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBHYD	187	187		N-LINKED (GLCNAC. .) (POTENTIAL).
FT	VARIANT	66	66		L -> R.
FT	VARIANT	66	66		/FTIG=VAR_008799.
FT	VARIANT	157	157		L -> H.
FT	VARIANT	176	176		F -> V.
FT	VARIANT				/FTId=VAR_008801.
FT	VARIANT				F -> V (in dbSNP:396991).
FT	VARIANT				/FTId=VAR_003960.
FT	VARIANT				/FTId=VAR_003960.
SQ	SEQUENCE	254 AA;	29089 MW;	D38DL78D32C67337 CRC64;	
	Query Match	30.1%;	Score 418;	DB 1:	Length 254;
	Best Local Similarity	40.9%;	Pred. No. 2e-27;		
	Matches	94;	Conservative	34;	Mismatches 92; Indels 10; Gaps 3;
Qy	10	LLCVALLFPADGVLAVPQPK-	-VSLNPWNRIKCGNTVLICNGNNFEVSSTKKFHN	67	
Db	5	LLPTLLLLLSAG-MRTEDLPKA	WFLPEQPWKLESDVTLCQGAYSPEDNSTQWFHN	63	
Qy	68	GSLSEETNSLNIWNAKFDSGEY	KCHQQNVSEPVLYEFSDWILLQAESAEEVMGQP	127	
Db	64	ESLISSOASSYFDAAITVDSDS	GEYRCQTNLSTLSDPQLVHIGWLLOAPRWVFKEBDP	123	
Qy	128	LFRCHGWNRNDVKVIYYKDGA	LKYENHNISITNAVDESGTYICTKWQLDYES	187	
Db	124	IHLRCHSWKTALHKVTVYLON	GKGKRYFHNSDFYIPKATLKDGSGYFCRLFGSKNVS	183	
Qy	188	EPLNITVIKPREKMYLQFIPI	P-----LLWLIFAVDTGLFITSTOOQU	230	
Db	184	ETVNITTOGLAVSTISSFFPG	QVQSFCIWMULLFAVDIGLYSVXTNI	233	
	RESULT 6				
	FCG3 BOVIN				
ID	_FCG3 BOVIN	STANDARD;	PRT;	250 AA.	
DC	P9107;				
AT	30-MAY-2000 (Rel. 39,	Created)			
DT	30-MAY-2000 (Rel. 39,	Last sequence update)			
DT	10-OCT-2003 (Rel. 42,	Last annotation update)			
DE	Low affinity immunoglobulin gamma Fc receptor III precursor				
DE	(IgG Fc receptor III) (Fc-gamma RIII) (FCRIII).				
GN	FCGR3 OR FCGRIII				
OS	Bos taurus (Bovine).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;				
OC	Bovidae; Bos.				
OX	NCBI_TaxID=9913;				
RX	[n]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=Lymph node;				
RX	MEDLINE=97246739; PubMed=9089104;				
RA	Collins R.A., Gelder K.I., Howard C.J.;				
RT	"Nucleotide sequence of cattle FCGRIII: its identification in gammadelta T cells";				
RL	Immunogenetics 45:440-443(1997).				
CC	!- FUNCTION: IS A RECEPTOR FOR THE FC REGION OF IGG. BINDS COMPLEXED OR AGGREGATED IGG AND ALSO MONOMERIC IGG. ALSO MEDIATES ANTIBODY-DEPENDENT CELLULAR TOXICITY (BY SIMILARITY).				
CC	!- SUBCELLULAR LOCATION: Type I membrane protein (Potential).				
CC	!- TISSUE SPECIFICITY: EXPRESSED IN GAMMA-DELTA T CELLS.				
CC	!- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.				
CC	!- CAUTION: IT IS NOT SURE IF THE VARIANTS ARE DUE TO DIFFERENT ALLELES OR TO THE EXISTENCE OF AT LEAST TWO GENES.				
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DR EMBL; X99695; CA68026.1; -.
DR HSP; P12319; IALS.
DR InterPro; IPR007110; Ig-like.
DR Pfam; PF00047; Ig; 2.
DR PROSITE; PS0835; IG LIKE; 2.
KW IgG-binding protein; Receptor; Transmembrane; Glycoprotein; Signal;
KW Immunoglobulin domain; Repeat; Polymorphism.
FT SIGNAL 1 16
FT CHAIN 17 250
FT DOMAIN 17 208
FT TRANSMEM 209 225
FT DOMAIN 226 250
FT DOMAIN 23 105
FT DOMAIN 99 189
FT DISULFID 47 89
FT DISULFID 128 172
FT CARBOHYD 56 56
FT CARBOHYD 63 63
FT CARBOHYD 180 180
FT VARIANT 11 11
FT VARIANT 12 12
FT VARIANT 46 46
FT VARIANT 107 107
FT VARIANT 114 114
FT VARIANT 229 229
SQ SEQUENCE 250 AA; 28050 MW; D5625139E889E207 CRC64;

Query Match 30.0%; Score 417; DB 1; Length 250;
Best Local Similarity 38.2%; Pred. No. 2.4e-27;
Matches 91; Conservative 38; Mismatches 93; Indels 16; Gaps 3;

QY 1 MAPAMESPTLLCVALLPAPDGLAVPKPKVSLNPPWNRIFKGVNTLCNGNPFVS 60
DB 4 LILPAALPLV-----SADTQADFSKAVLLDPQWNVLTNRVTLKQGDYFVEDN 56
QY 61 STKWFHNGSLSEETNSLNIYNAKPEDSGEYKQHQVNESEPYLVEFSDWLLQASAE 120
DB 57 STKWFHNGTLSSQTPSYFIADVQDSGEYKQKQGLSAPSDPKLEHVHGLLQVAQR 116
QY 121 VVMGQPLFLCHGRWVDVYKLYYKDGALKYWNENHISITNATVEDSGTYCTGKV 180
DB 117 VNVGKPIRLCKHSHKKTTPVAKVQYFNGRGKYSNGNSDFHPEAKLHSGSYFCRGII 176
QY 181 WQDYSESPNLNITVIKAPREKYNLQFTIP-----LLVVLFAVDTLGFIQTQQV 230
DB 177 GSKNESSEVQITV-QAPETLQTVSSFPFPWHQITFCLVGVLFVAVDTGLYFSVRHL 233

RESULT 7
FC3B HUMAN
ID FC3B HUMAN STANDARD; PRT; 233 AA.
AC O75015;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Low affinity immunoglobulin gamma Fc region receptor III-B precursor
DE (IgG Fc receptor III-1) (Fc-gamma RII-beta) (Fc-gamma RIIIB)
DE (FCRIIB) (Fc-gamma RIII) (FCRII) (CD16-B) (FCR-10).
DE FCGR3B OR FCGR3 OR IGR3 OR CD16B.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (VARIANT NA-2).
RX MEDLINE=89328325; PubMed=2526846;
RA Ravetch J.V., Perussia B.

RT "Alternative membrane forms of Fc gamma RIII(CD16) on human natural
RT killer cells and neutrophils. Cell type-specific expression of two
RT genes that differ in single nucleotide substitutions.";
RL J Exp. Med. 170:481-497(1989).
RN [2]
RP SEQUENCE FROM N.A. (VARIANT NA-2).
RC TISSUE=Placenta;
RX MEDLINE=88232937; PubMed=2967436;
RA Simmons D., Seed B.;
RT "The Fc gamma receptor of natural killer cells is a phospholipid-
RT linked membrane protein.";
RL Nature 333:568-570(1988).
RN [3]
RP ERRATUM.
RA Simmons D., Seed B.;
RL Nature 340:662-662(1989).
RN [4]
RP SEQUENCE FROM N.A. (VARIANT NA-1).
RC TISSUE=Leukocyte;
RX MEDLINE=89128838; PubMed=2521732;
RA Feltz G.A., Grundy H.O., Lebo R.V., Yssel H., Barsh G.S., Moore K.W.;
RT "Human Fc-gamma-RIII: Cloning, expression, and identification of the
RT chromosomal locus of two Fc receptors for IgG.";
RL Proc. Natl. Acad. Sci. U.S.A. 86:1013-1017(1989).
RN [5]
RP SEQUENCE OF 1-72 FROM N.A. (VARIANT NA-2).
RC TISSUE=Placenta;
RX MEDLINE=95138131; PubMed=7836402;
RA Gessner J.E., Grussenmeyer T., Kolanus W., Schmidt R.E.;
RT "The human low affinity immunoglobulin G Fc receptor III-A and III-B
RT genes. Molecular characterization of the promoter regions.";
RL J. Biol. Chem. 270:1350-1361(1995).
RN [6]
RP X-RAY CRYSTALLOGRAPHY (3.2 ANGSTROMS) IN COMPLEX WITH IGG1 FC.
RX MEDLINE=20372189; PubMed=10917521;
RA Sondermann P., Huber R., Oosthuizen V., Jacob U.;
RT "The 3.2-A crystal structure of the human IgG1 Fc fragment-Fc
RT gammaRIII complex.";
RL Nature 406:267-273(2000).
RN [7]
RP X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS) OF 19-192.
RX MEDLINE=20471519; PubMed=11021536;
RA Zhang Y., Boesen C.C., Radaev S., Brooks A.G., Fridman W.H.,
RA Sautes-Fridman C., Sun P.D.;
RT "Crystal structure of the extracellular domain of a human Fc gamma
RT RIII.";
RL Immunity 13:387-395(2000).
RN [8]
RP VARIANT SH ASP-78.
RX MEDLINE=97180159; PubMed=9028335;
RA Bux J., Stein E.L., Bierling P., Fromont P., Clay M., Stroncek D.,
RA Santos S.;
RT "Characterization of a new alloantigen (SH) on the human neutrophil Fc
RT gamma receptor IIIB.";
RL Blood 89:1027-1034(1997).
CC -!- FUNCTION: RECEPTOR FOR THE FC REGION OF IMMUNOGLOBULINS GAMMA. LOW
CC AFFINITY RECEPTOR. BINDS COMPLEXED OR AGGREGATED IGG AND ALSO
CC MONOMERIC IGG. CONTRARY TO III-A, IS NOT CAPABLE TO MEDIATE
CC ANTIBODY-DEPENDENT CYTOTOXICITY AND PHAGOCYTOSIS. MAY SERVE AS A
CC TRAP FOR IMMUNE COMPLEXES IN THE PERIPHERAL CIRCULATION WHICH DOES
CC NOT ACTIVATE NEUTROPHILS.
CC -!- SUBUNIT: Monomer.
CC -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.
CC EXISTS ALSO AS A SOLUBLE RECEPTOR, PRODUCED BY A PROTEOLYTIC
CC CLEAVAGE.
CC -!- TISSUE SPECIFICITY: EXPRESSED SPECIFICALLY BY POLYMORPHONUCLEAR
CC LEUKOCYTES (NEUTROPHILS). ALSO EXPRESSED BY STIMULATED
CC EOSINOPHILS.
CC -!- PTM: GLYCOSYLATED. GLYCOSYLATION PLAYS AN INHIBITORY ROLE IN THE
CC INTERACTION WITH IGG3.
CC -!- PTM: The soluble form is produced by a proteolytic cleavage.
CC -!- POLYMORPHISM: There are three allelic forms of FCGR3B: NA-1, NA-2
CC (shown here) and SH. NA-1 and NA-2 are detectable with antibodies

Db	5	LLPTALLLVASAG-NRTEDLPKPAWLEFPQWVSLEKDSVLLKCKQGAISPEDNSIQWPHN	63
Qy	68	GSLSSEETNSLNIWNAKFSDSGEYKCHQHQVNESEFPVILEVFSDFWLLLOASAEVVMGQP	127
Db	64	ESLISQASYSFFDAATVNDSDGEYRCQTNLSTLSDPQVLEHIGWLLLOAPRWVKEEDP	123
Qy	128	LFURCHGRNWDVYKVIYKDKGALKYWNHNISITNAIVDSGTYYCTGKYWQLDYES	187
Db	124	IHLRCHSWKNTALHKVYTLQNGKDRKYFHNSDFHIPKATLKDSGYSFRCGLVSGKNVSS	193
Qy	188	EPINIVIKAPREKYWLQFPF-----LLVWLVFAVDTGLTSTQOQV	230
Db	184	ETVNIITQGLAVSTISSPSPGQYQVSCVCLVMVLLFAVDTGLFVSVKTN	233

RESULT 8

FCG2_BOVIN	STANDARD;	PRT;	296 AA.
ID_FCG2_BOVIN	Q28110;		
AC	Q28110;		
DT	01-NOV-1997 (Rel. 35, Created)		
DT	01-NOV-1997 (Rel. 35, Last sequence update)		
DT	10-OCT-2003 (Rel. 42, Last annotation update)		
DE	Low affinity immunoglobulin gamma Fc region receptor II precursor (Fc-gamma RII) (FCRII) (IG Fc receptor II).		
DE	FCGR2.		
GN	Bos taurus (Bovine).		
OS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovioidea;		
OC	Bovidae; Bovinae; Bos.		
OX	NCBI TaxID=9913;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=94245284; PubMed=8189320;		
RA	Zhang G., Young J.R., Tregaskes C.R., Howard C.J.;		
RT	"Cattle Fc gamma RII: Molecular cloning and ligand specificity. ";		
RL	Immunogenetics 39:423-427(1994).		
CC	FUNCTION: Binds to the Fc region of immunoglobulins gamma. Low affinity receptor.		
CC	CELLULAR LOCATION: Type I membrane protein.		
CC	TISSUE SPECIFICITY: Higher expression is found in macrophages than in neutrophils (Probable).		
CC	DOMAIN: Contains 1 copy of a cytoplasmic motif that is referred to as the immunoreceptor tyrosine-based inhibitor motif (ITIM).		
CC	This motif is involved in downmodulation of cellular responses.		
CC	The phosphorylated ITIM motif binds to the SH2 domain of PTPN6(SHP-1).		
CC	SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.		
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DR	EMBL; X75671; CAA53367.1; -		
DR	PIR; I46021; I46021.		
DR	HSSP; P12319; 1ALS.		
DR	InterPro; IPR007110; IG-like.		
DR	InterPro; IPR003599; IG.		
DR	Pfam; PF00047; IG; 2.		
DR	SMART; SM00409; IG; 2.		
DR	PROSITE; PS50835; IG Like; 2.		
KW	IG-binding protein; Receptor; Transmembrane; Glycoprotein; Signal; Immunoglobulin domain; Repeat.		
KW	IMMUNOGLOBULIN DOMAIN; REPEAT.		
FT	SIGNAL	1	42
FT	CHAIN	43	296
FT	FT		
FT	DOMAIN	43	225
FT	TRANSMEM	226	246
FT	DOMAIN	247	296
FT	DOMAIN	47	129

LOW AFFINITY IMMUNOGLOBULIN GAMMA FC REGION RECEPTOR II. EXTRACELLULAR (POTENTIAL). POTENTIAL. CYTOPLASMIC (POTENTIAL). IG-LIKE C2-TYPE 1.

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FT DOMAIN 130 212 IG-LIKE C2-TYPE 2.
FT SITE 273 278 ITIM MOTIF.
FT DISULFID 70 112 BY SIMILARITY.
FT DISULFID 151 195 BY SIMILARITY.
FT CARBOHYD 79 79 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 86 86 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 105 105 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 179 179 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 186 186 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 210 210 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 296 AA; 33020 MW; A61A40A611F71ED5 CRC64;

Query Match 29.1%; Score 405; DB 1; Length 296;
Best Local Similarity 42.2%; Pred. No. 2.9e-26;
Matches 79; Conservative 33; Mismatches 71; Indels 4; Gaps 2;

QY 10 LLCVALLFPADGVLAVPQPK--VSLNPPNRRIFKGNVTLTCNGNNFFVSTKWFH 67
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
29 LLWTALLFLAP--VSGKPDLPKAVVTIQPAWINVLREDHVTLCQGTFSAGNLTTFHN 86
QY 68 GSLSEETNSSLNIVNAKFDGSEYKCOHQVNESEPVYLEVFSDWLLLOASAEVVMGEP 127
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
87 GSSHTQKQPSVSPAGNDGSGRCQREQLSDPVLHVDVLSWLLLOTPSLVFQGE 146
QY 128 LFLCHGRWMDVYKVIYKDGKALKYENHNISITNATVEDSGTYCTGKVMQLDYES 187
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
147 IMLCHSRWNOPLNKITFYQDRKSKIFSQRTNFSIPRANLSHSGQYHCTAFIGKMLHSS 206
QY 188 RPLNITY 194
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
207 QPVNITY 213

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RESULT 9
FCG3 MOUSE
ID_FCG3 MOUSE STANDARD; PRT; 261 AA.
AC P08508;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-AUG-1988 (Rel. 08, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Low affinity immunoglobulin gamma Fc region receptor III precursor
DE (IGG Fc receptor III) (Fc-gamma RIII) (FCRIII).
GN FCGR3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87042761; PubMed=2946078;
RA Ravetch J.V., Luster A.D., Weinshank R., Kochan J., Pavlovic A.,
RA Portney D.A., Hulmes J., Pan Y.-C.E., Unkeless J.C.;
RT "Structural heterogeneity and functional domains of murine
RT immunoglobulin G Fc receptors."
RL Science 234:718-725 (1986).
RN [2]
RP SEQUENCE OF 1-29 FROM N.A.
RC STRAIN=BALE/c; TISSUE=Liver;
RA Soares H.J., Onken M.D., Kulczycki A. Jr.;
RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Receptor for the Fc region of complexed immunoglobulins
CC gamma. Low affinity receptor.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
CC -!- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
CC
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CC use by non-profit institutions as long as its content is in no way
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CC

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DR EMBL; M14215; AAA37604.1; -.
DR EMBL; X60929; CAA43266.1; -.
DR PIR; S29360; S29360.
DR HSP; P12319; IALS.
DR MGD; MGI:95500; Fcgr3.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003599; Ig.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00409; Ig; 2.
DR PROSITE; PS00835; IG-LIKE; 2.
KW IGG-binding protein; Receptor; Transmembrane; Glycoprotein; Signal;
KW Immunoglobulin domain; Repeat.
FT SIGNAL 1 30 POTENTIAL.
FT CHAIN 31 261 LOW AFFINITY IMMUNOGLOBULIN GAMMA FC
REGION RECEPTOR III.
FT DOMAIN 31 215 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 216 235 POTENTIAL.
FT DOMAIN 236 261 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 33 110 IG-LIKE C2-TYPE 1.
FT DOMAIN 116 198 IG-LIKE C2-TYPE 2.
FT DISULFID 56 98 BY SIMILARITY.
FT DISULFID 137 181 BY SIMILARITY.
FT CARBOHYD 64 64 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 91 91 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 165 165 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 172 172 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 261 AA; 30036 MW; 757FB83668E41069 CRC64;

Query Match 28.9%; Score 401.5; DB 1; Length 261;
Best Local Similarity 35.6%; Pred. No. 4.8e-26;
Matches 90; Conservative 44; Mismatches 104; Indels 15; Gaps 5;

QY 11 LCVALLFPADGVLAVPQPKVSLNPPNRRIFKGNVTLTCNGNNFFVSTKWFHNG-S 69
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
16 LTILLFAPADQSAALPKAVVKLDPPIQVLKDMVTLMCEGTNPGNSSTQWFHNGS 75
QY 70 LSEETNSSLNIVNAKFDGSEYKCOHQVNESEPVYLEVFSDWLLLOASAEVVMGQPLF 129
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
76 IRSQVQASYTF-KATVNDGSEYRCQEQRLSDPVLGVIDSWLLLOTPPQVFLGEIT 134
QY 130 LRCHGRWMDVYKVIYKDGKALKYENHNISITNATVEDSGTYCTGKVMQLDYES 189
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
135 LRCHSRWKNLNRISGFHNEKSVRHHYKSNFSPKANHSISGDYCYGSLGSTQHQSKP 194
QY 190 LNITY----IKAPREKYWLQFPIPLVVLFAVDLTGLFISTQQQVTLKIKRTEKGR- 244
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
195 VTIITQDPATTSISLWHTAFSLVMCLLFAVDLTGLFYVRR-----NLQTPREYWRK 248
QY 245 --LLNPHKPKPNPK 255
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
249 SLIRKHAQAPQDK 261

```

```

RESULT 10
FCG3 RAT
ID_FCG3 RAT STANDARD; PRT; 267 AA.
AC P27645; Q04798; Q63204;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Low affinity immunoglobulin gamma Fc region receptor III precursor
DE (IGG Fc receptor III) (Fc-gamma RIII) (FCRIII).
GN FCGR3.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS B; C AND D).
RC STRAIN=Sprague-Dawley;
RX MEDLINE=91250730; PubMed=1710249;
RA Farber D.L., Sears D.W.;
RT "Rat CD16 is defined by a family of class III Fc gamma receptors

```


RT isoforms of guinea pig Fc receptor for IgG1 and IgG2.1;
RL J. Immunol. 151:2014-2023(1993).
CC -!- FUNCTION: Binds to the Fc region of immunoglobulins gamma. Low
CC affinity receptor.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=3;
CC Name=2R-B3;
CC IsoId=Q0513-1; Sequence=Displayed;
CC Name=2R-B1; IsoId=Q0513-2; Sequence=VSP_002639;
CC Name=2R-B2;
CC Name=2R-B2;
CC TISSUE SPECIFICITY: Macrophages and polymorphonuclear leukocytes
CC express preferentially isoform 2R-B1. B lymphocytes express
CC isoform 2R-B1, isoform 2R-B2 and isoform 2R-B3.
CC -!- DOMAIN: Contains 1 copy of a cytoplasmic motif that is referred
CC to as the immunoreceptor tyrosine-based inhibitor motif (ITIM).
CC This motif is involved in downmodulation of cellular responses.
CC -!- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
CC
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CC
CC -----
CC EMBL; D13693; BAA02852.1; -;
CC EMBL; D13692; BAA02851.1; -;
CC EMBL; D13691; BAA02850.1; -;
CC EMBL; M35272; AAA37036.1; ALT_INIT.
CC HSSP; P12319; IALS.
CC InterPro; IPR007110; Ig-like.
CC Pfam; PF00047; ig; 2.
CC PROSITE; PS50835; IG_LIKE; 2.
KW IgG-binding protein; Receptor; Transmembrane; Glycoprotein; Signal;
KW Immunoglobulin domain; Repeat; Alternative splicing.
FT SIGNAL 1 42
FT CHAIN 43 341
FT FT
FT DOMAIN 43 224
FT TRANSMEM 225 245
FT DOMAIN 246 341
FT DOMAIN 48 125
FT DOMAIN 131 213
FT SITE 318 323
FT DISULFID 71 113
FT DISULFID 152 196
FT CARBOHYD 79 79
FT CARBOHYD 106 106
FT CARBOHYD 180 180
FT CARBOHYD 187 187
FT CARBOHYD 195 195
FT VARSPPLIC 273 301
FT FT
FT FT
FT VARSPLIC 257 301
FT GNPERENGELPDPGYSVVFSGSWMSCGPLDGLPAR
FT TDL5 -> A (in isoform 2R-B1).
FT /FTId=VSP_002639.
FT
FT CONFLICT 114 114 Q -> QVLPYSYRFTAKGNDSEYRCQ (IN REF. 1).
FT SEQUENCE 341 AA; 37091 MW; 5137E3271D443B84 CRC64;
Query Match 28.4%; Score 395; DB 1; Length 341;
Best Local Similarity 38.2%; Pred. No. 2.3e-25;
Matches 96; Conservative 33; Mismatches 106; Indels 16; Gaps 5;
QY 7 SPTLLCVALLFPAP-DGVLAVPQPKVSLNPPNWRIFKXENVTLCNGNFFEVSSTKWF 65
DB 26 SHMLLWITVFLAPVAGTSADPPKAVVLEPPWQVLGRDVRTLTCEGSPGNHSTQWL 85
QY 66 HNGSUSEETNSLNTVNAKFDESGYKQHQOVNESEPVYLEVFSDWLLQLQASAEVWNEG 125

Db 86 HNGRLPTQVLPYSRFTAKGNDSEYRCQAGCTSLSDPVRLDVSDWLVLTQSILFQEG 145
QY 126 QELFLRCHWRNDVYKVIYKDGALKYVENHNISITNATVEDSGTYCTGKWQLDY 185
Db 146 DIVLFRCHSWNNWPLAKVTFFYHNGVAKYFSSKQFSPQANSHSGAYNCTGLIGRTSH 205
QY 186 ESEPLNITVIKAPREKYWLFQFPIPLVILFVAVDFTGLFISTQQQVTFLLKIRTRKGRFL 245
Db 206 TSPPVITV-QGPKSS-----DSSMWVIVAAVIG--IATAIIVAVVAICLKK--- 252
QY 246 LNPHPKPNPN 256
Db 253 --KQPPGNPEH 261
RESULT 12
FCGI_HUMAN STANDARD; PRT; 374 AA.
AC P12314; P12315;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE High affinity immunoglobulin gamma Fc receptor I precursor (Fc-gamma
DE RI) (FcRI) (IgG Fc receptor I) (CD64 antigen).
GN FCGR1A OR FCGR1 OR FCGL OR IGFR1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89098339; PubMed=2974947;
RA Allen J.M., Seed B.;
RT "Nucleotide sequence of three cDNAs for the human high affinity Fc
RT receptor (FcRI).";
RL Nucleic Acids Res. 16:11824-11824(1988).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=89100284; PubMed=2911749;
RA Allen J.M., Seed B.;
RT "Isolation and expression of functional high-affinity Fc receptor
RT complementary DNAs.";
RL Science 243:378-381(1989).
CC -!- FUNCTION: Binds to the Fc region of immunoglobulins gamma. High
CC affinity receptor.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=A;
CC IsoId=P12314-1; Sequence=Displayed;
CC Name=B;
CC IsoId=P12314-2; Sequence=VSP_002637;
CC -!- TISSUE SPECIFICITY: Monocyte/macrophage specific.
CC -!- SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.
CC -!- DATABASE: NAME=PROW; NOTE=CD guide CD64 entry;
CC WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd64.htm".
CC
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CC
CC -----
CC EMBL; X14356; CAA32537.1; -;
CC EMBL; X14355; CAA32536.1; -;
CC PIR; A41357; A41357.
CC HSSP; P12319; IALS.
CC Genew; HGNC:3613; FCGR1A.
CC MIM; 145760; -;
CC GO; GO:0005057; Fc receptor signaling protein activity; TAS.

Db 132 LRCHGWKRLVNVYFRNGKSFQP-SSDSEVAILKTNLSHG1YHCSG-TGRHRYTSAG 189
 QY 190 LNVIT 194
 Db 190 VSITV 194

RESULT 14
 FCGH HUMAN STANDARD; PRT; 310 AA.
 AC P31594; O95649; CBN1A1;
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Low affinity immunoglobulin gamma Fc region receptor II-b precursor
 DE (Fc-gamma RII-b) (FCRII-b) (Ig Fc receptor II-b) (Fc-gamma-RIIb)
 DE (CD32 antigen) (CDw32).
 GN FCGR2B OR FCG2 OR IGR2 OR CD32.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 ON NCBI_TaxID=9606;
 RX MEDLINE=90059865; PubMed=2531080;
 RA Mellman I.;
 RT "Human IgG Fc receptor (hFcRII; CD32) exists as multiple isoforms in
 RT macrophages, lymphocytes and IgG-transporting placental epithelium.";
 RL EMBO J. 8:3657-3666(1989).
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORMS IIB1; IIB2 AND IIB3).
 RC TISSUE=Lymphocytes;
 RA Ng S., Sinclair N.R.S., Anderson C., Bell D.A., Cairns E.;
 RT "Fc-gamma-RIIb nucleotide sequences in SLE and non-SLE humans in vivo
 RT derived lymphocytes.";
 RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM IIB2).
 RC TISSUE=Placenta;
 RX MEDLINE=90059865; PubMed=2531080;
 RA Stuart S.G., Simster N.E., Clarkson S.B., Kacinski B.M., Shapiro M.,
 RT "Human IgG Fc receptor (hFcRII; CD32) exists as multiple isoforms in
 RT macrophages, lymphocytes and IgG-transporting placental epithelium.";
 RL EMBO J. 8:3657-3666(1989).
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORMS IIB1; IIB2 AND IIB3).
 RC TISSUE=Lymphocytes;
 RX MEDLINE=90010791; PubMed=2529942;
 RA Brooks D.G., Qiu W.Q., Luster A.D., Ravetch J.V.;
 RT "Structure and expression of human IgG FcRII (CD32). Functional
 RT heterogeneity is encoded by the alternatively spliced products of
 RT multiple genes.";
 RL J. Exp. Med. 170:1369-1385(1989).
 RN [4]
 RP SEQUENCE FROM N.A. (ISOFORM IIB2).
 RC TISSUE=Placenta;
 RX MEDLINE=90316181; PubMed=2142460;
 RA Engelhardt W., Geerds C., Frey J.;
 RT "Distribution, inducibility and biological function of the cloned and
 RT expressed human beta 2 Fc receptor II.";
 RL Eur. J. Immunol. 20:1367-1377(1990).
 RN [5]
 RP SEQUENCE FROM N.A. (ISOFORM IIB1).
 RC TISSUE=Skin;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Sherman C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalilus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [6]
 RP SEQUENCE OF 132-253 FROM N.A., AND VARIANT THR-232.
 RX MEDLINE=22109090; PubMed=12115230;
 RA Kyogoku C., Dijkstra O.H.M., Tsuchiya N., Hata Y., Kato H.,
 RA Yamaguchi A., Fukazawa T., Jansen M.D., Hashimoto H.,
 RA van de Winkel J.G.J., Kallenberg C.G.M., Tokunaga K.;
 RT "Fc gamma receptor gene polymorphisms in Japanese patients with
 RT systemic lupus erythematosus: contribution of FCGR2B to genetic
 RT susceptibility.";
 RL Arthritis Rheum. 46:1242-1254(2002).
 RN [7]
 RP VARIANT ASP-258.
 RX MEDLINE=93222096; PubMed=8466861;
 RA Warmerdam P.A., van den Herik-Oudijk I.E., Parren P.W.,
 RA Westerdaal N.A., van de Winkel J.G., Capel P.J.;
 RT "Interaction of a human Fc gamma RIIB1 (CD32) isoform with murine and
 RT human IgG subclasses.";
 RL Int. Immunol. 5:239-247(1993).
 CC -1- FUNCTION: Receptor for the Fc region of complexed or aggregated
 CC immunoglobulins gamma. Low affinity receptor. Involved in a
 CC variety of effector and regulatory functions such as phagocytosis
 CC of immune complexes and modulation of antibody production by B-
 CC cells. Binding to this receptor results in downmodulation of
 CC previous state of cell activation triggered via antigen receptors
 CC on B cells (BCR), T cells (TCR) or via another Fc receptor.
 CC Isoform IIB1 fails to mediate endocytosis or phagocytosis. Isoform
 CC IIB2 does not trigger phagocytosis.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=3;
 CC Name=IIB1;
 CC IsoID=P31994-1; Sequence=Displayed;
 CC Name=IIB2;
 CC IsoID=P31994-2; Sequence=VSP_002643;
 CC Name=IIB3;
 CC IsoID=P31994-3; Sequence=VSP_002642;
 CC -1- TISSUE SPECIFICITY: Is the most broadly distributed Fc-gamma-
 CC receptor. Expressed in monocyte, neutrophils, macrophages,
 CC basophils, eosinophils, Langerhans cells, B cells, platelets
 CC cells and placenta (endothelial cells). Not detected in natural
 CC killer cells.
 CC -1- DOMAIN: Contains 1 copy of a cytoplasmic motif that is referred
 CC to as the immunoreceptor tyrosine-based inhibitor motif (ITIM).
 CC This motif is involved in downmodulation of cellular responses.
 CC The phosphorylated ITIM motif binds to the SH2 domain of
 CC PTPN6/SHP-1.
 CC -1- DISEASE: Involved in a follicular lymphoma through a chromosomal
 CC translocation t(1;22)(q22;q11) which leads to the hyperexpression
 CC of the receptor. This may play a role in the tumor progression.
 CC -1- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
 CC -1- CAUTION: Has sometime been attributed to correspond to FCR-IIC.
 CC -1- DATABASE: NAME=PROW; NOTE=CD guide CD32 entry;
 CC WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd32.htm".
 CC -1- DATABASE: NAME=Atlas Genet. Cytogenet. Oncol. Haematol.;
 CC WWW="http://www.infobiogen.fr/services/chronocancer/Genes/FCGR2BID397.html".
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 CC -----
 CC EMBL; U87560; AAD00627.1; -
 CC EMBL; U87561; AAD00628.1; -
 CC EMBL; U87562; AAD00629.1; -
 DR
 DR

Search completed: October 6, 2004, 09:03:36
Job time : 10.6865 secs

QY	103	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
QY	103	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100

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OM protein - protein search, using sw model

Run on: October 6, 2004, 08:59:38 ; Search time 58.1096 Seconds
(without alignments)
1249.617 Million cell updates/sec

Title: US-10-763-400-2

Perfect score: 1390

Sequence: 1 MAPAMESPTLLCVALLFPAP.....RTRKGFRLNPHKPNKNN 257

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_29Jan04:*

- 1: Geneseq1980s:*
- 2: Geneseq1990s:*
- 3: Geneseq2000s:*
- 4: Geneseq2001s:*
- 5: Geneseq2002s:*
- 6: Geneseq2003s:*
- 7: Geneseq2003b:*
- 8: Geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1390	100.0	257	1 AAP90385	Alpha sub
2	1390	100.0	257	2 AAR05025	Alpha sub
3	1390	100.0	257	2 AAR14772	Human Fc
4	1390	100.0	257	2 AAR42336	Human Fce
5	1390	100.0	257	2 AAW24066	Alpha sub
6	1390	100.0	257	2 AAW61190	The alpha
7	1390	100.0	257	4 AAB74667	Human imm
8	1390	100.0	257	4 AAB31584	Amino aci
9	1390	100.0	257	5 ABG32801	Human IGS
10	1390	100.0	257	6 ABO01301	Human pro
11	1390	100.0	257	7 ADD48674	Human Pro
12	1390	100.0	260	3 AAY96230	Human Fc
13	1385	99.6	257	2 AAW48094	Human IGE
14	1377	99.1	257	7 ADB85536	Human imm
15	1264	90.9	222	4 AAB31585	Amino aci
16	1225	88.1	247	2 AAR30483	Human hig
17	1157.5	83.3	218	6 ABO01302	Human pro
18	1117	80.4	978	2 AAW48096	Human ser
19	1117	80.4	978	5 ABG32803	Human IGE
20	1107.5	79.7	235	2 AAR26064	Human FCE
21	1073	77.2	197	2 AAR45778	Human dih
22	1073	77.2	197	4 AAB31586	Amino aci
23	1073	77.2	660	4 AAB31593	Fc epsilo
24	1073	77.2	756	4 AAB31590	Amino aci
25	1039	74.7	193	2 AAR89281	IGE high

26	1008	72.5	183	3 AAY96232	Recombina
27	1006	72.4	182	3 AAY96234	Recombina
28	969	69.7	176	3 AAY94210	Human PhF
29	969	69.7	176	4 AAG65597	Amino aci
30	947	68.1	172	2 AAY33185	Human SFC
31	947	68.1	172	3 AAY94211	Human PhF
32	947	68.1	172	4 AAB31587	A Fc epsi
33	947	68.1	635	4 AAB31594	Fc epsilo
34	947	68.1	731	4 AAB31591	Amino aci
35	944	67.9	175	4 AAG65598	Amino aci
36	832.5	59.9	255	2 AAY27058	Equine FC
37	799.5	57.5	236	2 AAY27060	Equine FC
38	775	55.8	281	2 AAR13867	Hybrid FC
39	705	50.7	253	2 AAW81113	Canine FC
40	679	48.8	281	2 AAR13870	Hybrid FC
41	676	48.6	229	2 AAW81114	Canine FC
42	639	46.0	281	2 AAR13872	Fc(gamma)
43	617	44.4	201	2 AAY27061	Recombina
44	606	43.6	281	2 AAR13869	Hybrid FC
45	597.5	43.0	245	1 AAP90386	Alpha sub

ALIGNMENTS

RESULT 1
AAP90385
ID AAP90385 standard; protein; 257 AA.
XX
AC AAP90385;
XX
DT 24-OCT-2003 (revised)
DT 25-MAR-2003 (revised)
DT 01-NOV-1989 (first entry)
XX
DE Alpha subunit of human mast cell IGE surface receptor.
XX
KW Immunoglobulin E receptor alpha subunit; allergies;
KW non-peptide drug design; human.
XX
OS Homo sapiens; (Human); mast cell line.
OS KU812.
XX
FN WO8905352-A.
XX
PD 15-JUN-1989.
XX
PF 29-NOV-1988; 88WO-US004255.
XX
PR 01-DEC-1987; 87US-00127214.
XX
PA (HARD) HARVARD COLLEGE.
XX
PI (USSH) NAT INST OF HEALTH.
XX
PI Leder P; Benfey P;
XX
DR WPI; 1989-192698/26.
XX
DR N-PSDB; AAN90126.
XX
PT CDNA encoding IGE receptor alpha-sub-unit - used to treat allergies.
XX
PS Disclosure; Fig 4; 17pp; English.
XX
CC Immunoglobulin E receptor alpha subunit of human mast cell IGE surface
CC receptor (see corresp. AAN90126). Used to produce antibodies which can
CC diagnose IGE receptor levels, measure and treat allergies, and design non
CC -peptide drugs. (Updated on 25-MAR-2003 to correct PA field.) (Updated on
XX 24-OCT-2003 to standardise OS field)
SQ Sequence 257 AA;
XX

Query Match 100.0%; Score 1390; DB 1; Length 257;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;

Matches 257; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAPAMESPTLLCVALLFPAPDGLAVPQPKVSLNPPWNRIFKGENVTLCNGNFFEVS 60
 DB 1 MAPAMESPTLLCVALLFPAPDGLAVPQPKVSLNPPWNRIFKGENVTLCNGNFFEVS 60
 QY 61 STKWFHNGSLSEETNSSLNIVNAKPEDSGEYKCOHQVNESEPVYLEVFSWLLQLQASAE 120
 DB 61 STKWFHNGSLSEETNSSLNIVNAKPEDSGEYKCOHQVNESEPVYLEVFSWLLQLQASAE 120
 QY 121 VVMEQOPLFLRCHGWRNDVYKVIYKDGKALKYWYENHNISITNATVEDSGTYICTGKV 180
 DB 121 VVMEQOPLFLRCHGWRNDVYKVIYKDGKALKYWYENHNISITNATVEDSGTYICTGKV 180
 QY 181 WOLDYSEPLNITVIKAPREKYWLQFFIPLLVILFAVDTGIFISTQQQVTFLLKIKRTR 240
 DB 181 WOLDYSEPLNITVIKAPREKYWLQFFIPLLVILFAVDTGIFISTQQQVTFLLKIKRTR 240
 QY 241 KGFRLLNPHKPNPKNN 257
 DB 241 KGFRLLNPHKPNPKNN 257

RESULT 2
 AAR05025
 ID AAR05025 standard; protein; 257 AA.
 AC AAR05025;
 XX
 DT 02-OCT-1990 (first entry)
 XX
 DE Alpha subunit of human high affinity Ige receptor.
 XX
 KW high affinity Ige receptor; alpha subunit of Ige receptor; human;
 KW allergic response; ss.
 XX
 OS Synthetic.
 PN WO9004640-A.
 XX
 PD 03-MAY-1990.
 XX
 PF 18-OCT-1988; 88US-00259065.
 XX
 PR 18-OCT-1988; 88US-00259065.
 XX
 PA (USDC) US SEC OF COMMERCE.
 XX
 PI Kinet JP, Metzger H;
 XX
 XX WPI; 1990-164023/21.
 DR N-PSDB; AAQ04644.
 XX
 DNA sequences for sub-unit peptide(s) of high affinity Ige receptor - and
 derived polypeptides, for therapy and diagnosis of allergies, and studies
 of Ige receptor interaction.
 XX
 PS Disclosure; Page ?; -pp; English.
 XX
 CC The high affinity receptor is a tetrameric complex consisting of 2 gamma
 subunits and one each of subunits alpha and beta. It is expressed on mast
 cells and is involved in the allergic response. COS-7 cells cotransfected
 with cDNA for all 3 intact subunit types (derived from rat basophilic
 leukaemia cells) express receptor on their surfaces. Detailed study of
 the receptors is now possible. See also AAQ04643 and AAQ04645-6
 XX
 SQ Sequence 257 AA;
 Query Match 100.0%; Score 1390; DB 2; Length 257;
 Best Local Similarity 100.0%; Pred. No. 3.3e-103;
 Matches 257; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAPAMESPTLLCVALLFPAPDGLAVPQPKVSLNPPWNRIFKGENVTLCNGNFFEVS 60

DB 1 MAPAMESPTLLCVALLFPAPDGLAVPQPKVSLNPPWNRIFKGENVTLCNGNFFEVS 60
 QY 61 STKWFHNGSLSEETNSSLNIVNAKPEDSGEYKCOHQVNESEPVYLEVFSWLLQLQASAE 120
 DB 61 STKWFHNGSLSEETNSSLNIVNAKPEDSGEYKCOHQVNESEPVYLEVFSWLLQLQASAE 120
 QY 121 VVMEQOPLFLRCHGWRNDVYKVIYKDGKALKYWYENHNISITNATVEDSGTYICTGKV 180
 DB 121 VVMEQOPLFLRCHGWRNDVYKVIYKDGKALKYWYENHNISITNATVEDSGTYICTGKV 180
 QY 181 WOLDYSEPLNITVIKAPREKYWLQFFIPLLVILFAVDTGIFISTQQQVTFLLKIKRTR 240
 DB 181 WOLDYSEPLNITVIKAPREKYWLQFFIPLLVILFAVDTGIFISTQQQVTFLLKIKRTR 240
 QY 241 KGFRLLNPHKPNPKNN 257
 DB 241 KGFRLLNPHKPNPKNN 257

RESULT 3
 AAR14772
 ID AAR14772 standard; protein; 257 AA.
 XX
 AC AAR14772;
 XX
 DT 25-MAR-2003 (revised)
 DT 17-DEC-2001 (revised)
 DT 03-FEB-1992 (first entry)
 XX
 DE Human Fc(epsilon)RI alpha subunit.
 XX
 KW Immunoglobulin; receptor; high affinity receptor.
 XX
 OS Homo sapiens.
 XX
 FH Key
 FH Peptide Location/Qualifiers
 FT 1..25 /label= signal
 FT 26..257 /label= alpha_subunit
 FT 80..104 /label= homologous_domain
 FT /note= "homologous to residues 163-190"
 FT 163..190 /label= homologous_domain
 FT /note= "homologous to residues 80-104"
 FT 205..224 /label= transmembrane
 FT 225..257 /label= cytoplasmic
 XX
 PN USN7626704-N.
 XX
 PD 15-OCT-1991.
 XX
 PF 14-DEC-1990; 90US-00626704.
 XX
 PR 14-DEC-1990; 90US-00626704.
 XX (USSH) NAT INST OF HEALTH.
 XX
 PI Kinet JP, Metzger H;
 XX
 DR WPI; 1991-346755/47.
 DR N-PSDB; AAQ14736.
 XX
 PT DNA coding alpha, beta and gamma-units of ige high affinity receptor -
 PT are used to prepare recombinant polypeptide(s) for treating allergy, drug
 screening or monitoring Ige level.
 PS Disclosure; Fig 1; 58pp; English.
 XX

CC A lambda gtl1 library was prepared from poly-A RNA isolated from KUB12
 CC cells. Screening was by a cDNA fragment from the rat Fc(epsilon)RI alpha
 CC cDNA corresponding to nucleotides 119-781. Positive clones were subcloned
 CC and sequenced. This amino acid sequence was deduced from the cDNA clone.
 CC (Note: Revised entry submitted to correct the patent number format of US
 CC Government-owned NTIS applications to prevent clashes with ongoing US
 CC Government-owned NTIS applications. For further information please visit the Derwent
 CC web site at www.derwent.com/dwpi/updates/ntis_us.html.) (Updated on 25-
 CC MAR-2003 to correct pf field.)

XX SQ Sequence 257 AA;

Query Match 100.0%; Score 1390; DB 2; Length 257;
 Best Local Similarity 100.0%; Pred. No. 3.3e-103;
 Matches 257; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAPAMESPTLLCVALLFFAPDGVLAVPQPKVSLNPPNRIFKGENVLTTCGNNFFEVS 60
 DB 1 MAPAMESPTLLCVALLFFAPDGVLAVPQPKVSLNPPNRIFKGENVLTTCGNNFFEVS 60
 QY 61 STKWFHNGSLSEETNSLINVNAKFDSDGEYKCOHQVNESEPVYLEVFSDWLLLOASAE 120
 DB 61 STKWFHNGSLSEETNSLINVNAKFDSDGEYKCOHQVNESEPVYLEVFSDWLLLOASAE 120
 QY 121 VMGEGQLFLRCHGWRNDVYKVIYKDGKALKYWEHNHISITNATVEDSGTYCTGKV 180
 DB 121 VMGEGQLFLRCHGWRNDVYKVIYKDGKALKYWEHNHISITNATVEDSGTYCTGKV 180
 QY 181 WOLDYSEPLNITVIKAPREKYLQFFIPLLVLVILFAVDGLFISTQQQVTFLLKIKRTR 240
 DB 181 WOLDYSEPLNITVIKAPREKYLQFFIPLLVLVILFAVDGLFISTQQQVTFLLKIKRTR 240
 QY 241 KGFRLNPHPKPNKN 257
 DB 241 KGFRLNPHPKPNKN 257

RESULT 4

AAW42336
 ID AAR42336 standard; protein; 257 AA.

XX AC AAR42336;

XX 25-MAR-2003 (revised)

DT 21-JUN-1994 (first entry)

XX DE Human FcεRI alpha.

XX KW IgE; immunoglobulin E receptor; beta subunit; basophils; allergy;
 KW aggregation; signal transduction; diagnosis; antagonist.

XX OS Homo sapiens.

XX PN WO9321317-A1.

XX PD 28-OCT-1993.

XX PF 16-APR-1993; 93WO-US003419.

XX PR 16-APR-1992; 92US-00869933.

XX PA (USSH) US DEPT HEALTH & HUMAN SERVICE.

XX PI Kinet JP;

XX DR WPT; 1993-351727/44.

XX DR N-PSDB; AAQ51020.

XX FT Immunoglobulin E receptor human beta sub-unit isolation - using 1st
 PT strand reverse transcripts from human basophils as templates for a
 PT polymerase chain reaction, used to treat and diagnose allergic diseases.

XX PS Claim 5; Fig 1; 154pp; English.

XX CC The sequence is that of the human FcεRI alpha subunit, isolated by using
 CC first strand reverse transcriptase from human basophils by PCR. The gene
 CC and its prod. can be used to identify human beta subunit FcεRI inhibitors
 CC (immunoglobulin E receptor) which inhibit the binding of IgE to its
 CC receptor and inhibit the aggregation function of the receptor or the
 CC signal transducing function related to allergic response. Such inhibitors
 CC can be used for the treatment or prevention of allergic disease. See also
 CC AAR42337-42. (Updated on 25-MAR-2003 to correct PN field.)

XX SQ Sequence 257 AA;

Query Match 100.0%; Score 1390; DB 2; Length 257;
 Best Local Similarity 100.0%; Pred. No. 3.3e-103;
 Matches 257; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAPAMESPTLLCVALLFFAPDGVLAVPQPKVSLNPPNRIFKGENVLTTCGNNFFEVS 60
 DB 1 MAPAMESPTLLCVALLFFAPDGVLAVPQPKVSLNPPNRIFKGENVLTTCGNNFFEVS 60
 QY 61 STKWFHNGSLSEETNSLINVNAKFDSDGEYKCOHQVNESEPVYLEVFSDWLLLOASAE 120
 DB 61 STKWFHNGSLSEETNSLINVNAKFDSDGEYKCOHQVNESEPVYLEVFSDWLLLOASAE 120
 QY 121 VMGEGQLFLRCHGWRNDVYKVIYKDGKALKYWEHNHISITNATVEDSGTYCTGKV 180
 DB 121 VMGEGQLFLRCHGWRNDVYKVIYKDGKALKYWEHNHISITNATVEDSGTYCTGKV 180
 QY 181 WOLDYSEPLNITVIKAPREKYLQFFIPLLVLVILFAVDGLFISTQQQVTFLLKIKRTR 240
 DB 181 WOLDYSEPLNITVIKAPREKYLQFFIPLLVLVILFAVDGLFISTQQQVTFLLKIKRTR 240
 QY 241 KGFRLNPHPKPNKN 257
 DB 241 KGFRLNPHPKPNKN 257

RESULT 5

AAW24066
 ID AAW24066 standard; protein; 257 AA.

XX AC AAW24066;

XX 04-FEB-1998 (first entry)

XX DE Alpha subunit of human high affinity receptor for IgE (human FcεRI).

XX KW alpha subunit; human high affinity receptor; IgE; FcεRI; antigen;
 KW preformed mediator; histamine; serotonin; leukotriene; IgE level;
 KW allergic condition; therapy; allergic response; drug screening;
 KW DNA probe; diagnostic assay.

XX OS Homo sapiens.

XX FH Location/Qualifiers

XX FT Peptide

XX FT 1..25 /label= signal_peptide

XX FT 26..257 /label= mature_peptide

XX FT 26..204 /label= extracellular_portion_of_protein

XX FT 80..104 /label= homologous_domain_1

XX FT 163..190 /note= "this region is homologous with amino acids 163-190"

XX FT 104..205 /label= homologous_domain_2

XX FT 205..224 /note= "this region is homologous with amino acids 80-104"

XX FT 225..257 /label= transmembrane_segment

XX FT 225..257 /label= cytoplasmic_domain

XX US5639660-A.
 XX 17-JUN-1997.
 XX
 XX 24-FEB-1988; 88US-00160457.
 XX
 XX 24-FEB-1988; 88US-00160457.
 XX
 XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX (HOFF) HOFFMANN LA ROCHE INC.
 XX
 XX Kochan JP, Kinet JP;
 XX WPI; 1997-332052/30.
 XX N-PSDB; AAT85615.
 XX
 XX DNA encoding alpha sub-unit of high affinity receptor for immunoglobulin E - used for producing polypeptide(s) which can be used for therapy or to prevent allergic responses or in diagnostic and screening assays.
 XX
 XX Claim 7; Fig 1A-B; 15pp; English.
 XX
 XX This sequence represents the alpha subunit of the human high affinity receptor for IgE (FcERI). FcERI is found exclusively on mast cells, basophils and related cells. Aggregation of IgE occupied FcERI by antigen triggers both the release of of preformed mediators such as histamine and serotonin, as well as stimulating the synthesis of leukotrienes. It is the release of these mediators that results in an allergic condition. The DNA can be used to produce the human FcERI alpha polypeptides which can be used for therapy or to prevent allergic responses, in drug screening assays or for monitoring IgE levels in patients. The DNA encoding this protein can also be used to produce DNA probes useful in diagnostic assays
 XX
 XX SQ Sequence 257 AA;

Query Match 100.0%; Score 1390; DB 2; Length 257;
 Best Local Similarity 100.0%; Pred. No. 3.3e-103;
 Matches 257; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAPAMESPTLLCVALLFFAPDGVLPQPKVSLNPPWNRIFKGENVTLTCNGNPFVEVS 60
 DB 1 MAPAMESPTLLCVALLFFAPDGVLPQPKVSLNPPWNRIFKGENVTLTCNGNPFVEVS 60
 QY 61 STKWFHNGSLSEETNSLNIVNAKFEDSGEYKQHQQVNESEPVYLEVPSDWLLQLQASAE 120
 DB 61 STKWFHNGSLSEETNSLNIVNAKFEDSGEYKQHQQVNESEPVYLEVPSDWLLQLQASAE 120
 QY 121 VMEGQPLFLRCHGRWNRWDVYKVIYKDGKALKYWYENHNISITNATVEDSGTYCTGKV 180
 DB 121 VMEGQPLFLRCHGRWNRWDVYKVIYKDGKALKYWYENHNISITNATVEDSGTYCTGKV 180
 QY 181 WQLDYSEPLNITVIKAPREKYLQFFIPLLVILFAVDTLGLFISTQQQVTFLLKIKRTR 240
 DB 181 WQLDYSEPLNITVIKAPREKYLQFFIPLLVILFAVDTLGLFISTQQQVTFLLKIKRTR 240
 QY 241 KGFRLNPHKPNKPN 257
 DB 241 KGFRLNPHKPNKPN 257

RESULT 6
 AAW61190
 ID AAW61190 standard; protein; 257 AA.
 XX
 AC AAW61190;

XX 07-OCT-1998 (first entry)
 XX The alpha chain of a Fc epsilon receptor.
 XX Alpha chain; human; Fc epsilon receptor; canine; equine; feline;

KW immunoglobulin E: IgE; detection; diagnose; allergy; atopic disease;
 KW hyper-IgE syndrome; internal parasitic infection; B cell neoplasia;
 KW flea allergy; heartworm infection.
 XX
 XX Homo sapiens.
 XX
 XX WO9823964-A1.
 XX
 XX 04-JUN-1998.
 XX
 XX 24-NOV-1997; 97WO-US021651.
 XX
 XX 26-NOV-1996; 96US-C0756387.
 XX
 XX (HESK-) HESKA CORP.
 XX
 XX Frank RG, Porter JP, Rushlow KE, Wassom DL;
 XX WPI; 1998-322873/28.
 XX N-PSDB; AAV36343.
 XX
 XX Detection of non-human immunoglobulin E - by complex formation with human Fc epsilon receptor, used for, e.g. diagnosis of allergy and atopic disease.
 XX
 XX Disclosure; Page 37-38; 70pp; English.

XX The present sequence represents the alpha chain of the human Fc epsilon receptor. Detection of canine, equine or feline immunoglobulin E (IgE) comprises reacting isolated human Fc epsilon receptor with the test sample and detecting formation of a IgE-receptor complex. Detection of IgE is used to diagnose allergy, atopic disease, hyper-IgE syndrome, internal parasitic infections or B cell neoplasia, and for measuring effect of treatments. Most particularly flea allergy in dogs and cats is detected, and also heartworm infection
 XX
 XX SQ Sequence 257 AA;

Query Match 100.0%; Score 1390; DB 2; Length 257;
 Best Local Similarity 100.0%; Pred. No. 3.3e-103;
 Matches 257; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAPAMESPTLLCVALLFFAPDGVLPQPKVSLNPPWNRIFKGENVTLTCNGNPFVEVS 60
 DB 1 MAPAMESPTLLCVALLFFAPDGVLPQPKVSLNPPWNRIFKGENVTLTCNGNPFVEVS 60
 QY 61 STKWFHNGSLSEETNSLNIVNAKFEDSGEYKQHQQVNESEPVYLEVPSDWLLQLQASAE 120
 DB 61 STKWFHNGSLSEETNSLNIVNAKFEDSGEYKQHQQVNESEPVYLEVPSDWLLQLQASAE 120
 QY 121 VMEGQPLFLRCHGRWNRWDVYKVIYKDGKALKYWYENHNISITNATVEDSGTYCTGKV 180
 DB 121 VMEGQPLFLRCHGRWNRWDVYKVIYKDGKALKYWYENHNISITNATVEDSGTYCTGKV 180
 QY 181 WQLDYSEPLNITVIKAPREKYLQFFIPLLVILFAVDTLGLFISTQQQVTFLLKIKRTR 240
 DB 181 WQLDYSEPLNITVIKAPREKYLQFFIPLLVILFAVDTLGLFISTQQQVTFLLKIKRTR 240
 QY 241 KGFRLNPHKPNKPN 257
 DB 241 KGFRLNPHKPNKPN 257

RESULT 7
 AAB74667
 ID AAB74667 standard; protein; 257 AA.
 XX
 AC AAB74667;
 XX
 DT 19-JUN-2001 (first entry)
 XX Human immunoglobulin E receptor I alpha subunit protein.
 XX

KW Human; polymorphism; immunoglobulin E receptor I alpha subunit; IGERA;
 KW single nucleotide polymorphism; SNP; allele specific oligonucleotide;
 KW immunoassay; detection.
 XX
 OS Homo sapiens.
 XX
 PN WO200111010-A2.
 XX
 PD 15-FEB-2001.
 XX
 PF 02-AUG-2000; 2000WO-US021097.
 XX
 PR 09-AUG-1999; 99US-0147860P.
 XX
 PA (GENA-) GENAISSANCE PHARM INC.
 XX
 PI Chew A, Denton RR, Duda A, Kliem SE, Lanz EM, Nandabalan K;
 PI Stephens JC;
 XX
 XX WPI; 2001-202766/20.
 DR N-PSDB; AAF97964.
 XX
 XX New polynucleotide for gene therapy, comprises nucleotide polymorphisms
 in the immunoglobulin E receptor I alpha subunit gene.
 PT
 PT
 PS Claim 10; Fig 3; 99pp; English.
 XX
 CC The present invention describes an isolated polynucleotide (I) comprising
 a nucleotide sequence (S) which is a polymorphic variant of a reference
 sequence for the human immunoglobulin E receptor I alpha subunit (IGERA)
 gene or its fragment. The polymorphic variant comprises at least one
 polymorphism selected from guanine (G) at polymorphic site (PS) 1, PS9,
 PS10 or PS21, cytosine (C) at PS2, PS3, PS6, PS12, PS18 or PS20, adenine
 (A) at PS5, PS7, PS11, PS13, PS14, PS15, PS19, or PS22 and thymine (T) at
 PS4, PS8, PS16 or PS17, or (G) at a position corresponding to nucleotide
 251, (A) at a position corresponding to nucleotide 302 or 741, and (T) at
 a position corresponding to nucleotide 530. (I) can be used in gene
 therapy. (I) is useful for therapeutic purposes. A polypeptide (II)
 encoded by (I) is useful in drug screening assays and in assays to
 measure the binding affinity of one or more candidate drugs targeting
 CC (II). An antibody (III) to (II) is useful to immunoprecipitate (II) from
 solution and also reacts with (II) on Western or immunoblots of
 polyacrylamide gels on membrane supports or substrates. (III) is also
 useful in immunoassays to detect (II) in biological samples. AAF97965 to
 AAF98096 represent IGERA allele specific oligonucleotide probes; AAF98097
 to AAF98140 represent IGERA gene polymorphism detection primers; and
 AAF98141 to AAF98180 represent IGERA gene PCR primers which are used in
 the exemplification of the present invention. The present sequence
 CC represents the human IGERA protein used in the present invention
 XX
 SQ Sequence 257 AA;
 Query Match 100.0%; Score 1390; DB 4; Length 257;
 Best Local Similarity 100.0%; Pred. No. 3.3e-103;
 Matches 257; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MAPAMESPTLLCVALLFPAPDGLVAPQKPKVSLNPPNRIKGENVTLTCGNNFVEYS 60
 DB 1 MAPAMESPTLLCVALLFPAPDGLVAPQKPKVSLNPPNRIKGENVTLTCGNNFVEYS 60
 QY 61 STKWFHNGSLSEETNSLNIVNAKFDSDGEYKCOHQQVNESEFPVYLEVFSDWLLLLQASAE 120
 DB 61 STKWFHNGSLSEETNSLNIVNAKFDSDGEYKCOHQQVNESEFPVYLEVFSDWLLLLQASAE 120
 QY 121 VMMEGQPLFLRCHGRNWDVVKVYKDGKALYWNENHISITNATVEDSGTYCTGKV 180
 DB 121 VMMEGQPLFLRCHGRNWDVVKVYKDGKALYWNENHISITNATVEDSGTYCTGKV 180
 QY 181 WQLDYSEPLNITVIKAPREKYLQFFIPLLVILFAVDGLFISTQQQVTFLLKIKRTR 240
 DB 181 WQLDYSEPLNITVIKAPREKYLQFFIPLLVILFAVDGLFISTQQQVTFLLKIKRTR 240
 QY 241 KGFELNPHKPNKPN 257

Db 241 KGFELNPHKPNKPN 257
 RESULT 8
 AAB31584
 ID AAB31584 standard; protein; 257 AA.
 XX
 AC AAB31584;
 XX
 DT 30-APR-2001 (first entry)
 XX
 DE Amino acid sequence of a human Fc epsilon receptor alpha-chain.
 XX
 KW Fc epsilon receptor; Fc epsilonR; immunoglobulin E; IgE; atopic disease;
 KW luminescence inducing protein; allergy; hyper IgE syndrome;
 KW internal parasite infection; B cell neoplasia.
 XX
 OS Homo sapiens.
 XX
 XX WO200104310-A1.
 XX
 PD 18-JAN-2001.
 XX
 PF 13-JUL-2000; 2000WO-US019070.
 XX
 PR 13-JUL-1999; 99US-0143612P.
 PR 02-MAR-2000; 2000US-0186412P.
 XX
 PA (HESK-) HESKA CORP.
 XX
 PI Weber ER, Wood KV, Hall MP;
 XX
 XX WPI; 2001-103082/11.
 DR N-PSDB; AAF24911.
 XX
 PT A fusion protein, comprising an Fc epsilon receptor domain and a
 PT luminescence inducing protein domain that induces a LP substrate to emit
 PT light when contacted with the LP domain, useful for detecting
 PT immunoglobulin (Ig) E.
 XX
 XX Claim 16; Page 60; 105pp; English.
 XX
 CC The present sequence represents a human Fc epsilon receptor (Fc epsilonR)
 CC alpha-chain protein, that binds to immunoglobulin (Ig) E. The Fc epsilonR
 CC domain is used to produce a fusion protein, which also comprises a
 CC luminescence inducing protein domain that induces a substrate to emit
 CC light when contacted with the luminescence inducing protein domain. The
 CC fusion protein may be used to detect IgE. It may also be used to identify
 CC a compound capable of inhibiting Fc epsilonR protein activity. IgE
 CC antibody production is indicative of diseases such as allergies, atopic
 CC disease, hyper IgE syndrome, internal parasite infections and B cell
 CC neoplasia. Detection of IgE production in an animal following therapy is
 CC indicative of the efficacy of the treatment, for example when using
 CC treatments intended to disrupt IgE production
 XX
 SQ Sequence 257 AA;
 Query Match 100.0%; Score 1390; DB 4; Length 257;
 Best Local Similarity 100.0%; Pred. No. 3.3e-103;
 Matches 257; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MAPAMESPTLLCVALLFPAPDGLVAPQKPKVSLNPPNRIKGENVTLTCGNNFVEYS 60
 DB 1 MAPAMESPTLLCVALLFPAPDGLVAPQKPKVSLNPPNRIKGENVTLTCGNNFVEYS 60
 QY 61 STKWFHNGSLSEETNSLNIVNAKFDSDGEYKCOHQQVNESEFPVYLEVFSDWLLLLQASAE 120
 DB 61 STKWFHNGSLSEETNSLNIVNAKFDSDGEYKCOHQQVNESEFPVYLEVFSDWLLLLQASAE 120
 QY 121 VMMEGQPLFLRCHGRNWDVVKVYKDGKALYWNENHISITNATVEDSGTYCTGKV 180

Db 121 VMGQPLFLRCHGWRNWDVYVYKDGKALKYWYENHNSITNATVEDSGTYCTGKV 180
 QY 181 WOLDYSEPLNITVTKAPREKYWLOFFPLLVILFAVDGTLFTSTOOVTFLLKIKRTR 240
 Db 181 WOLDYSEPLNITVTKAPREKYWLOFFPLLVILFAVDGTLFTSTOOVTFLLKIKRTR 240
 QY 241 KGFRLNPHKPNKPN 257
 Db 241 KGFRLNPHKPNKPN 257

RESULT 9
 ID ABG32801 standard; protein; 257 AA.
 AC ABG32801;
 XX
 DT 29-NOV-2002 (first entry)
 DE Human IgE receptor FcεpsilonR1alpha.
 XX
 KW Human; IgE; receptor; FcεpsilonR1alpha; HSA; human serum albumin;
 KW anti-allergic; dermatological; anti-inflammatory; antiasthmatic;
 KW IgE binding domain; systemic allergy; IgE-receptor-mediated disorder;
 KW atopic dermatitis; atopic asthma; chronic urticaria.
 OS Homo sapiens.
 XX
 FH Key
 FT Peptide
 FT 1. 25
 FT /label= Signal_peptide
 FT Protein
 FT 26-257
 FT /label= Mature_FcεpsilonR1alpha
 FT Region
 FT 26..204
 FT /label= IgE_binding_domain
 FT /note= "This region is specifically claimed in claim 5"
 XX
 FN US6423512-B1.
 XX
 PD 23-JUL-2002.
 XX
 PF 21-JUL-1997; 97US-00897956.
 XX
 PR 26-JUL-1996; 96US-0022689P.
 XX
 PA (NOVS) NOVARTIS AG.
 XX
 PI Digan ME, Lake P, Gram H;
 XX
 DR WPI; 2002-672940/72.
 DR N-PSDB; ABS52959.
 XX
 PT New fusion IgE-binding polypeptide, useful for the prevention and
 PT treatment of systemic allergy and/or other IgE-receptor-mediated
 PT disorders such as atopic dermatitis, atopic asthma and chronic urticaria.
 XX
 PS Claim 5; Fig 13; 49pp; English.
 XX
 CC The invention relates to a new fusion polypeptide or its pharmaceutically
 CC acceptable salt comprises at least one IgE-binding domain fused to at
 CC least one human serum albumin (HSA) component, where the IgE-binding
 CC domain is the sequence (a) defined residues Val26-Leu204 of the protein
 CC sequence appearing as ABG32801, or a truncation at the carboxy terminus
 CC by 1-12 amino acids. Also included are: (1) a fusion polypeptide defined
 CC by residues Val26-Leu978 of the protein appearing as ABG32803; (2) a
 CC polynucleotide sequence encoding the fusion protein; (3) a host cell
 CC transformed with the polynucleotide; (4) a method of preparing the fusion
 CC protein comprising transforming a host cell with a vector comprising a
 CC polynucleotide encoding the fusion polypeptide, expressing the fusion
 CC polypeptide in the cell, and recovering the fusion polypeptide from the
 CC host cell, optionally in the form of its salt; and (5) a vector for
 CC expressing a polynucleotide sequence encoding a fusion polypeptide of
 CC formula (I), (II), (III), (IV), or (V) or its salts (R₁-L-R₂ (I), R₂-

CC L-R₁ (II), R₁-L-R₂-L-R₁ (III), R₁-L-R₁-L-R₂ (IV), R₂-L-R₁-L-R₁
 CC (V), where R₁ = the polypeptide (a) or its truncation at the carboxy
 CC terminus by 1-12 amino acids and R₂ = a polypeptide selected from the
 CC sequence defined by residues Asp25-Leu609 the human HSA sequence
 CC appearing as ABG32802, or its truncation at the carboxy terminus by 1-10
 CC amino acids and L = independently a chemical bond, where the vector is
 CC PXMT3-R1a-HAS-R1a). The compositions and methods of the present invention
 CC are useful for the prevention and treatment of systemic allergy and other
 CC IgE-receptor-mediated disorders such as atopic dermatitis, atopic asthma
 CC and chronic urticaria. The IgE-binding polypeptide have a more prolonged
 CC effective serum life, more improved clinical utility in the treatment of
 CC allergy, as well as improved activity in a more efficient and cost-
 CC effective manner. The present sequence is the human IgE receptor
 CC FcεpsilonR1alpha used to make the fusion protein of the invention
 XX
 SQ Sequence 257 AA;

Query Match 100.0%; Score 1390; DB 5; Length 257;
 Best Local Similarity 100.0%; Pred. No. 3.3e-103;
 Matches 257; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAPAESPTLLCVALLFFAPDGVLAPOKPKVSLNPPWNRIFKGVNTLTCGNPFVS 60
 Db 1 MAPAESPTLLCVALLFFAPDGVLAPOKPKVSLNPPWNRIFKGVNTLTCGNPFVS 60
 QY 61 STKWFHNGSLSEETNSSLNIVNAKFEDSGEYKCOHQVNESEPVYLVFSDWLLQASAE 120
 Db 61 STKWFHNGSLSEETNSSLNIVNAKFEDSGEYKCOHQVNESEPVYLVFSDWLLQASAE 120
 QY 121 VMGQPLFLRCHGWRNWDVYVYKDGKALKYWYENHNSITNATVEDSGTYCTGKV 180
 Db 121 VMGQPLFLRCHGWRNWDVYVYKDGKALKYWYENHNSITNATVEDSGTYCTGKV 180
 QY 181 WOLDYSEPLNITVTKAPREKYWLOFFPLLVILFAVDGTLFTSTOOVTFLLKIKRTR 240
 Db 181 WOLDYSEPLNITVTKAPREKYWLOFFPLLVILFAVDGTLFTSTOOVTFLLKIKRTR 240
 QY 241 KGFRLNPHKPNKPN 257
 Db 241 KGFRLNPHKPNKPN 257

RESULT 10

ABG01301
 ID ABG01301 standard; protein; 257 AA.

AC ABG01301;

DT 07-AUG-2003 (first entry)

DE Human protein NOV8a.

XX Human; NOV8; cardiomyopathy; atherosclerosis; hypertension;
 KW congenital heart defect; prostate cancer; diabetes; metabolic disorder;
 KW neoplasm; graft versus host disease; AIDS; bronchial asthma;
 KW Crohn's disease; multiple sclerosis; infectious disease; anorexia;
 KW cancer-associated cachexia; neurodegenerative disorder;
 KW Alzheimer's disease; Parkinson's disease; immune disorder;
 KW haematopoietic disorder; dyslipidaemia; wasting disorder; gene therapy.

OS Homo sapiens.

XX WO2003023008-A2.

XX 20-MAR-2003.

XX 09-SEP-2002; 2002WO-US028596.

XX 07-SEP-2001; 2001US-0318120P.

PR 07-SEP-2001; 2001US-0318130P.

PR 10-SEP-2001; 2001US-0318430P.

PR 12-SEP-2001; 2001US-0318765P.

PR 17-SEP-2001; 2001US-0322781P.

17-SEP-2001; 2001US-0322816P.
19-SEP-2001; 2001US-0323519P.
20-SEP-2001; 2001US-0323631P.
20-SEP-2001; 2001US-0323636P.
25-SEP-2001; 2001US-0324969P.
25-SEP-2001; 2001US-0325081P.
26-SEP-2001; 2001US-0324990P.
15-FEB-2002; 2002US-0357303P.
28-FEB-2002; 2002US-0360973P.
20-MAR-2002; 2002US-0366131P.
25-MAR-2002; 2002US-0367753P.
02-APR-2002; 2002US-0369479P.
10-MAY-2002; 2002US-0379532P.
17-MAY-2002; 2002US-0381664P.
28-MAY-2002; 2002US-0381672P.
19-JUN-2002; 2002US-0384851P.
29-MAY-2002; 2002US-0384012P.
06-SEP-2002; 2002US-0390155P.
PA (CURA-) CURAGEN CORP.
XX
PI Zhong M, Li L, Gorman L, Spytek KA, Kekuda R, Taupier RJ;
PI Anderson DW, Vernet CAM, Catterton E, Miller CE, Shenoy SG;
PI Faturajan M, Pena CEA, Tchernov VT, Padigaru M, Gusev VY;
PI Malyankar UM, Burgess CE, Gerlach VL, Casman SJ, Rieger DK;
PI Grosse WM, Smithson G, Peyman JA, Starling G, Rothenberg ME;
PI Larocheille WJ, Shinkets RA, Crabtree J, Rastelli L, Voss EZ;
PI Boldog FL, Edinger SR, Millet I, Macdougall JR, Ellerman K;
PI Chapoval A;
XX
XX WPI; 2003-313246/30.
DR N-PSDB; ACD06182.
XX
XX
XX
PT
PT
PT
PT
PT
PT
PS Claim 2; Page 133; 849pp; English.
XX
XX The invention relates to an isolated polypeptide comprising one of 127 sequences (appearing as ABO1288-ABO1414) designated as NOVX, a mature form of NOVX, an amino acid sequence which is at least 95% identical to NOVX or an amino acid sequence comprising one or more conservative substitutions in NOVX. Also included are nucleic acids encoding NOVX proteins, determining the presence or amount of NOVX or NOVX DNA in a sample (by introducing the sample to an antibody that binds immunospecifically to the polypeptide), and determining the presence or amount of antibody bound to the polypeptide), determining the presence or predisposition to a disease associated with altered levels of expression of NOVX or NOVX DNA in a first mammalian subject, identifying an agent that binds to NOVX, identifying a potential therapeutic agent for treatment of a pathology related to aberrant expression or aberrant physiological interactions of NOVX, screening for a modulator of activity of or of latency or predisposition to a pathology associated with NOVX, a vector comprising NOVX DNA, a cell comprising the vector (used to produce NOVX) and an anti-NOVX antibody. The NOVX nucleic acids and polypeptides are useful as a marker for cell or tissue type, and in diagnosing and treating pathologies, diseases, conditions or disorders associated with NOVX sequences, including cardiomyopathy, atherosclerosis, hypertension, congenital heart defects, prostate cancer, diabetes, metabolic disorders, neoplasia, graft versus host disease, AIDS, bronchial asthma, Crohn's disease, multiple sclerosis, infectious diseases, anorexia, cancer-associated cachexia, neurodegenerative disorders (e.g. Alzheimer's disease or Parkinson's disease), immune disorders, haematopoietic disorders, dyslipidaemias, and wasting disorders associated with chronic diseases. These may also be used to screen for molecules which inhibit or enhance NOVX activity or function, and for detecting specific cell types. These may also be used in chromosome mapping, gene therapy, tissue typing, and in forensic biology. The present sequence represents a NOVX protein

SQ Sequence 257 AA;
Query Match 100.0%; Score 1390; DB 6; Length 257;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
Matches 257; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAPAMESPTLLCVALLFFADPGVLAPOKPKSLNPPNRIKGENVTLTCGNPFVEVS 60
DB 1 MAPAMESPTLLCVALLFFADPGVLAPOKPKSLNPPNRIKGENVTLTCGNPFVEVS 60
QY 61 STKWFHNGSLSEETNSLNIIVNAKFDSEYKCKHQOVNESEPVYLEVFSDWLLQASAE 120
DB 61 STKWFHNGSLSEETNSLNIIVNAKFDSEYKCKHQOVNESEPVYLEVFSDWLLQASAE 120
QY 121 VVMEGQPLFLRCHGRNWDVYKVIYKDGKALKYVENENISITNATVDSGTYYCTGKV 180
DB 121 VVMEGQPLFLRCHGRNWDVYKVIYKDGKALKYVENENISITNATVDSGTYYCTGKV 180
QY 191 WQLDYSESEPLNITVIKAPREKYWLQFFIPLLVVILFAVDTLGLFISTQQQVTFLLKIKRTR 240
DB 191 WQLDYSESEPLNITVIKAPREKYWLQFFIPLLVVILFAVDTLGLFISTQQQVTFLLKIKRTR 240
QY 241 KGFRLNPHPKPKPKNN 257
DB 241 KGFRLNPHPKPKPKNN 257
RESULT 11
ADD48674
ID ADD48674 standard; protein; 257 AA.
XX
XX ADD48674;
AC
XX
DT 29-JAN-2004 (first entry)
XX
DS Human Protein P12319, SEQ ID NO 14381.
XX
KW Human; pain; neuronal tissue; gene therapy;
KW spinal segmental nerve injury; chronic constriction injury; CCI;
KW spared nerve injury; SNI; Chung.
XX
OS Homo sapiens.
XX
XX WO2003016475-A2.
XX
PD 27-FEB-2003.
XX
PF 14-AUG-2002; 2002WO-US025765.
XX
PR 14-AUG-2001; 2001US-0312147P.
PR 01-NOV-2001; 2001US-0346382P.
PR 26-NOV-2001; 2001US-0333347P.
XX
XX (GEHO) GEN HOSPITAL CORP.
XX (FARB) BAYER AG.
XX
XX Woolf C, D'urso D, Befort K, Costigan M;
XX
XX WPI; 2003-268312/26.
XX GENBANK; P12319.
XX
XX New composition comprising two or more isolated polypeptides, useful for preparing a medicament for treating pain in an animal.
PT
XX
XX Claim 1; Page; 1017pp; English.
XX
XX The invention discloses a composition comprising two or more isolated rat or human polynucleotides or a polynucleotide which represents a fragment, or derivative of allelic variation of the nucleic acid sequence. Also claimed are a vector comprising the novel polynucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a kit to perform the method, an array, a method for identifying an agent

CC that increases or decreases the expression of the polynucleotide sequence
 CC that is differentially expressed in neuronal tissue of a first animal
 CC subjected to pain, a method for identifying a compound which regulates
 CC the expression of a polynucleotide sequence which is differentially
 CC expressed in an animal subjected to pain, a method for identifying a
 CC compound that regulates the activity of one or more of the
 CC polynucleotides, a method for producing a pharmaceutical composition, a
 CC method for identifying a compound or small molecule that regulates the
 CC activity in an animal of one or more of the polypeptides given in the
 CC specification, a method for identifying a compound useful in treating
 CC pain and a pharmaceutical composition comprising the one or more
 CC polypeptides or their antibodies. The polynucleotide or the compound that
 CC modulates its activity is useful for preparing a medicament for treating
 CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
 CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
 CC therapy). The sequence presented is a human protein (shown in table 2 of
 CC the specification) which is differentially expressed during pain. Note:
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic form directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 257 AA;

Query Match 100.0%; Score 1390; DB 7; Length 257;

Best Local Similarity 100.0%; Pred. No. 3.3e-103;

Matches 257; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAPAMESPTLLCVALLFPAPDGVLAPOKPKVSLNPPWNRIFKGENVLTGCGNNFEVS 60
 DB 1 MAPAMESPTLLCVALLFPAPDGVLAPOKPKVSLNPPWNRIFKGENVLTGCGNNFEVS 60
 QY 61 STKWFHNGSLSEETNSSLNINAKFEDSGEYKCHQVWSEPVYLFVSDWLLQASAE 120
 DB 61 STKWFHNGSLSEETNSSLNINAKFEDSGEYKCHQVWSEPVYLFVSDWLLQASAE 120
 QY 121 VMGQPLFLRCHGWRNDVYKVIYKDGKALKYWYENHNISITNATVEDSGTYCTGKV 180
 DB 121 VMGQPLFLRCHGWRNDVYKVIYKDGKALKYWYENHNISITNATVEDSGTYCTGKV 180
 QY 181 WLDYSEPLNITVIKAPREKYLQFFIPLLVILFAVDGLFISTQQQVTFLLKIKRTR 240
 DB 181 WLDYSEPLNITVIKAPREKYLQFFIPLLVILFAVDGLFISTQQQVTFLLKIKRTR 240
 QY 241 KGFRLNPHKPNKPN 257
 DB 241 KGFRLNPHKPNKPN 257

RESULT 12

AAV96230

ID AAV96230 standard; protein; 260 AA.

XX AAV96230;

XX 11-SEP-2000 (first entry)

DE Human Fc receptor, FcepsilonRIa.

XX Human; Fc receptor; FcepsilonRIa; immunoglobulin; infection;

KW immune response; HIV; IGG; immunosuppressive; antirheumatic;

KW antinflammatory; AIDS; SLE; multiple myeloma; rheumatoid arthritis;

KW systemic lupus erythematosus; tumour.

XX Homo sapiens.

OS EP1006183-A1.

PN 07-JUN-2000.

PD 03-DEC-1998; 98EP-00122969.

XX 03-DEC-1998; 98EP-00122969.

PR 03-DEC-1998; 98EP-00122969.

XX

PA (PIAC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.

XX WPI; 2000-367968/32.

DR N-PSDB; AAA27470.

XX Novel Fc receptor lacking transmembrane domains, a signal peptide, and

PT glycosylation, useful for diagnosing and treating immune disorders and

PT cancer.

XX Disclosure; Page 40-41; 60pp; English.

XX The present sequence is the human Fc receptor, FcepsilonRIa. Fc receptors

CC play an important role in defending the body against infections. First,

CC pathogens are opsonised by serum immunoglobulins. The resulting complex

CC then binds to cells expressing Fc receptors. Upon Fc receptor activation,

CC immune effector pathways are activated, leading to immune response. The

CC present sequence may be modified to produce recombinant versions. The

CC recombinant Fc receptor consist only of the extracellular portion of the

CC receptor and are not glycosylated i.e. they do not have transmembrane

CC domains or signal peptides. The recombinant proteins may be used in

CC immunoassays to determine the immune status of patients with chronic

CC diseases of the immune system, e.g. AIDS, systemic lupus erythematosus

CC (SLE), multiple myeloma (MM), or rheumatoid arthritis. In addition,

CC pharmaceutical compositions containing recombinant proteins may be used

CC to treat or prevent autoimmune diseases, allergies or tumours, especially

CC AIDS, rheumatoid arthritis or MM

XX Sequence 260 AA;

Query Match 100.0%; Score 1390; DB 3; Length 260;

Best Local Similarity 100.0%; Pred. No. 3.4e-103;

Matches 257; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAPAMESPTLLCVALLFPAPDGVLAPOKPKVSLNPPWNRIFKGENVLTGCGNNFEVS 60
 DB 4 MAPAMESPTLLCVALLFPAPDGVLAPOKPKVSLNPPWNRIFKGENVLTGCGNNFEVS 63
 QY 61 STKWFHNGSLSEETNSSLNINAKFEDSGEYKCHQVWSEPVYLFVSDWLLQASAE 120
 DB 64 STKWFHNGSLSEETNSSLNINAKFEDSGEYKCHQVWSEPVYLFVSDWLLQASAE 123
 QY 121 VMGQPLFLRCHGWRNDVYKVIYKDGKALKYWYENHNISITNATVEDSGTYCTGKV 180
 DB 124 VMGQPLFLRCHGWRNDVYKVIYKDGKALKYWYENHNISITNATVEDSGTYCTGKV 183
 QY 181 WLDYSEPLNITVIKAPREKYLQFFIPLLVILFAVDGLFISTQQQVTFLLKIKRTR 240
 DB 184 WLDYSEPLNITVIKAPREKYLQFFIPLLVILFAVDGLFISTQQQVTFLLKIKRTR 243
 QY 241 KGFRLNPHKPNKPN 257
 DB 244 KGFRLNPHKPNKPN 260

RESULT 13

AAW48094

ID AAW48094 standard; protein; 257 AA.

XX AAW48094;

XX 20-JUL-1998 (first entry)

XX Human IgE receptor Fc-epsilon-RI alpha chain.

DE Fc-epsilon RI alpha chain; IgE receptor; human serum albumin;

KW fusion protein; allergy; atopic dermatitis; asthma; urticaria; hay fever;

KW eczema; anaphylaxis; gene therapy; diagnosis; transgenic animal.

XX Homo sapiens.

XX Key

FT Location/Qualifiers

FT Peptide 1..25

FT /label= sig_peptide

FT Protein 26. .257
 FT /label= Mat_protein
 FT Domain 26. .204
 FT /note= "extracellular domain"
 XX
 XX WO9804718-A1.
 XX
 XX PD 05-FEB-1998.
 XX
 XX PF 25-JUL-1997; 97WO-EP004066.
 XX
 XX PR 26-JUL-1996; 96US-00690216.
 XX
 XX PA (NOVS) NOVARTIS AG.
 XX
 XX PI Digan ME, Lake P, Gram H;
 XX
 XX DR WPI; 1998-130705/12.
 XX DR N-PSDB; AAV20402.
 XX
 XX PT New fusion polypeptide for, e.g. diagnosing allergies - comprises
 XX PT immunoglobulin E-binding domain fused to human serum albumin.
 XX
 XX PS Claim 2; Page 44; 77pp; English.
 XX
 CC This is the amino acid sequence of the dominant form of full-length
 CC native human IGE receptor Fc-epsilon RI alpha chain. A claimed fusion
 CC protein (FP) comprises an IGE binding domain fused to at least one human
 CC serum albumin (HSA) component (see AA038095), optionally via a peptide
 CC linker, and is especially a dimeric FP (see AA048096) comprising HSA
 CC fused, at each of its N- and C-termini, to the extracellular domain of Fc
 CC -epsilon RI alpha chain. Also claimed are: nucleic acids encoding the FP
 CC (see AAV20404); a vector; a process for preparing the FP; a method of
 CC performing gene therapy in humans that comprises removing somatic cells
 CC from a patient, genetically modifying them in culture by insertion of a
 CC polynucleotide that encodes the FP, and reintroducing the modified cells
 CC into the patient so that the FP is expressed by the cells of the patient;
 CC and use of the FP in an in vitro diagnostic assay to determine the level
 CC of IGE or auto-antibodies to Fc epsilon RI in a sample. The products can
 CC be used in the prevention and/or treatment of IGE-mediated allergic
 CC diseases and related disorders such as atopic dermatitis, atopic asthma,
 CC chronic urticaria, hayfever and eczema. Compared with using IGE binding
 CC domain alone, the FP has a longer serum life, and thus greater activity,
 CC without a loss of ability to bind serum IGE or circulating auto-
 CC antibodies
 XX
 XX SQ Sequence 257 AA;

Query Match 99.6%; Score 1385; DB 2; Length 257;
 Best Local Similarity 99.6%; Pred. No. 8.3e-103;
 Matches 256; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MAPAMESPTLLCVALLFPADPGVLAVPQPKVSLNPPNRRIFKGENVTLTCGNNEFFVS 60
 DB 1 MAPAMESPTLLCVALLFPADPGVLAVPQPKVSLNPPNRRIFKGENVTLTCGNNEFFVS 60
 QY 61 STKWFHNGSLSEETNSSLNIVNAKFEDSGEYKCOHQVNESEPVYLEVFSDFMLLQASAE 120
 DB 61 STKWFHNGSLSEETNSSLNIVNAKFEDSGEYKCOHQVNESEPVYLEVFSDFMLLQASAE 120
 QY 121 VMNEGQPLFLRCHGNWVYKVIYKDGKALKWYENHNISITNATVEDSGFYCTGKV 180
 DB 121 VMNEGQPLFLRCHGNWVYKVIYKDGKALKWYENHNISITNATVEDSGFYCTGKV 180
 QY 181 WOLDYSEPLNITVIKAPREYVQLQFTPLLWILFVADTGLFISTQQQVTFLLKIKRTR 240
 DB 181 WOLDYSEPLNITVIKAPREYVQLQFTPLLWILFVADTGLFISTQQQVTFLLKIKRTR 240
 QY 241 KGRLLNPHNPKNKN 257
 DB 241 KGRLLNPHNPKNKN 257

RESULT 14
 ADB85536
 ID ADB85536 standard; protein; 257 AA.
 XX
 XX AC ADB85536;
 XX
 XX DT 04-DEC-2003 (first entry)
 XX
 XX DE Human immunoglobulin E high affinity receptor alpha subunit protein.
 XX
 XX KW alpha subunit; high affinity receptor for immunoglobulin E; FcERI;
 XX KW mast cell; basophil; histamine; serotonin; allergic condition;
 XX KW antiallergic; allergic response; drug screening assay; immunoglobulin E;
 XX KW human.
 XX
 XX OS Homo sapiens.
 XX
 XX FH Key
 XX FT Misc-difference 221 Location/Qualifiers
 XX FT /note= "Encoded by GGA"
 XX FT Misc-difference 253
 XX FT /note= "Encoded by AAC"
 XX
 XX PN US6602983-B1.
 XX
 XX PD 05-AUG-2003.
 XX
 XX PF 22-SEP-1994; 94US-00310902.
 XX
 XX PR 24-FEB-1988; 86US-00160457.
 XX PR 30-OCT-1991; 91US-00785127.
 XX PR 29-MAY-1993; 93US-00066640.
 XX
 XX PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX
 XX PI Kinet JP, Kochan JP;
 XX
 XX DR WPI; 2003-669612/63.
 XX DR N-PSDB; ADB85535.
 XX
 XX New alpha subunit of the human high affinity receptor for immunoglobulin
 XX E polypeptides, useful as antagonists to prevent allergic response, as
 XX reagents in drug screening assays, or for monitoring immunoglobulin E
 XX levels in patients.
 XX
 XX PS Claim 1; Fig 1; 9pp; English.
 XX
 CC This invention relates to a novel purified polypeptide corresponding to
 CC the alpha subunit of the human high affinity receptor for immunoglobulin
 CC E (FcERI) and the DNA sequence which encodes it. The receptor of the
 CC invention is found exclusively on mast cells, basophils and related
 CC cells. Activation of the receptor triggers the release of preformed
 CC mediators such as histamine and serotonin which may result in allergic
 CC conditions. Compounds which modulate FcERI activity may have antiallergic
 CC activity. The polypeptide of the invention may be useful as an antagonist
 CC for preventing allergic response, as a reagent in drug screening assays,
 CC as a therapeutic or for monitoring immunoglobulin E levels in patients.
 CC The DNA sequences may be useful for producing the polypeptide or for
 CC synthesizing cDNA sequences to construct DNA probes used in diagnostic
 CC assays. The present sequence is the amino acid sequence of the alpha
 CC subunit of the human FcERI receptor of the invention.

SQ Sequence 257 AA;

Query Match 99.1%; Score 1377; DB 7; Length 257;
 Best Local Similarity 99.2%; Pred. No. 3.6e-102;
 Matches 255; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MAPAMESPTLLCVALLFPADPGVLAVPQPKVSLNPPNRRIFKGENVTLTCGNNEFFVS 60
 DB 1 MAPAMESPTLLCVALLFPADPGVLAVPQPKVSLNPPNRRIFKGENVTLTCGNNEFFVS 60
 QY 61 STKWFHNGSLSEETNSSLNIVNAKFEDSGEYKCOHQVNESEPVYLEVFSDFMLLQASAE 120

Db 61 STKWFHNGSLSEETSSLNIVAKEDSGEYKCOHQVNESEPVYLEVFSWLLLOASAE 120
 QY 121 VMEGQPLFLRCHGRNWDVYKVIYKDGELKQWYENHNISITNATVEDSGTYCTGKV 180
 Db 121 VMEGQPLFLRCHGRNWDVYKVIYKDGELKQWYENHNISITNATVEDSGTYCTGKV 180
 QY 181 WOLDVESEPLNTVIKAPREKYNWLOFFPIPLLVILFAVDTGIFISTQQVTFLLKIKETR 240
 Db 181 WOLDVESEPLNTVIKAPREKYNWLOFFPIPLLVILFAVDTELFISTQQVTFLLKIKETR 240
 QY 241 KGFRLLNPHKPNPKNN 257
 Db 241 KGFRLLNPHKPNPKNN 257

RESULT 15

AAB31585
 ID AAB31585 standard; protein; 232 AA.

XX AC AAB31585;

XX DT 30-APR-2001 (first entry)

XX DE Amino acid sequence of Fc epsilon receptor alpha-chain mature protein.

XX KW Fc epsilon receptor; FcepsilonR; immunoglobulin E; IgE; atopic disease;
 XX KW luminescence inducing protein; allergy; hyper IgE syndrome;
 XX KW internal parasite infection; B cell neoplasia.

XX OS Homo sapiens.

XX PN WO200104310-A1.

XX PD 18-JAN-2001.

XX PF 13-JUL-2000; 2000WO-US019070.

XX PR 13-JUL-1999; 99US-0143612P.

XX PR 02-MAR-2000; 2000US-0186412P.

XX XX (HESK-) HESKA CORP.

XX PA (PROM-) PROMEGA CORP.

XX PI Weber ER, Wood KV, Hall MP;

XX DR WPI; 2001-103082/11.

XX DR N-PSDE; AAF24913.

XX PT A fusion protein, comprising an Fc epsilon receptor domain and a
 XX PT luminescence inducing protein domain that induces a LP substrate to emit
 XX PT light when contacted with the LP domain, useful for detecting
 XX PT immunoglobulin (Ig) E.

XX PS Claim 16; Page 62-63; 105pp; English.

XX CC The present sequence represents a human Fc epsilon receptor (FcepsilonR)
 XX CC alpha-chain mature protein, that binds to immunoglobulin (Ig) E). The
 XX CC FcepsilonR domain is used to produce a fusion protein, which also
 XX CC comprises a luminescence inducing protein domain that induces a substrate
 XX CC to emit light when contacted with the luminescence inducing protein
 XX CC domain. The fusion protein may be used to detect IgE. It may also be used
 XX CC to identify a compound capable of inhibiting FcepsilonR protein activity.
 XX CC IgE antibody production is indicative of diseases such as allergies,
 XX CC atopic disease, hyper IgE syndrome, internal parasite infections and B
 XX CC cell neoplasia. Detection of IgE production in an animal following
 XX CC therapy is indicative of the efficacy of the treatment, for example when
 XX CC using treatments intended to disrupt IgE production

XX SQ Sequence 232 AA;

Query Match 90.9%; Score 1264; DB 4; Length 232;
 Best Local Similarity 100.0%; Pred. No. 3.6e-93;

Matches 232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 26 VPQPKVSLNPPWNRIFKGENVTLCNNGNFFEVSTKWFHNGSLSEETSSLNIVNAKF 85
 Db 1 VPQPKVSLNPPWNRIFKGENVTLCNNGNFFEVSTKWFHNGSLSEETSSLNIVNAKF 60
 QY 86 EDSGEYKCOHQVNESEPVYLEVFSWLLLOASAEVMEGQPLFLRCHGRNWDVYKVIY 145
 Db 61 EDSGEYKCOHQVNESEPVYLEVFSWLLLOASAEVMEGQPLFLRCHGRNWDVYKVIY 120
 QY 146 YKDGELKQWYENHNISITNATVEDSGTYCTGKWQLDYSEPLNTVIKAPREKYNWLO 205
 Db 121 YKDGELKQWYENHNISITNATVEDSGTYCTGKWQLDYSEPLNTVIKAPREKYNWLO 180
 QY 206 FFIPLLVILFAVDTGIFISTQQVTFLLKIKRTRKGFRLNPHKPNPKNN 257
 Db 181 FFIPLLVILFAVDTGIFISTQQVTFLLKIKRTRKGFRLNPHKPNPKNN 232

Search completed: October 6, 2004, 09:03:04
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OM protein - protein search, using sw model

Run on: October 6, 2004, 08:59:40 ; Search time 16.7739 Seconds
(without alignments)
790.984 Million cell updates/sec

Title: US-10-763-400-2
Perfect score: 1390
Sequence: 1 MAPAMESPTLLCVALLFPAP.....RTRKGFRLLNPHKPNKPN 257

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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3: /cgn2_6/prodata/2/iaa/6A-COMB.pep:*
4: /cgn2_6/prodata/2/iaa/6B-COMB.pep:*
5: /cgn2_6/prodata/2/iaa/PCTUS-COMB.pep:*
6: /cgn2_6/prodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1390	100.0	257	1	US-07-869-933-11
2	1390	100.0	257	2	US-08-756-387B-2
3	1390	100.0	257	3	US-09-103-663-11
4	1390	100.0	257	4	US-09-285-873-2
5	1390	100.0	257	4	US-08-897-956A-1
6	1390	100.0	257	4	US-09-944-277A-2
7	1264	90.9	232	1	US-07-869-933-13
8	1264	90.9	232	2	US-08-756-387B-6
9	1264	90.9	232	3	US-09-103-663-13
10	1264	90.9	232	4	US-09-285-873-6
11	1264	90.9	232	4	US-09-944-277A-6
12	1117	80.4	197	4	US-08-897-956A-3
13	1073	77.2	197	4	US-08-756-387B-11
14	1073	77.2	197	4	US-09-285-873-11
15	1073	77.2	197	4	US-09-944-277A-11
16	1067	76.8	197	3	US-08-788-954-2
17	1039	74.7	193	2	US-08-765-536-1
18	1039	74.7	193	5	PCT-US95-08401-1
19	947	68.1	172	2	US-08-756-387B-13
20	947	68.1	172	4	US-09-285-873-13
21	947	68.1	172	4	US-09-245-764-9
22	947	68.1	172	4	US-09-944-277A-13
23	832.5	59.9	255	3	US-09-015-734-2
24	832.5	59.9	255	4	US-09-515-311-2
25	799.5	57.5	236	3	US-09-015-734-7
26	799.5	57.5	236	4	US-09-515-311-7
27	722	51.9	263	2	US-08-768-964-2

28	722	51.9	263	3	US-09-005-299-2	Sequence 2, Appli
29	722	51.9	263	3	US-09-515-431-2	Sequence 2, Appli
30	705	50.7	253	3	US-08-833-488B-20	Sequence 20, Appl
31	690.5	49.7	238	2	US-08-768-964-7	Sequence 7, Appli
32	690.5	49.7	238	3	US-09-005-299-7	Sequence 7, Appli
33	690.5	49.7	238	3	US-09-515-431-7	Sequence 7, Appli
34	676	48.6	229	3	US-08-833-488B-24	Sequence 24, Appl
35	617	44.4	201	3	US-09-015-734-12	Sequence 12, Appl
36	617	44.4	201	4	US-09-515-311-12	Sequence 12, Appl
37	587.5	42.3	227	1	US-07-869-933-14	Sequence 14, Appl
38	587.5	42.3	227	3	US-09-103-663-14	Sequence 12, Appl
39	576.5	41.5	222	1	US-07-869-933-12	Sequence 28, Appl
40	576.5	41.5	222	1	US-07-869-933-28	Sequence 12, Appl
41	576.5	41.5	222	3	US-09-103-663-12	Sequence 28, Appl
42	576.5	41.5	222	3	US-09-103-663-28	Sequence 12, Appl
43	554	39.9	199	3	US-08-833-488B-14	Sequence 14, Appl
44	546	39.3	431	4	US-09-592-998C-9	Sequence 9, Appli
45	546	39.3	435	4	US-09-592-998C-10	Sequence 10, Appl

ALIGNMENTS

RESULT 1
US-07-869-933-11
; Sequence 11, Application US/07869933
; Patent No. 5770396
; GENERAL INFORMATION:
; APPLICANT: KINET, Jean-Pierre
; TITLE OF INVENTION: ISOLATION, CHARACTERIZATION, AND USE OF
; TITLE OF INVENTION: THE HUMAN B SUBUNIT OF THE HIGH AFFINITY RECEPTOR FOR
; TITLE OF INVENTION: IMMUNOGLOBULIN
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Foley & Lardner
; STREET: 1800 Diagonal Road, Suite 500
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/869,933
; FILING DATE: 19920416
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 40399/154 NIHD
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)836-9300
; TELEFAX: (703)683-4109
; TELEX: 899149
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 257 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-07-869-933-11

Query Match 100.0%; Score 1390; DB 1; Length 257;
Best Local Similarity 100.0%; Pred. No. 6.1e-127; Indels 0; Gaps 0;
Matches 257; Conservative 0; Mismatches 0;

QY 1 MAPAMESPTLLCVALLFPAPDGLAVPQPKVSLNPPNRRIFKGENVLTGNNFFEVS 60
DB 1 MAPAMESPTLLCVALLFPAPDGLAVPQPKVSLNPPNRRIFKGENVLTGNNFFEVS 60

QY 61 STKWFHNGSLSEETNSSLNINAKFEDSGEYKCOHQVNESEPVYLEVFSWLLQASAE 120
 DB 61 STKWFHNGSLSEETNSSLNINAKFEDSGEYKCOHQVNESEPVYLEVFSWLLQASAE 120
 QY 121 VMEGQPLFLRCHGWRNDVYKVIYKDGKALKYWYENHNISITNATVEDSGTYCTGKV 180
 DB 121 VMEGQPLFLRCHGWRNDVYKVIYKDGKALKYWYENHNISITNATVEDSGTYCTGKV 180
 QY 181 WQLDYSEPLNITVIKAPREKYLQFFIPLLVILFAVDTGLFISTQQQVTFLLKIKRTR 240
 DB 181 WQLDYSEPLNITVIKAPREKYLQFFIPLLVILFAVDTGLFISTQQQVTFLLKIKRTR 240
 QY 241 KGFRLLNHPKPNPKNN 257
 DB 241 KGFRLLNHPKPNPKNN 257

RESULT 2

US-08-756-387B-2
 ; Sequence 2, Application US/08756387B
 ; Patent No. 5945294
 ; GENERAL INFORMATION:
 ; APPLICANT: Frank, Glenn R.
 ; APPLICANT: Porter, James P.
 ; APPLICANT: Rushlow, Keith E.
 ; APPLICANT: Wassom, Donald L.
 ; TITLE OF INVENTION: Method to Detect Ige
 ; NUMBER OF SEQUENCES: 13
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Carol Talkington Verser, Ph.D.
 ; ADDRESSEE: Heska Corporation
 ; STREET: 1825 Sharp Point Drive
 ; CITY: Fort Collins
 ; STATE: Colorado
 ; COUNTRY: USA
 ; ZIP: 80525
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: Windows 95
 ; SOFTWARE: WordPerfect for Windows, Version 7.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/756,387B
 ; FILING DATE: No. 5945294ember 26, 1996
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Verser, Carol Talkington
 ; REGISTRATION NUMBER: 37,459
 ; REFERENCE/DOCKET NUMBER: DI-1
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 970/493-7272
 ; TELEFAX: 970/484-9505
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 257 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-756-387B-2

Query Match 100.0%; Score 1390; DB 2; Length 257;
 Best Local Similarity 100.0%; Pred. No. 6.1e-127;
 Matches 257; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MAPAMESPTLLCVALLFFAPDGLVAVPQPKVSLNPPNRRIFKGENVTLTCNNGNFFEVS 60
 DB 1 MAPAMESPTLLCVALLFFAPDGLVAVPQPKVSLNPPNRRIFKGENVTLTCNNGNFFEVS 60
 QY 61 STKWFHNGSLSEETNSSLNINAKFEDSGEYKCOHQVNESEPVYLEVFSWLLQASAE 120
 DB 61 STKWFHNGSLSEETNSSLNINAKFEDSGEYKCOHQVNESEPVYLEVFSWLLQASAE 120
 QY 121 VMEGQPLFLRCHGWRNDVYKVIYKDGKALKYWYENHNISITNATVEDSGTYCTGKV 180

DB 121 VMEGQPLFLRCHGWRNDVYKVIYKDGKALKYWYENHNISITNATVEDSGTYCTGKV 180
 QY 181 WQLDYSEPLNITVIKAPREKYLQFFIPLLVILFAVDTGLFISTQQQVTFLLKIKRTR 240
 DB 181 WQLDYSEPLNITVIKAPREKYLQFFIPLLVILFAVDTGLFISTQQQVTFLLKIKRTR 240
 QY 241 KGFRLLNHPKPNPKNN 257
 DB 241 KGFRLLNHPKPNPKNN 257

RESULT 3

US-09-103-663-11
 ; Sequence 11, Application US/09103663D
 ; Patent No. 6171803
 ; GENERAL INFORMATION:
 ; APPLICANT: Kinet et al.
 ; TITLE OF INVENTION: Isolation, characterization, and use of the human beta
 ; TITLE OF INVENTION: subunit of the high affinity receptor for
 ; TITLE OF INVENTION: immunoglobulin E.
 ; FILE REFERENCE: 50490
 ; CURRENT APPLICATION NUMBER: US/09/103,663D
 ; CURRENT FILING DATE: 1998-06-23
 ; EARLIER APPLICATION NUMBER: 07/869,933
 ; EARLIER FILING DATE: 1992-04-16
 ; NUMBER OF SEQ ID NOS: 35
 ; SOFTWARE: Patent in Ver. 2.1
 ; SEQ ID NO 11
 ; LENGTH: 257
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-09-103-663-11

Query Match 100.0%; Score 1390; DB 3; Length 257;
 Best Local Similarity 100.0%; Pred. No. 6.1e-127;
 Matches 257; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MAPAMESPTLLCVALLFFAPDGLVAVPQPKVSLNPPNRRIFKGENVTLTCNNGNFFEVS 60
 DB 1 MAPAMESPTLLCVALLFFAPDGLVAVPQPKVSLNPPNRRIFKGENVTLTCNNGNFFEVS 60
 QY 61 STKWFHNGSLSEETNSSLNINAKFEDSGEYKCOHQVNESEPVYLEVFSWLLQASAE 120
 DB 61 STKWFHNGSLSEETNSSLNINAKFEDSGEYKCOHQVNESEPVYLEVFSWLLQASAE 120
 QY 121 VMEGQPLFLRCHGWRNDVYKVIYKDGKALKYWYENHNISITNATVEDSGTYCTGKV 180
 DB 121 VMEGQPLFLRCHGWRNDVYKVIYKDGKALKYWYENHNISITNATVEDSGTYCTGKV 180
 QY 181 WQLDYSEPLNITVIKAPREKYLQFFIPLLVILFAVDTGLFISTQQQVTFLLKIKRTR 240
 DB 181 WQLDYSEPLNITVIKAPREKYLQFFIPLLVILFAVDTGLFISTQQQVTFLLKIKRTR 240
 QY 241 KGFRLLNHPKPNPKNN 257
 DB 241 KGFRLLNHPKPNPKNN 257

RESULT 4

US-09-285-873-2
 ; Sequence 2, Application US/09285873
 ; Patent No. 6309832
 ; GENERAL INFORMATION:
 ; APPLICANT: Frank, Glenn R.
 ; APPLICANT: Porter, James P.
 ; APPLICANT: Rushlow, Keith E.
 ; APPLICANT: Wassom, Donald L.
 ; TITLE OF INVENTION: Method to Detect Ige
 ; NUMBER OF SEQUENCES: 13
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Carol Talkington Verser, Ph.D.
 ; ADDRESSEE: Heska Corporation

```
; STREET: 1825 Sharp Point Drive
; CITY: Fort Collins
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80525
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: Windows 95
; SOFTWARE: WordPerfect for Windows, Version 7.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/285,873
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/756,387
; FILING DATE: No. 6309832ember 26, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Verser, Carol Talkington
; REGISTRATION NUMBER: 37,459
; REFERENCE/DOCKET NUMBER: DI-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 970/493-7272
; TELEFAX: 970/484-9505
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 257 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-285-873-2

Query Match      100.0%; Score 1390; DB 4; Length 257;
Best Local Similarity 100.0%; Pred. No. 6.1e-127;
Matches 257; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAPAMESPTLLCVALLFFAPDGVLAVPQPKVSLNPPWNRIFKGENVTITCNGNNFFEVS 60
DB 1 MAPAMESPTLLCVALLFFAPDGVLAVPQPKVSLNPPWNRIFKGENVTITCNGNNFFEVS 60
QY 61 STKWFHNGSLSEETNSSLNIVNAKFEDSGEYKCOHQVNESEPVYLEVFSMDLLLOASAE 120
DB 61 STKWFHNGSLSEETNSSLNIVNAKFEDSGEYKCOHQVNESEPVYLEVFSMDLLLOASAE 120
QY 121 VMWEGQPLFLRCHGWRNWDVYKVIYKDGKALKYWYENHNISITNATVEDSGTYICTGKV 180
DB 121 VMWEGQPLFLRCHGWRNWDVYKVIYKDGKALKYWYENHNISITNATVEDSGTYICTGKV 180
QY 181 WOLDYSEPLNITVIKAPREKYWLQFFIPLLVILPAVDTGFLISTQQQVTFLLKIKRTR 240
DB 181 WOLDYSEPLNITVIKAPREKYWLQFFIPLLVILPAVDTGFLISTQQQVTFLLKIKRTR 240
QY 241 KGFRLNPHKPNPKNN 257
DB 241 KGFRLNPHKPNPKNN 257

RESULT 5
US-08-897-956A-1
; Sequence 1, Application US/08897956A
; Patent No. 6423512
; GENERAL INFORMATION:
; APPLICANT: Mary Ellen Digan
; APPLICANT: Philip Lake
; APPLICANT: Hermann Gram
; TITLE OF INVENTION: Fusion Polypeptides
; FILE REFERENCE: 600-7244/CFA
; CURRENT APPLICATION NUMBER: US/08/897,956A
; CURRENT FILING DATE: 1997-07-21
; PRIOR APPLICATION NUMBER: 60/022,689
; PRIOR FILING DATE: 1996-07-26
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 1
; LENGTH: 257
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-08-897-956A-1

Query Match      100.0%; Score 1390; DB 4; Length 257;
Best Local Similarity 100.0%; Pred. No. 6.1e-127;
Matches 257; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAPAMESPTLLCVALLFFAPDGVLAVPQPKVSLNPPWNRIFKGENVTITCNGNNFFEVS 60
DB 1 MAPAMESPTLLCVALLFFAPDGVLAVPQPKVSLNPPWNRIFKGENVTITCNGNNFFEVS 60
QY 61 STKWFHNGSLSEETNSSLNIVNAKFEDSGEYKCOHQVNESEPVYLEVFSMDLLLOASAE 120
DB 61 STKWFHNGSLSEETNSSLNIVNAKFEDSGEYKCOHQVNESEPVYLEVFSMDLLLOASAE 120
QY 121 VMWEGQPLFLRCHGWRNWDVYKVIYKDGKALKYWYENHNISITNATVEDSGTYICTGKV 180
DB 121 VMWEGQPLFLRCHGWRNWDVYKVIYKDGKALKYWYENHNISITNATVEDSGTYICTGKV 180
QY 181 WOLDYSEPLNITVIKAPREKYWLQFFIPLLVILPAVDTGFLISTQQQVTFLLKIKRTR 240
DB 181 WOLDYSEPLNITVIKAPREKYWLQFFIPLLVILPAVDTGFLISTQQQVTFLLKIKRTR 240
QY 241 KGFRLNPHKPNPKNN 257
DB 241 KGFRLNPHKPNPKNN 257

GENERAL INFORMATION:
APPLICANT: Frank, Glenn R.
Porter, James P.
Rushlow, Keith E.
Wassom, Donald L.
TITLE OF INVENTION: Method to Detect Ige
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Carol Talkington Verser, Ph.D.
STREET: 1825 Sharp Point Drive
CITY: Fort Collins
STATE: Colorado
COUNTRY: USA
ZIP: 80525
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: WordPerfect for Windows, Version 7.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/944,277A
FILING DATE: 30-Aug-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/285,873
FILING DATE: 1999-03-31
ATTORNEY/AGENT INFORMATION:
NAME: Verser, Carol Talkington
REGISTRATION NUMBER: 37,459
REFERENCE/DOCKET NUMBER: DI-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 970/493-7272
TELEFAX: 970/484-9505
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 257 amino acids
TYPE: amino acid
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/
/
/ MOLECULE TYPE: linear
/ SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-944-277A-2

Query Match      100.0%; Score 1390; DB 4; Length 257;
Best Local Similarity 100.0%; Pred. No. 6.1e-127;
Matches 257; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAPAESSTLLCVALLEAPGVLAPOKPKVSLNPPNRIKGENVTLCNGNNFFVS 60
Db 1 MAPAESSTLLCVALLEAPGVLAPOKPKVSLNPPNRIKGENVTLCNGNNFFVS 60
QY 61 STKPFHNGSLSEETNSSLNIVNAKFSDSGEYKCOHQVNESEPVYLEVFSDDLLOASAE 120
Db 61 STKPFHNGSLSEETNSSLNIVNAKFSDSGEYKCOHQVNESEPVYLEVFSDDLLOASAE 120
QY 121 VMGEOPIFLCHGWRNDVYKVIYKDGKALKYWHNNHNSITNATVEDSGTYCTGKV 180
Db 121 VMGEOPIFLCHGWRNDVYKVIYKDGKALKYWHNNHNSITNATVEDSGTYCTGKV 180
QY 181 WQDYSEPLNITVIKAPREKYWLQFFIPLLWILFAVDLGLFISTQQVTFLLKIKRTR 240
Db 181 WQDYSEPLNITVIKAPREKYWLQFFIPLLWILFAVDLGLFISTQQVTFLLKIKRTR 240
QY 241 KGFLLNPPHPPKPNKN 257
Db 241 KGFLLNPPHPPKPNKN 257

RESULT 7
US-07-869-933-13
; Sequence 13, Application US/07869933
; Patent No. 5770396
; GENERAL INFORMATION:
; APPLICANT: KINET, Jean-Pierre
; TITLE OF INVENTION: ISOLATION, CHARACTERIZATION, AND USE OF
; TITLE OF INVENTION: THE HUMAN B SUBUNIT OF THE HIGH AFFINITY RECEPTOR FOR
; TITLE OF INVENTION: IMMUNOGLOBULIN
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 1800 Diagonal Road, Suite 500
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/869,933
; FILING DATE: 19920416
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 40399/154 NIHD
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)836-9300
; TELEFAX: (703)836-4109
; TELEX: 899149
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 232 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; ORGANISM: homo sapien
; STRAIN: FcR1 alpha subunit

US-07-869-933-13
; Sequence 6, Application US/08756387B
; Patent No. 5945294
; GENERAL INFORMATION:
; APPLICANT: Frank, Glenn R.
; APPLICANT: Porter, James P.
; APPLICANT: Rushlow, Keith E.
; APPLICANT: Wassom, Donald L.
; TITLE OF INVENTION: Method to Detect IgE
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carol Talkington Verser, Ph.D.
; ADDRESSEE: Heeka Corporation
; STREET: 1825 Sharp Point Drive
; CITY: Fort Collins
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80525
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: WordPerfect for Windows, Version 7.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/756,387B
; FILING DATE: No. 5945294ember 26, 1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Verser, Carol Talkington
; REGISTRATION NUMBER: 37,459
; REFERENCE/DOCKET NUMBER: DI-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 970/493-7272
; TELEFAX: 970/484-9505
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 232 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-756-387B-6

Query Match      90.9%; Score 1264; DB 2; Length 232;
Best Local Similarity 100.0%; Pred. No. 8.9e-115;
Matches 232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 26 VPQPKVSLNPPNRIKGENVTLCNGNNFFVSSTKWFHNGSLSEETNSSLNIVNAKF 85
Db 1 VPQPKVSLNPPNRIKGENVTLCNGNNFFVSSTKWFHNGSLSEETNSSLNIVNAKF 60
QY 86 EDSGEYKCOHQVNESEPVYLEVFSDDLLOASAEVVMGQPLFLRCHGWRNDVYKVIY 145
Db 61 EDSGEYKCOHQVNESEPVYLEVFSDDLLOASAEVVMGQPLFLRCHGWRNDVYKVIY 120
QY 146 YKDGKALKYWHNNHNSITNATVEDSGTYCTGKVWQDYSEPLNITVIKAPREKYWLQ 205
Db 121 YKDGKALKYWHNNHNSITNATVEDSGTYCTGKVWQDYSEPLNITVIKAPREKYWLQ 180
QY 206 FFIPLLWILFAVDLGLFISTQQVTFLLKIKRTRKGFLLNPPHPPKPNKN 257
Db 181 FFIPLLWILFAVDLGLFISTQQVTFLLKIKRTRKGFLLNPPHPPKPNKN 232

RESULT 8
US-08-756-387B-6
; Sequence 6, Application US/08756387B
; Patent No. 5945294
; GENERAL INFORMATION:
; APPLICANT: Frank, Glenn R.
; APPLICANT: Porter, James P.
; APPLICANT: Rushlow, Keith E.
; APPLICANT: Wassom, Donald L.
; TITLE OF INVENTION: Method to Detect IgE
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carol Talkington Verser, Ph.D.
; ADDRESSEE: Heeka Corporation
; STREET: 1825 Sharp Point Drive
; CITY: Fort Collins
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80525
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: WordPerfect for Windows, Version 7.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/756,387B
; FILING DATE: No. 5945294ember 26, 1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Verser, Carol Talkington
; REGISTRATION NUMBER: 37,459
; REFERENCE/DOCKET NUMBER: DI-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 970/493-7272
; TELEFAX: 970/484-9505
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 232 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-756-387B-6

Query Match      90.9%; Score 1264; DB 2; Length 232;
Best Local Similarity 100.0%; Pred. No. 8.9e-115;
Matches 232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 26 VPQPKVSLNPPNRIKGENVTLCNGNNFFVSSTKWFHNGSLSEETNSSLNIVNAKF 85
Db 1 VPQPKVSLNPPNRIKGENVTLCNGNNFFVSSTKWFHNGSLSEETNSSLNIVNAKF 60
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Qy	86	EDSGEYKCOHQVNESEFPYILEVSDMLLQASAEVVMGQPLFLRCHGWNDDVKVY	145
Db	61	EDSGEYKCOHQVNESEFPYILEVSDMLLQASAEVVMGQPLFLRCHGWNDDVKVY	120
Qy	146	YKDGALKYWNHNHISITNATVEDSGPYCTGKWOLDYSEBPLNTVTIKAPREKYWQ	205
Db	121	YKDGALKYWNHNHISITNATVEDSGPYCTGKWOLDYSEBPLNTVTIKAPREKYWQ	180
Qy	206	FPILVLWILFAVDTLGLISTQQQVTFLLKIKRTKRGFLNHPKPNKN	257
Db	181	FPILVLWILFAVDTLGLISTQQQVTFLLKIKRTKRGFLNHPKPNKN	232

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RESULT 9
US-09-103-663-13
; Sequence 13, Application US/09103663D
; Patent No. 6171803
; GENERAL INFORMATION:
; APPLICANT: Kinest et al.
; TITLE OF INVENTION: Isolation, characterization, and use of the human beta
; TITLE OF INVENTION: subunit of the high affinity receptor for
; TITLE OF INVENTION: immunoglobulin E.
; FILE REFERENCE: 50490
; CURRENT APPLICATION NUMBER: US/09/103,663D
; CURRENT FILING DATE: 1998-06-23
; EARLIER APPLICATION NUMBER: 07/869,933
; EARLIER FILING DATE: 1992-04-16
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 2282
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-103-663-13

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RESULT 10
US-09-285-873-6
; Sequence 6, Application US/09285873
; Patent No. 6308932
; GENERAL INFORMATION:
; APPLICANT: Frank, Glenn R.
; APPLICANT: Porter, James P.
; APPLICANT: Rushlow, Keith E.
; APPLICANT: Wasson, Donald L.
; TITLE OF INVENTION: Method to Detect Ige
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carol Talkington Verser, Ph.D.
; ADDRESSEE: Heskia Corporation
; STREET: 1825 Sharp Point Drive
; CITY: Fort Collins

```

STATE: Colorado
COUNTRY: USA
ZIP: 80525
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: wordPerfect for Windows, Version 7.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/285,873
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/756,387
FILING DATE: No. 6309832ember 26, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Verser, Carol Talkington
REGISTRATION NUMBER: 37,453
REFERENCE/DOCKET NUMBER: DI-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 970/493-7272
TELEFAX: 970/484-9505
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 232 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-285-873-6

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RESULT 11
US-09-944-277A-6
Sequence 6, Application US/09944277A
Patent No. 6652894
GENERAL INFORMATION:
APPLICANT: Frank, Glenn R.
Porter, James P.
Rushlow, Keith E.
Wassom, Donald L.
TITLE OF INVENTION: Method to Detect IGE
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESS: Carol Talkington Verser, Ph.D.
STREET: 1825 Sharp Point Drive
City: Fort Collins
STATE: Colorado
COUNTRY: USA
ZIP: 80525
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

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OPERATING SYSTEM: Windows 95
 SOFTWARE: WordPerfect for Windows, Version 7.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/944,277A
 FILING DATE: 30-Aug-2001
 CLASSIFICATION: <unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 09/285,873
 FILING DATE: 1999-03-31
 ATTORNEY/AGENT INFORMATION:
 NAME: Verser, Carol Talkington
 REGISTRATION NUMBER: 37,459
 REFERENCE/DOCKET NUMBER: DI-1
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 970/493-7272
 TELEFAX: 970/484-9505
 INFORMATION FOR SEQ ID NO: 6:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 232 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 SEQUENCE DESCRIPTION: SEQ ID NO: 6:
 US-09-944-277A-6

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 Best Local Similarity 100.0%; Pred. No. 8.9e-115;
 Matches 232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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 DB 1 VPQPKVSLNPPNRIKGENVTLCNGNNFFVSTKWFHNGSLSEETNSSLINVNAKF 60
 QY 86 EDGEYKQCOQVNESEPVVLEFVSDWLLQASAEVVMGQPLFLRCHGRNWDVYKVIY 145
 DB 61 EDGSEYKQCOQVNESEPVVLEFVSDWLLQASAEVVMGQPLFLRCHGRNWDVYKVIY 120
 QY 146 YKDGKALKWYENHNISITNATVEDSGTYCTGKWQLDYSEPLNITVIKAPREKYWLQ 205
 DB 121 YKDGKALKWYENHNISITNATVEDSGTYCTGKWQLDYSEPLNITVIKAPREKYWLQ 180
 QY 206 FTIPLLVILFAVDTGLFTSTQQVTFLLKIKRTRKGFRLNPHPKPNKNN 257
 DB 181 FTIPLLVILFAVDTGLFTSTQQVTFLLKIKRTRKGFRLNPHPKPNKNN 232

RESULT 12
 US-08-897-956A-3
 Sequence 3, Application US/08897956A
 Patent No. 6423512
 GENERAL INFORMATION:
 APPLICANT: Mary Ellen Digan
 APPLICANT: Philip Lake
 APPLICANT: Hermann Gram
 TITLE OF INVENTION: Fusion Polypeptides
 FILE REFERENCE: 600-7244/CPA
 CURRENT APPLICATION NUMBER: US/08/897,956A
 CURRENT FILING DATE: 1997-07-21
 PRIOR APPLICATION NUMBER: 60/022,689
 PRIOR FILING DATE: 1996-07-26
 NUMBER OF SEQ ID NOS: 38
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO 3
 LENGTH: 978
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Fusion polypeptide
 US-08-897-956A-3

Query Match 80.4%; Score 1117; DB 4; Length 978;
 Best Local Similarity 100.0%; Pred. No. 1.2e-99;
 Matches 204; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAPAMESPTLLCVALLFPADGVLAPOKPKVSLNPPNRIKGENVTLCNGNNFFVSV 60
 DB 1 MAPAMESPTLLCVALLFPADGVLAPOKPKVSLNPPNRIKGENVTLCNGNNFFVSV 60
 QY 61 STKWFHNGSLSEETNSSLINVNAKFEDSGEYKQCOQVNESEPVVLEFVSDWLLQASAE 120
 DB 61 STKWFHNGSLSEETNSSLINVNAKFEDSGEYKQCOQVNESEPVVLEFVSDWLLQASAE 120
 QY 121 VMEGQPLFLRCHGRNWDVYKVIYKDGKALKWYENHNISITNATVEDSGTYCTGKV 180
 DB 121 VMEGQPLFLRCHGRNWDVYKVIYKDGKALKWYENHNISITNATVEDSGTYCTGKV 180
 QY 181 WOLDYSESEPLNITVIKAPREKYWL 204
 DB 181 WOLDYSESEPLNITVIKAPREKYWL 204

RESULT 13
 US-08-756-387B-11
 Sequence 11, Application US/08756387B
 Patent No. 5945294
 GENERAL INFORMATION:
 APPLICANT: Frank, Glenn R.
 APPLICANT: Porter, James P.
 APPLICANT: Rushlow, Keith E.
 APPLICANT: Wassom, Donald L.
 TITLE OF INVENTION: Method to Detect IgE
 NUMBER OF SEQUENCES: 13
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Carol Talkington Verser, Ph.D.
 ADDRESSEE: Heskia Corporation
 STREET: 1825 Sharp Point Drive
 CITY: Fort Collins
 STATE: Colorado
 COUNTRY: USA
 ZIP: 80525
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: Windows 95
 SOFTWARE: WordPerfect for Windows, Version 7.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/756,387B
 FILING DATE: No. 5945294ember 26, 1996
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Verser, Carol Talkington
 REGISTRATION NUMBER: 37,459
 REFERENCE/DOCKET NUMBER: DI-1
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 970/493-7272
 TELEFAX: 970/484-9505
 INFORMATION FOR SEQ ID NO: 11:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 197 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-756-387B-11

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 Best Local Similarity 100.0%; Pred. No. 2.4e-96;
 Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 14

US-09-285-873-11
; Sequence 11, Application US/09285873
; Patent No. 6309832
; GENERAL INFORMATION:
; APPLICANT: Frank, Glenn R.
; APPLICANT: Porter, James P.
; APPLICANT: Rushlow, Keith E.
; APPLICANT: Wassom, Donald L.
; TITLE OF INVENTION: Method to Detect Ige
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carol Talkington Verser, Ph.D.
; STREET: 1825 Sharp Point Drive
; CITY: Fort Collins
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80525
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: Wordperfect for Windows, Version 7.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/285,873
; FILING DATE:
; CLASSIFICATION:

PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/756,387
; FILING DATE: NO. 6309832ember 26, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Verser, Carol Talkington
; REGISTRATION NUMBER: 37,459
; REFERENCE/DOCKET NUMBER: DI-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 970/493-7272
; TELEFAX: 970/484-9505
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 197 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-285-873-11

Query Match 77.2%; Score 1073; DB 4; Length 197;
Best Local Similarity 100.0%; Pred. No. 2.4e-96;
Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 121 VMGQPLFLRCHGWNWDVYKVIYKDGKALKYWYENHNISITNATVEDSGTYCTGKV 180
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Db 181 WQDYSEPLNITVIKA 197
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US-09-944-277A-11
; Sequence 11, Application US/09944277A
; Patent No. 6682894
; GENERAL INFORMATION:
; APPLICANT: Frank, Glenn R.
; APPLICANT: Porter, James P.
; APPLICANT: Rushlow, Keith E.
; APPLICANT: Wassom, Donald L.
; TITLE OF INVENTION: Method to Detect Ige
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carol Talkington Verser, Ph.D.
; STREET: 1825 Sharp Point Drive
; CITY: Fort Collins
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80525
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: Wordperfect for Windows, Version 7.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/944,277A
; FILING DATE: 30-Aug-2001
; CLASSIFICATION: <unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/285,873
; FILING DATE: 1999-03-31
; ATTORNEY/AGENT INFORMATION:
; NAME: Verser, Carol Talkington
; REGISTRATION NUMBER: 37,459
; REFERENCE/DOCKET NUMBER: DI-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 970/493-7272
; TELEFAX: 970/484-9505
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 197 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 11:

US-09-944-277A-11
Query Match 77.2%; Score 1073; DB 4; Length 197;
Best Local Similarity 100.0%; Pred. No. 2.4e-96;
Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 121 VMGQPLFLRCHGWNWDVYKVIYKDGKALKYWYENHNISITNATVEDSGTYCTGKV 180
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Db 121 VMGQPLFLRCHGWNWDVYKVIYKDGKALKYWYENHNISITNATVEDSGTYCTGKV 180
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QY 181 WQDYSEPLNITVIKA 197
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Db 181 WQDYSEPLNITVIKA 197
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Search completed: October 6, 2004, 09:04:36
Job time : 17.7739 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 6, 2004, 09:03:44 ; Search time 78.4779 Seconds
(without alignments)
1053.831 Million cell updates/sec

Title: US-10-763-400-2
Perfect score: 1390
Sequence: 1 MAPAMESPTLLCVALLFP.....RTRKGFRLPHKPNKNN 257

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1351062 seqs, 321799191 residues
Total number of hits satisfying chosen parameters: 1351062

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:
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2: /cgn2_6/ptodata/2/pubaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/2/pubaa/US03_NEW_PUB.pep.*
4: /cgn2_6/ptodata/2/pubaa/US06_PUBCOMB.pep.*
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8: /cgn2_6/ptodata/2/pubaa/US08_PUBCOMB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1390	100.0	257	9	US-09-944-277A-2
2	1390	100.0	257	12	US-10-236-392-28
3	1390	100.0	257	14	US-10-384-850-45
4	1264	90.9	232	9	US-09-944-277A-6
5	1157.5	83.3	218	12	US-10-236-392-30
6	1073	77.2	197	9	US-09-944-277A-11
7	969	69.7	176	10	US-09-809-715-2
8	969	69.7	176	12	US-10-293-992-2
9	947	68.1	172	9	US-09-944-277A-13
10	947	68.1	172	12	US-10-293-992-4
11	947	68.1	172	12	US-10-687-109-9
12	947	68.1	172	10	US-09-809-715-4
13	944	67.9	176	10	US-10-434-817-2
14	832.5	59.9	255	15	US-10-434-817-2
15	799.5	57.5	236	15	US-10-434-817-7

16	617	44.4	201	15	US-10-434-817-12
17	423	30.4	254	15	US-10-449-566-117
18	419	30.1	254	14	US-10-027-736A-20
19	418	30.1	254	14	US-10-384-850-44
20	418	30.1	254	14	US-10-027-736A-21
21	418	30.1	254	15	US-10-449-566-116
22	411	29.6	233	15	US-10-193-377-6
23	409.5	29.5	234	14	US-10-027-736A-69
24	383.5	27.6	257	14	US-10-027-736A-9
25	380.5	27.4	294	14	US-10-027-736A-18
26	379	27.3	374	12	US-09-836-544-23
27	379	27.3	374	14	US-10-027-736A-10
28	379	27.3	404	15	US-10-193-377-7
29	376	27.1	374	14	US-10-308-279-30
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31	374.5	26.9	336	14	US-10-027-736A-65
32	374	26.9	291	14	US-10-027-736A-19
33	374	26.9	291	16	US-10-322-696-96
34	372	26.8	339	9	US-09-925-301-1128
35	372	26.8	339	14	US-10-106-698-5782
36	371.5	26.7	310	14	US-10-384-850-42
37	371.5	26.7	310	16	US-10-322-696-180
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39	367.5	26.4	210	15	US-10-449-566-29
40	366	26.3	298	16	US-10-322-696-93
41	358	25.8	252	14	US-10-027-736A-68
42	357	25.7	174	9	US-09-245-764-8
43	357	25.7	174	12	US-10-687-109-8
44	357	25.7	261	9	US-09-245-764-7
45	357	25.7	261	12	US-10-687-109-7

ALIGNMENTS

RESULT 1
US-09-944-277A-2
; Sequence 2, Application US/09944277A
; Patent No. US20020034771A1
; GENERAL INFORMATION:

APPLICANT: Frank, Glenn R.
Porter, James P.
Rushlow, Keith E.
Wassom, Donald L.
TITLE OF INVENTION: Method to Detect Ige
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Carol Talkington Verser, Ph.D.
STREET: 1825 Sharp Point Drive
CITY: Fort Collins
STATE: Colorado
COUNTRY: USA
ZIP: 80525

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: WordPerfect for Windows, Version 7.0
CURRENT APPLICATION NUMBER: US/09/944,277A
FILING DATE: 30-Aug-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/285,873
FILING DATE: 1999-03-31
ATTORNEY/AGENT INFORMATION:
NAME: Verser, Carol Talkington
REGISTRATION NUMBER: 37,459
REFERENCE/DOCKET NUMBER: DI-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 970/493-7272
TELEFAX: 970/484-9505

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; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 257 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-944-277A-2

Query Match      100.0%; Score 1390; DB 9; Length 257;
Best Local Similarity 100.0%; Pred. No. 3.3e-111;
Matches 257; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAPAMESPTLLCVALLFFADGVLAVPQPKVSLNPPWNRIFKGENVTLCNNGNPFVS 60
DB 1 MAPAMESPTLLCVALLFFADGVLAVPQPKVSLNPPWNRIFKGENVTLCNNGNPFVS 60
QY 61 STKWFHNGSLSEETNSLNIVNAKFEDSGYKQHQQVNESEPVYLEVFSDWLLQASAE 120
DB 61 STKWFHNGSLSEETNSLNIVNAKFEDSGYKQHQQVNESEPVYLEVFSDWLLQASAE 120
QY 121 VMGEGQPLFLRCHGRWMDVYKVIYKDGKALKYWENHNISITNATVEDSGTYCTGKV 180
DB 121 VMGEGQPLFLRCHGRWMDVYKVIYKDGKALKYWENHNISITNATVEDSGTYCTGKV 180
QY 181 WLDYSEPLNITVIKAPREKYLQFFIPLLVILFAVDTLGLFISTQQQVTFLLKIKRTR 240
DB 181 WLDYSEPLNITVIKAPREKYLQFFIPLLVILFAVDTLGLFISTQQQVTFLLKIKRTR 240
QY 241 KGFRLNPHKPNPKNN 257
DB 241 KGFRLNPHKPNPKNN 257

RESULT 2
US-10-236-392-28
; Sequence 28, Application US/10236392
; Publication No. US20040067490A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, David W
; APPLICANT: Boldog, Ferenc L
; APPLICANT: Burgess, Catherine, E
; APPLICANT: Casman, Stacie J
; APPLICANT: Catterton, Blina
; APPLICANT: Chapoval, Andrei
; APPLICANT: Crabtree, Julie
; APPLICANT: Edinger, Shlomit, R
; APPLICANT: Ellerman, Karen
; APPLICANT: Gerlach, Valerie
; APPLICANT: Gorman, Linda
; APPLICANT: Gusev, Vladimir
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Larochele, William J
; APPLICANT: Li, Li
; APPLICANT: MacDougall, John R
; APPLICANT: Malvankar, Uriel M
; APPLICANT: Miller, Charles E
; APPLICANT: Millet, Isabelle
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Patturajan, Meera
; APPLICANT: Pena, Carol A
; APPLICANT: Peyman, John A
; APPLICANT: Rastelli, Luca
; APPLICANT: Reiger, Daniel K
; APPLICANT: Rothenberg, Mark E
; APPLICANT: Shenoy, Suresh
; APPLICANT: Shinkets, Richard A
; APPLICANT: Smithson, Glenda
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-442A
; CURRENT FILING DATE: 2002-09-06

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; PRIOR APPLICATION NUMBER: US09/540,763
; PRIOR FILING DATE: 2000-03-30
; PRIOR APPLICATION NUMBER: US60/390,155
; PRIOR FILING DATE: 2002-06-19
; PRIOR APPLICATION NUMBER: US09/635,949
; PRIOR FILING DATE: 2000-08-10
; PRIOR APPLICATION NUMBER: US60/318,765
; PRIOR FILING DATE: 2001-09-12
; PRIOR APPLICATION NUMBER: US60/357,303
; PRIOR FILING DATE: 2002-02-15
; PRIOR APPLICATION NUMBER: US60/367,753
; PRIOR FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER: US60/369,479
; PRIOR FILING DATE: 2002-04-02
; PRIOR APPLICATION NUMBER: US09/659,634
; PRIOR FILING DATE: 2000-09-12
; PRIOR APPLICATION NUMBER: US60/318,120
; PRIOR FILING DATE: 2001-09-07
; PRIOR APPLICATION NUMBER: US60/318,130
; PRIOR FILING DATE: 2001-09-07
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 794
; SOFTWARE: Custom
; SEQ ID NO 28
; LENGTH: 257
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-236-392-28

Query Match      100.0%; Score 1390; DB 12; Length 257;
Best Local Similarity 100.0%; Pred. No. 3.3e-111;
Matches 257; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAPAMESPTLLCVALLFFADGVLAVPQPKVSLNPPWNRIFKGENVTLCNNGNPFVS 60
DB 1 MAPAMESPTLLCVALLFFADGVLAVPQPKVSLNPPWNRIFKGENVTLCNNGNPFVS 60
QY 61 STKWFHNGSLSEETNSLNIVNAKFEDSGYKQHQQVNESEPVYLEVFSDWLLQASAE 120
DB 61 STKWFHNGSLSEETNSLNIVNAKFEDSGYKQHQQVNESEPVYLEVFSDWLLQASAE 120
QY 121 VMGEGQPLFLRCHGRWMDVYKVIYKDGKALKYWENHNISITNATVEDSGTYCTGKV 180
DB 121 VMGEGQPLFLRCHGRWMDVYKVIYKDGKALKYWENHNISITNATVEDSGTYCTGKV 180
QY 181 WLDYSEPLNITVIKAPREKYLQFFIPLLVILFAVDTLGLFISTQQQVTFLLKIKRTR 240
DB 181 WLDYSEPLNITVIKAPREKYLQFFIPLLVILFAVDTLGLFISTQQQVTFLLKIKRTR 240
QY 241 KGFRLNPHKPNPKNN 257
DB 241 KGFRLNPHKPNPKNN 257

RESULT 3
US-10-384-850-45
; Sequence 45, Application US/10384850
; Publication No. US20030175890A1
; GENERAL INFORMATION:
; APPLICANT: C. Fraser
; TITLE OF INVENTION: FAIL MOLECULES AND USES THEREOF
; FILE REFERENCE: 7853-217
; CURRENT APPLICATION NUMBER: US/10/384,850
; CURRENT FILING DATE: 2003-03-10
; PRIOR APPLICATION NUMBER: US/09/702,021
; PRIOR FILING DATE: 2000-10-30
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 45
; LENGTH: 257
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-384-850-45

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Query Match 100.0%; Score 1390; DB 14; Length 257;
Best Local Similarity 100.0%; Pred. No. 3.3e-111; Indels 0; Gaps 0;
Matches 257; Conservative 0; Mismatches 0;

QY 1 MAPAMESPTLCVALLFPADQVLAVPOKPKVSLNPPNRIKGENVTLCNGNFFEVS 60
Db 1 MAPAMESPTLCVALLFPADQVLAVPOKPKVSLNPPNRIKGENVTLCNGNFFEVS 60

QY 61 STKWFHNGSLSETNSSLNINAKEDSGEYKCHQCHQVNESEPPVYLEVFSWLLQLQASAE 120
Db 61 STKWFHNGSLSETNSSLNINAKEDSGEYKCHQCHQVNESEPPVYLEVFSWLLQLQASAE 120

QY 121 VVMEGQPLFLRCHGRNMDVYVYIKDGEALKYWYENHNSITNATVEDSGTYCTGV 180
Db 121 VVMEGQPLFLRCHGRNMDVYVYIKDGEALKYWYENHNSITNATVEDSGTYCTGV 180

QY 181 WOLDYSEPLNTVTKAPREKYWLOFFFIPLLVVILFAVDTGLFISTQQOVTFLKIKRTR 240
Db 181 WOLDYSEPLNTVTKAPREKYWLOFFFIPLLVVILFAVDTGLFISTQQOVTFLKIKRTR 240

QY 241 KGFRLLNPHKPNKPN 257
Db 241 KGFRLLNPHKPNKPN 257

RESULT 4
US-09-944-277A-6
; Sequence 6, Application US/09944277A
; Patent No. US20020034771A1

GENERAL INFORMATION:

APPLICANT: Frank, Glenn R.
Porter, James P.
Rushlow, Keith E.
Wassom, Donald L.
TITLE OF INVENTION: Method to Detect Ige
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Carol Talkington Verser, Ph.D.

STREET: 1825 Sharp Point Drive
CITY: Fort Collins
STATE: Colorado
COUNTRY: USA
ZIP: 80525

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: WordPerfect for Windows, Version 7.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/944,277A
FILING DATE: 30-Aug-2001
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/285,873
FILING DATE: 1999-03-31

ATTORNEY/AGENT INFORMATION:

NAME: Verser, Carol Talkington
REGISTRATION NUMBER: 37,459
REFERENCE/DOCKET NUMBER: DI-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 970/493-7272
TELEFAX: 970/484-9505

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:
LENGTH: 232 amino acids
TYPE: amino acid
TOPOLOGY: linear

MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 6:

US-09-944-277A-6

Query Match 90.9%; Score 1264; DB 9; Length 232;
Best Local Similarity 100.0%; Pred. No. 1.9e-100; Indels 0; Gaps 0;
Matches 232; Conservative 0; Mismatches 0;

QY 26 VPQKPKVSLNPPNRIKGENVTLCNGNFFEVSSTKWFHNGSLSETNSSLNINAKF 85
Db 1 VPQKPKVSLNPPNRIKGENVTLCNGNFFEVSSTKWFHNGSLSETNSSLNINAKF 60

QY 86 EDSEYKCHQCHQVNESEPPVYLEVFSWLLQLQASAEVVMGQPLFLRCHGRNMDVYVY 145
Db 61 EDSEYKCHQCHQVNESEPPVYLEVFSWLLQLQASAEVVMGQPLFLRCHGRNMDVYVY 120

QY 146 YKGEALKYWYENHNSITNATVEDSGTYCTGVKQWQDYSEPLNTVTKAPREKYWLO 205
Db 121 YKGEALKYWYENHNSITNATVEDSGTYCTGVKQWQDYSEPLNTVTKAPREKYWLO 180

QY 206 FFIPLLVVILFAVDTGLFISTQQOVTFLKIKRTRGFRLLNPHKPNKPN 257
Db 181 FFIPLLVVILFAVDTGLFISTQQOVTFLKIKRTRGFRLLNPHKPNKPN 232

RESULT 5

US-10-236-392-30
; Sequence 30, Application US/10236392
; Publication No. US20040067490A1

GENERAL INFORMATION:

APPLICANT: Anderson, David W
APPLICANT: Boldog, Ferenc L
APPLICANT: Burgess, Catherine, E
APPLICANT: Casman, Stacie J
APPLICANT: Catterton, Elina
APPLICANT: Chapoval, Andrei
APPLICANT: Crabtree, Julie
APPLICANT: Edinger, Shlomit, R
APPLICANT: Ellerman, Karen
APPLICANT: Gerlach, Valerie
APPLICANT: Gorman, Linda
APPLICANT: Grosse, William M
APPLICANT: Gusev, Vladimir
APPLICANT: Kekuda, Ramesh
APPLICANT: Larchelle, William J
APPLICANT: Li, Li
APPLICANT: MacDougall, John R
APPLICANT: Malyankar, Uriel M
APPLICANT: Miller, Charles E
APPLICANT: Millet, Isabelle
APPLICANT: Padigaru, Muralidhara
APPLICANT: Patturajan, Meera
APPLICANT: Pena, Carol A
APPLICANT: Peyman, John A
APPLICANT: Rastelli, Luca
APPLICANT: Reiger, Daniel K
APPLICANT: Rothenberg, Mark E
APPLICANT: Shenoy, Suresh
APPLICANT: Shinkets, Richard A
APPLICANT: Smithson, Glennda
TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME
FILE REFERENCE: 21402-442A
CURRENT APPLICATION NUMBER: US/10/236,392
CURRENT FILING DATE: 2002-09-06
PRIOR APPLICATION NUMBER: US09/540,763
PRIOR FILING DATE: 2000-03-30
PRIOR APPLICATION NUMBER: US60/390,155
PRIOR FILING DATE: 2002-06-19
PRIOR APPLICATION NUMBER: US09/635,949
PRIOR FILING DATE: 2000-08-10
PRIOR APPLICATION NUMBER: US60/318,765
PRIOR FILING DATE: 2001-09-12
PRIOR APPLICATION NUMBER: US60/357,303
PRIOR FILING DATE: 2002-02-15
PRIOR APPLICATION NUMBER: US60/367,753
PRIOR FILING DATE: 2002-03-25
PRIOR APPLICATION NUMBER: US60/369,479

;; PRIOR FILING DATE: 2002-04-02
;; PRIOR APPLICATION NUMBER: US09/659,634
;; PRIOR FILING DATE: 2000-09-12
;; PRIOR APPLICATION NUMBER: US60/318,120
;; PRIOR FILING DATE: 2001-09-07
;; PRIOR APPLICATION NUMBER: US60/318,130
;; PRIOR FILING DATE: 2001-09-07
;; Remaining Prior Application data removed - See File Wrapper or PALM.
;; NUMBER OF SEQ ID NOS: 794
;; SOFTWARE: Custom
;; SEQ ID NO 30
;; LENGTH: 218
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-10-236-392-30

Query Match 83.3%; Score 1157.5; DB 12; Length 218;
Best Local Similarity 84.8%; Pred. No. 2.5e-91;
Matches 218; Conservative 0; Mismatches 0; Indels 39; Gaps 1;

QY 1 MAPAMESPTLLCVALLFPADGVLAVPQKPKVSLNPPNRRIFKGENVTLTCNGNNPFEVS 60
DB 1 MAPAMESPTLLCVALLFPADGVLAVPQKPKVSLNPPNRRIFKGENVTLTCNGNNPFEVS 60
QY 61 STKWFHNGSLSEETNSSLNINAKFDSGEYKCOHQVNESEPVYLEVFSDDLLOASAE 120
DB 61 STKWFHNGSLSEETNSSLNINAKFDSGEYK----- 92
QY 121 VMGEQPLFLRCHGWRNWDVYKVIYKDGALKYWNHNISITNATVEDSGTYCTGKV 180
DB 93 -----CHGWRNWDVYKVIYKDGALKYWNHNISITNATVEDSGTYCTGKV 141
QY 181 WLDYSEPLNITVIKAPREKYLWOPPIPLVILFAVDTGLFISTQQQVTFLLKIKRTR 240
DB 142 WLDYSEPLNITVIKAPREKYLWOPPIPLVILFAVDTGLFISTQQQVTFLLKIKRTR 201
QY 241 KGFLLNPHKPNPKNN 257
DB 202 KGFLLNPHKPNPKNN 218

RESULT 6
US-09-944-277A-11
; Sequence 11, Application US/09944277A
; Patent No. US20020034771A1
; GENERAL INFORMATION:
; APPLICANT: Frank, Glenn R.
; Porter, James P.
; Rushlow, Keith E.
; Wassom, Donald L.
; TITLE OF INVENTION: Method to Detect Ige
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carol Talkington Verser, Ph.D.
; STREET: 1825 Sharp Point Drive
; CITY: Fort Collins
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80525
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: WordPerfect for Windows, Version 7.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/944,277A
; FILING DATE: 30-Aug-2001
; CLASSIFICATION: <unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/285,873
; FILING DATE: 1999-03-31
; ATTORNEY/AGENT INFORMATION:

;; NAME: Verser, Carol Talkington
;; REGISTRATION NUMBER: 37,459
;; REFERENCE/DOCKET NUMBER: DI-1
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 970/493-7272
;; TELEFAX: 970/484-9505
;; INFORMATION FOR SEQ ID NO: 11:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 197 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-09-944-277A-11

Query Match 77.2%; Score 1073; DB 9; Length 197;
Best Local Similarity 100.0%; Pred. No. 4e-84;
Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAPAMESPTLLCVALLFPADGVLAVPQKPKVSLNPPNRRIFKGENVTLTCNGNNPFEVS 60
DB 1 MAPAMESPTLLCVALLFPADGVLAVPQKPKVSLNPPNRRIFKGENVTLTCNGNNPFEVS 60
QY 61 STKWFHNGSLSEETNSSLNINAKFDSGEYKCOHQVNESEPVYLEVFSDDLLOASAE 120
DB 61 STKWFHNGSLSEETNSSLNINAKFDSGEYKCOHQVNESEPVYLEVFSDDLLOASAE 120
QY 121 VMGEQPLFLRCHGWRNWDVYKVIYKDGALKYWNHNISITNATVEDSGTYCTGKV 180
DB 121 VMGEQPLFLRCHGWRNWDVYKVIYKDGALKYWNHNISITNATVEDSGTYCTGKV 180
QY 181 WLDYSEPLNITVIK 197
DB 181 WLDYSEPLNITVIK 197

RESULT 7
US-09-809-715-2
; Sequence 2, Application US/09809715
; Publication No. US20030003502A1
; GENERAL INFORMATION:
; APPLICANT: Jardtzy, Theodore S.
; APPLICANT: Garman, Scott Clayton
; APPLICANT: Wurzburg, Beth A.
; APPLICANT: Kinet, Jean-Pierre
; TITLE OF INVENTION: THREE-DIMENSIONAL MODEL OF A COMPLEX BETWEEN A PC
; TITLE OF INVENTION: EPSILON RECEPTOR ALPHA CHAIN AND A PC REGION OF AN IGE
; FILE REFERENCE: AL-8
; CURRENT APPLICATION NUMBER: US/09/809,715
; CURRENT FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: 60/189,853
; PRIOR FILING DATE: 2000-03-15
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 2
; LENGTH: 176
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-809-715-2

Query Match 69.7%; Score 969; DB 10; Length 176;
Best Local Similarity 100.0%; Pred. No. 3e-75;
Matches 176; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 26 VPQKPKVSLNPPNRRIFKGENVTLTCNGNNPFEVSSTKWFHNGSLSEETNSSLNINAKF 85
DB 1 VPQKPKVSLNPPNRRIFKGENVTLTCNGNNPFEVSSTKWFHNGSLSEETNSSLNINAKF 60
QY 86 EDGSEYKCOHQVNESEPVYLEVFSDDLLOASAEVVMGEQPLFLRCHGWRNWDVYKVIY 145
DB 61 EDGSEYKCOHQVNESEPVYLEVFSDDLLOASAEVVMGEQPLFLRCHGWRNWDVYKVIY 120


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QY 86 EDGSEYKCHQOQVNESEPVYLEVFSWLLLOASAEVVMGQPLFLRCHGWRNDVYKVIY 145
Db 61 EDGSEYKCHQOQVNESEPVYLEVFSWLLLOASAEVVMGQPLFLRCHGWRNDVYKVIY 120
QY 146 YKDGEALKYWEHNHISITNATVEDSGTYCTGKQWQLDYSEPLNITVIKA 197
Db 121 YKDGEALKYWEHNHISITNATVEDSGTYCTGKQWQLDYSEPLNITVIKA 172

RESULT 11
US-10-293-992-4
; Sequence 4, Application US/10293992
; Publication No. US2004003527A1
; GENERAL INFORMATION:
; APPLICANT: Jaretzky, Theodore S.
; APPLICANT: Garman, Scott Clayton
; APPLICANT: Kinet, Jean-Pierre
; TITLE OF INVENTION: METHODS OF USING A THREE-DIMENSIONAL MODEL OF A FC EPSILON RECEPTOR
; TITLE OF INVENTION: CHAIN
; FILE REFERENCE: AL-3-CI-1
; CURRENT APPLICATION NUMBER: US/10/293,992
; CURRENT FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: 09/434,193
; PRIOR FILING DATE: 1999-11-04
; PRIOR APPLICATION NUMBER: 60/107,219
; PRIOR FILING DATE: 1998-11-05
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 4
; LENGTH: 172
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-992-4

Query Match 68.1%; Score 947; DB 12; Length 172;
Best Local Similarity 100.0%; Pred. No. 2.2e-73;
Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 26 VPQPKVSLNPPNRRIFKGENVTLCNGNNFFVSSSTKWFHNGSLSEETNSSLNIVNAKF 85
Db 1 VPQPKVSLNPPNRRIFKGENVTLCNGNNFFVSSSTKWFHNGSLSEETNSSLNIVNAKF 60
QY 86 EDGSEYKCHQOQVNESEPVYLEVFSWLLLOASAEVVMGQPLFLRCHGWRNDVYKVIY 145
Db 61 EDGSEYKCHQOQVNESEPVYLEVFSWLLLOASAEVVMGQPLFLRCHGWRNDVYKVIY 120
QY 146 YKDGEALKYWEHNHISITNATVEDSGTYCTGKQWQLDYSEPLNITVIKA 197
Db 121 YKDGEALKYWEHNHISITNATVEDSGTYCTGKQWQLDYSEPLNITVIKA 172

RESULT 13
US-09-809-715-4
; Sequence 4, Application US/09809715
; Publication No. US20030003502A1
; GENERAL INFORMATION:
; APPLICANT: Jaretzky, Theodore S.
; APPLICANT: Garman, Scott Clayton
; APPLICANT: Wurzburg, Beth A.
; APPLICANT: Kinet, Jean-Pierre
; TITLE OF INVENTION: THREE-DIMENSIONAL MODEL OF A COMPLEX BETWEEN A FC
; TITLE OF INVENTION: EPSILON RECEPTOR ALPHA CHAIN AND A FC REGION OF AN IGE
; TITLE OF INVENTION: ANTI-BODY AND USES THEREOF
; FILE REFERENCE: AL-8
; CURRENT APPLICATION NUMBER: US/09/809,715
; CURRENT FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: 60/189,853
; PRIOR FILING DATE: 2000-03-15
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 4
; LENGTH: 176
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-809-715-4

Query Match 67.9%; Score 944; DB 10; Length 176;
Best Local Similarity 97.7%; Pred. No. 4.2e-73;
Matches 172; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 26 VPQPKVSLNPPNRRIFKGENVTLCNGNNFFVSSSTKWFHNGSLSEETNSSLNIVNAKF 85
Db 1 VPQPKVSLNPPNRRIFKGENVTLCNGNNFFVSSSTKWFHNGSLSEETNSSLNIVNAKF 60
QY 86 EDGSEYKCHQOQVNESEPVYLEVFSWLLLOASAEVVMGQPLFLRCHGWRNDVYKVIY 145
Db 61 EDGSEYKCHQOQVNESEPVYLEVFSWLLLOASAEVVMGQPLFLRCHGWRNDVYKVIY 120
QY 146 YKDGEALKYWEHNHISITNATVEDSGTYCTGKQWQLDYSEPLNITVIKA 197
Db 121 YKDGEALKYWEHNHISITNATVEDSGTYCTGKQWQLDYSEPLNITVIKA 176

RESULT 14
US-10-434-817-2
; Sequence 2, Application US/10434817
; Publication No. US20030235579A1
; GENERAL INFORMATION:
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QY 86 EDGSEYKCHQOQVNESEPVYLEVFSWLLLOASAEVVMGQPLFLRCHGWRNDVYKVIY 145
Db 61 EDGSEYKCHQOQVNESEPVYLEVFSWLLLOASAEVVMGQPLFLRCHGWRNDVYKVIY 120
QY 146 YKDGEALKYWEHNHISITNATVEDSGTYCTGKQWQLDYSEPLNITVIKA 197
Db 121 YKDGEALKYWEHNHISITNATVEDSGTYCTGKQWQLDYSEPLNITVIKA 172

RESULT 11
US-10-293-992-4
; Sequence 4, Application US/10293992
; Publication No. US2004003527A1
; GENERAL INFORMATION:
; APPLICANT: Jaretzky, Theodore S.
; APPLICANT: Garman, Scott Clayton
; APPLICANT: Kinet, Jean-Pierre
; TITLE OF INVENTION: METHODS OF USING A THREE-DIMENSIONAL MODEL OF A FC EPSILON RECEPTOR
; TITLE OF INVENTION: CHAIN
; FILE REFERENCE: AL-3-CI-1
; CURRENT APPLICATION NUMBER: US/10/293,992
; CURRENT FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: 09/434,193
; PRIOR FILING DATE: 1999-11-04
; PRIOR APPLICATION NUMBER: 60/107,219
; PRIOR FILING DATE: 1998-11-05
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 4
; LENGTH: 172
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-992-4

Query Match 68.1%; Score 947; DB 12; Length 172;
Best Local Similarity 100.0%; Pred. No. 2.2e-73;
Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 26 VPQPKVSLNPPNRRIFKGENVTLCNGNNFFVSSSTKWFHNGSLSEETNSSLNIVNAKF 85
Db 1 VPQPKVSLNPPNRRIFKGENVTLCNGNNFFVSSSTKWFHNGSLSEETNSSLNIVNAKF 60
QY 86 EDGSEYKCHQOQVNESEPVYLEVFSWLLLOASAEVVMGQPLFLRCHGWRNDVYKVIY 145
Db 61 EDGSEYKCHQOQVNESEPVYLEVFSWLLLOASAEVVMGQPLFLRCHGWRNDVYKVIY 120
QY 146 YKDGEALKYWEHNHISITNATVEDSGTYCTGKQWQLDYSEPLNITVIKA 197
Db 121 YKDGEALKYWEHNHISITNATVEDSGTYCTGKQWQLDYSEPLNITVIKA 172

RESULT 12
US-10-687-109-9
; Sequence 9, Application US/10687109
; Publication No. US20040034480A1
; GENERAL INFORMATION:
; APPLICANT: Hogarth, P. Mark
; APPLICANT: Powell, Maree S.
; APPLICANT: McKenzie, Ian F.C.
; APPLICANT: Maxwell, Kelly F.
; APPLICANT: Garrett, Thomas P.J.
; APPLICANT: Epa, Vidana
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES AND MODELS OF FC RECEPTORS
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: 4102-4
; CURRENT APPLICATION NUMBER: US/10/687,109
; CURRENT FILING DATE: 2003-10-15
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/245,764
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-02-05
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/099,994
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/073,972
```

APPLICANT: Weber, Eric R.
McCall, Catherine A.
TITLE OF INVENTION: NOVEL EQUINE FC EPSILON RECEPTOR ALPHA
CHAIN NUCLEIC ACID MOLECULES, PROTEINS AND USES THEREOF
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hesk Corporation
STREET: 1825 Sharp Point Drive
CITY: Fort Collins
STATE: Colorado
COUNTRY: USA
ZIP: 80525
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect for Windows, Version 7.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/434,817
FILING DATE: 08-May-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/015,734
FILING DATE: 29-JAN-1998
ATTORNEY/AGENT INFORMATION:
NAME: Verser, Carol Talkington
REGISTRATION NUMBER: 37,459
REFERENCE/DOCKET NUMBER: DI-4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 970/493-7272
TELEFAX: 970/484-9505
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 236 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: Protein
SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-10-434-817-7
CHAIN NUCLEIC ACID MOLECULES, PROTEINS AND USES THEREOF
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hesk Corporation
STREET: 1825 Sharp Point Drive
CITY: Fort Collins
STATE: Colorado
COUNTRY: USA
ZIP: 80525
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect for Windows, Version 7.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/434,817
FILING DATE: 08-May-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/015,734
FILING DATE: 29-JAN-1998
ATTORNEY/AGENT INFORMATION:
NAME: Verser, Carol Talkington
REGISTRATION NUMBER: 37,459
REFERENCE/DOCKET NUMBER: DI-4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 970/493-7272
TELEFAX: 970/484-9505
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 236 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: Protein
SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-10-434-817-7

Query Match 57.5%; Score 799.5; DB 15; Length 236;
Best Local Similarity 66.0%; Pred. No. 1.5e-60;
Matches 155; Conservative 29; Mismatches 46; Indels 5; Gaps 2;

QY 21 DGVAVPQKPKVSLNPPWNRIFKGNVTLTCNGNFFVSTKWFHNGSLSEETNSSLNI 80
Db 2 DGVPAIRKSTVSLNPPWNRIFKGNVTLTCNKKPKLGNSTENTYNTTLEVTSSLNI 61
QY 81 VNAKPEDSGEYKQHQVNESEPVYLEVFSWLLQLQASAEVVMGQPLFLCHGWRNDV 140
Db 62 TNASHRSSEYRCRNDNLNLSEAVHLEVFSDWLLQLQASAEVIEGKALVLRGKWDV 121
QY 141 YKVIYKGEALKYWHENHNISITNATVEDSGTYCTG----KWQLDYSEPLNITVIK 196
Db 122 PKVIYKDGKPLEYWKYENKNISISATTENSGTYCEGAFNFKRTSEYTSYDLNITVK 181
QY 197 APREK-YWLOFFIPLLVILFAVDTLGLFISTQQQVTLFLKIKRTRKGFRLNPHP 250
Db 182 AEQSKYWLQFIPLLVILFAVDTLGLFVSTQQQLTFLKIKRTRGRKLMDDPH 236
Search completed: October 6, 2004, 09:28:09
Job time : 80.4779 secs

QY 1 MAPAMESPTLLCVALLFPADGVLAVPQKPKVSLNPPWNRIFKGNVTLTCNGNFFVST 60
Db 1 MPAPMGSPALLWTFLFLSLDGVPAIRKSTVSLNPPWNRIFKGNVTLTCNKKPKLGN 60
QY 61 STKWFHNGSLSEETNSSLNI VNAKPEDSGEYKQHQVNESEPVYLEVFSWLLQLQASAE 120
Db 61 STEWTYNTTLEVTSSLNI TNASHRSSEYRCRNDNLNLSEAVHLEVFSDWLLQLQASAE 120
QY 121 VMGQPLFLCHGWRNDVYKVIYKGEALKYWHENHNISITNATVEDSGTYCTG-- 178
Db 121 EVIEGKALVLRGKWDVFKVIYKDGKPLEYWKYENKNISISATTENSGTYCEGAF 180
QY 179 --KWQLDYSEPLNITVIKAPREK-YWLOFFIPLLVILFAVDTLGLFISTQQQVTLFLK 235
Db 181 NFKETSEYTSYDLNITVIKAEQSKYWLQFIPLLVILFAVDTLGLFVSTQQQLTFLK 240
QY 236 IKRTRKGFRLNPHP 250
Db 241 IKRTRGRKLMDDPH 255

RESULT 15

US-10-434-817-7
Sequence 7, Application US/10434817
Publication No. US2003035579A1
GENERAL INFORMATION:
APPLICANT: Weber, Eric R.
McCall, Catherine A.
TITLE OF INVENTION: NOVEL EQUINE FC EPSILON RECEPTOR ALPHA

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 6, 2004, 09:03:14 ; Search time 14.0781 Seconds
(without alignments)
1756.007 Million cell updates/sec

Title: US-10-763-400-2

Perfect score: 1390

Sequence: 1 MAPAMESPTLLCVALLFPAP.....RTRKGFRLNHPKPNKKN 257

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR 78:**

2: PIR1:**

3: PIR2:**

4: PIR3:**

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1390	100.0	257	2 S00682	IgE Fc receptor al
2	626.5	45.1	250	2 A34342	IgE Fc receptor al
3	597.5	43.0	245	2 A30154	IgE receptor alpha
4	418	30.1	254	1 JLO107	Fc gamma (Igg) rec
5	406	29.2	233	1 JLO084	Fc gamma (Igg) rec
6	405	29.1	296	2 I46021	Fc-gamma receptor
7	403	29.0	280	2 I55577	Fc gamma (Igg) rec
8	401.5	28.9	261	2 S29360	Fc gamma (Igg) rec
9	399	28.7	267	2 I56110	Fc-gamma RIIB-alc
10	395	28.4	267	2 A35902	Fc gamma (Igg) rec
11	390.5	28.1	270	2 A34636	Fc-gamma receptor
12	380	27.3	267	2 I72882	Fc gamma (Igd) rec
13	379	27.3	336	2 I48471	Fc gamma (Igg) rec
14	379	27.3	404	2 A46480	Fc gamma (Igg) rec
15	376	27.1	344	2 A41357	Fc gamma (Igg) rec
16	376	27.1	374	1 A39878	Fc gamma (Igg) rec
17	371.5	26.7	323	2 S06946	Fc gamma (Igg) rec
18	368	26.5	285	2 S36903	Fc gamma (Igg) rec
19	367.5	26.4	310	2 JLO119	Fc gamma (Igg) rec
20	367	26.4	283	1 FCMSG1	Fc gamma (Igg) rec
21	367	26.4	330	2 A40071	Fc gamma (Igg) rec
22	367	26.4	330	2 I49660	Fc-gamma-1/gamma-2
23	348	25.0	157	2 D31327	IgE receptor alpha
24	347	25.0	317	2 JLO118	Fc gamma (Igg) rec
25	338	24.3	160	2 I47163	cytolytic trigger
26	271	19.5	159	2 I47164	cytolytic trigger
27	166	11.9	1694	2 S50065	sialoadhesin - mou
28	156	11.2	104	2 I47165	cytolytic trigger
29	137.5	9.9	458	1 WMSR1	biliary glycoprote

30 137.5 9.9 521 2 JC1508 biliary glycoprote
31 136.5 9.8 458 2 JC1509 biliary glycoprote
32 136.5 9.8 458 2 S23969 cell-adhesion mole
33 136.5 9.8 458 2 S68177 C-CAM2a protein is
34 136.5 9.8 519 2 A44783 ecto-ATPase precur
35 136.5 9.8 521 2 S34338 biliary glycoprote
36 134 9.6 7962 2 I38346 elastic titin - hu
37 133 9.6 538 2 JC2457 vascular cell adhe
38 129.5 9.3 344 2 A27681 nonspecific cross-
39 129.5 9.3 1239 1 A32579 neuroglian - fruit
40 126 9.1 1327 2 T09402 immunoglobulin-lik
41 125.5 9.0 978 2 S16395 macrophage colony-
42 124.5 9.0 1033 2 S19247 cell adhesion prot
43 123.5 8.9 264 2 I46020 FC gamma 2 recept
44 123.5 8.9 976 1 TVMSMD macrophage colony-
45 121.5 8.7 739 2 JS0675 vascular cell adhe

ALIGNMENTS

RESULT 1

S00682
Igs Fc receptor alpha chain precursor - human

NlAlternate names: Fc-epsilon receptor

C:Species: Homo sapiens (man)

C:Date: 31-Dec-1988 #sequence revision 31-Dec-1988 #text_change 23-Jul-1999

C:Accession: S00682; B30154; S42209

R:Kochan, J.; Pettine, L.F.; Hakimi, J.; Kishi, K.; Kinet, J.P.

Nucleic Acids Res. 16, 3584, 1988

A:Title: Isolation of the gene coding for the alpha subunit of the human high affinity I

A:Reference number: S00682; MUID:88233953; PMID:2967464

A:Accession: S00682

A:Molecule type: mRNA

A:Residues: 1-257 <KOC>

A:Cross-references: EMBL:X06948; NID:G31317; PIDN:CAA30025.1; PID:G31318

R:Shimizu, A.; Tepler, I.; Benfey, P.N.; Berenstein, E.H.; Siraganian, R.P.; Leder, P.

Proc. Natl. Acad. Sci. U.S.A. 85, 1907-1911, 1988

A:Title: Human and rat mast cell high-affinity immunoglobulin E receptors: Characterizat

A:Reference number: A94131; MUID:88158102; PMID:2964640

A:Accession: B30154

A:Molecule type: mRNA

A:Residues: 1-257 <SHI>

A:Cross-references: GJ:J03605; NID:G187449; PIDN:AAA36204.1; PID:G307164

R:Yagi, S.; Yanagida, M.; Tanida, I.; Hasegawa, A.; Okumura, K.; Ra, C.

Eur. J. Biochem. 220, 593-599, 1994

A:Title: High-level expression of the truncated alpha chain of human high-affinity rece

nant product.

A:Reference number: S42209; MUID:94170811; PMID:8125119

A:Accession: S42209

A:Molecule type: Protein

A:Residues: 26-197 <YAG>

A:Experimental source: purified recombinant protein

C:Genetics:

A:Gene: GDB:FCER1A

A:Cross-references: GDB:I119902; OMIM:147140

A:Map position: Iq23-Iq23

C:Superfamily: Fc gamma receptor III; immunoglobulin homology

C:Keywords: immunoglobulin receptor; transmembrane protein

F;1-25/Domain: signal sequence #status predicted <Sig>

F;26-257/Product: IgE Fc receptor alpha chain #status predicted <NAT>

F;44-95/Domain: immunoglobulin homology <IMM1>

F;125-178/Domain: immunoglobulin homology <IMM2>

Query Match 100.0%; Score 1390; DB 2; Length 257;

Best Local Similarity 100.0%; Fred. No. 5.2e-100; Indels 0; Gaps 0;

Matches 257; Conservative 0; Mismatches 0;

QY 1 MAPAMESPTLLCVALLFPAPDGVLPQPKVSLNPPNRIKGENVTLCNGNFFEVS 60

Db 1 MAPAMESPTLLCVALLFPAPDGVLPQPKVSLNPPNRIKGENVTLCNGNFFEVS 60

QY 61 STKWFNGSLSETNSSLNIVNAKFEDSCGEYQHQVNESEFVILEVSDMLLLQASAE 120

Db 61 STKWFHNGSLSEBTSNLSINVAKEFDSGEYKQHQVNESEPVYLFVSDWLLQASAE 120
 QY 121 VMEGQPLFLRCHGWRNDVKVIYKDGEGALKWYENHNISINATVSDSGTYCTGKV 180
 Db 121 VMEGQPLFLRCHGWRNDVKVIYKDGEGALKWYENHNISINATVSDSGTYCTGKV 180
 QY 181 WOLDYESPLNTITVIAKREKYWLOFPPLPLWILFAVDTGLFISTQOQVTFLLKIKRTR 240
 Db 181 WOLDYESPLNTITVIAKREKYWLOFPPLPLWILFAVDTGLFISTQOQVTFLLKIKRTR 240
 QY 241 KGFRLNPHPKPNPKNN 257
 Db 241 KGFRLNPHPKPNPKNN 257

RESULT 2

A34342
 IGE Fc receptor alpha chain precursor - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 15-Jun-1990 #sequence_revision 15-Jun-1990 #text_change 23-Jul-1999
 C:Accession: A34342; A61238
 R:Ra, C.; Jouvin, M.H.E.; Kinet, J.P.
 J. Biol. Chem. 264, 15323-15327, 1989
 A:Title: Complete structure of the mouse mast cell receptor for IGE (Fc-epsilon-RI) and A:Reference number: A34342; MUID:89359361; PMID:2527850
 A:Accession: A34342
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-250 <RAC>
 A:CROSS-references: GB:J05018; NID:9193236; PIDN:AAA37600.1; PID:9309224
 R:Robertson, M.W.; Menl, V.S.; Richards, M.L.; Liu, F.T.
 Int. Arch. Allergy Appl. Immunol. 96, 289-295, 1991
 A:Title: mRNA variants encoding multiple forms of the high-affinity IGE receptor alpha s
 A:Reference number: A61238; MUID:92234569; PMID:1839735
 A:Accession: A61238
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 125-194 <ROB>
 A:Superfamily: Fc gamma receptor III; immunoglobulin homology
 C:Keywords: alternative splicing; immunoglobulin receptor; transmembrane protein
 F:42-94/Domain: immunoglobulin homology <IMM>

Query Match 45.1%; Score 626.5; DB 2; Length 250;
 Best Local Similarity 51.9%; Pred. No. 3.7e-41;
 Matches 121; Conservative 46; Mismatches 63; Indels 3; Gaps 3;
 QY 11 LCVALFFAPDGVLAVPQKPKVSLNPPNRIFFKGENVTLCNGNPFV-SSTKWFHNGS 69
 Db 9 LCLALLFMSLDVLTATEKSVLTDLPPIRIFTEGKVTLLSCYGNHLMQNSTKWLHNGT 68
 QY 70 LSEBTSNLSINVAKEFDSGEYKQHQVNESEPVYLFVSDWLLQASAEVMEGQPLFL 129
 Db 69 VSENSSHLVIVSATQDSGKYICQKGLFKSPVYLVNTQDWLLLTQTSADMLIVHGSFD 128
 QY 130 LRCHGWRNDVKVIYKDGEGALKWYENHNISINATVSDSGTYCTGKVWOLDYESPP 189
 Db 129 IRCHGWRNDVKVIYKDGEGALKWYENHNISINATVSDSGTYCTGKVWOLDYESPP 187
 QY 190 LNTVIAKREK-YWLOFPPLPLWILFAVDTGLFISTQOQVTFLLKIKRTRK 241
 Db 188 FRAVVKAYCKYWLQIPLPLVAILFAVDTGLLSTSEQKSVLEIQTKG 240

RESULT 3

A30154
 IGE receptor alpha chain precursor - rat
 N:Alternate names: Fc-epsilon-R alpha chain precursor
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 18-Oct-1989 #sequence_revision 18-Oct-1989 #text_change 21-Jan-2000
 C:Accession: C31327; A30154; A27116; 155304
 R:Liu, F.T.; Albrandt, K.; Robertson, M.W.
 Proc. Natl. Acad. Sci. U.S.A. 85, 5639-5643, 1988

A:Title: cDNA heterogeneity suggests structural variants related to the high-affinity IGE A:Reference number: A94203; MUID:88289772; PMID:2969594
 A:Accession: C31327
 A:Molecule type: mRNA
 A:Residues: 1-245 <LIU>
 A:CROSS-references: GB:M21622; GB:J03811
 A:Experimental source: basophilic leukemia cell line, clone R3-4
 A:Accession: A31327
 A:Molecule type: mRNA
 A:Residues: 21-245 <LIU>
 A:CROSS-references: GB:M21622; NID:9204109; PIDN:AAA41146.1; PID:9204110; GB:J03811
 A:Experimental source: basophilic leukemia cell line
 R:Shimizu, A.; Tepler, I.; Benfey, P.N.; Berenstein, E.H.; Siraganian, R.P.; Leder, P.
 Proc. Natl. Acad. Sci. U.S.A. 85, 1907-1911, 1988
 A:Title: Human and rat mast cell high-affinity immunoglobulin E receptors: characterization A:Reference number: A94191; MUID:88158102; PMID:2964640
 A:Accession: A30154
 A:Molecule type: mRNA
 A:Residues: 1-245 <SHI>
 A:CROSS-references: GB:J03606; NID:9205331; PIDN:AAA41582.1; PID:9205332
 R:Kinet, J.P.; Metzger, H.; Hakimi, J.; Kochan, J.
 Biochemistry 26, 4605-4610, 1987
 A:Title: A cDNA presumptively coding for the alpha subunit of the receptor with high aff A:Reference number: A27116; MUID:88024987; PMID:2959318
 A:Accession: A27116
 A:Molecule type: mRNA
 A:Residues: 1, 'G', '3-236', 'N', '238-244', 'RLKPNs', <KIN>
 R:Tepler, I.; Shimizu, A.; Leder, P.
 J. Biol. Chem. 264, 5912-5915, 1989
 A:Title: The gene for the rat mast cell high affinity IGE receptor alpha chain. Structur A:Reference number: 155304; MUID:89174653; PMID:2522441
 A:Accession: 155304
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-16 <RES>
 A:CROSS-references: GB:M25334; NID:9341335; PIDN:AAA74562.1; PID:9556391
 C:Superfamily: Fc gamma receptor III; immunoglobulin homology
 C:Keywords: immunoglobulin receptor; transmembrane protein
 F:1-23/Domain: signal sequence #status predicted <SIG>
 F:24-245/Product: IGE receptor alpha chain #status predicted <MAT>
 F:42-93/Domain: immunoglobulin homology <IMM>

Query Match 43.0%; Score 597.5; DB 2; Length 245;
 Best Local Similarity 49.8%; Pred. No. 6.3e-39;
 Matches 116; Conservative 43; Mismatches 73; Indels 1; Gaps 1;
 QY 11 LCVALFFAPDGVLAVPQKPKVSLNPPNRIFFKGENVTLCNGNPFVSDSGTYCTGKVWOLDYESPP 70
 Db 9 LCLALVLSLGVMLTATQKSVVSLDPPWIRLTGDKVTLLCNGNSQMSNTKWIHNDI 68
 QY 71 SEETNSSLSINVAKEFDSGEYKQHQVNESEPVYLFVSDWLLQASAEVMEGQPLFL 130
 Db 69 SNVKSSSHVIVSATQDSGKYICQKGLFKSPVYLVNTQDWLLLTQTSADMLIVHGSFDI 128
 QY 131 RCHGWRNDVKVIYKDGEGALKWYENHNISINATVSDSGTYCTGKVWOLDYESPP 190
 Db 129 RCRGWRNDVKVIYKDGEGALKWYENHNISINATVSDSGTYCTGKVWOLDYESPP 188
 QY 191 NITVIAKREK-YWLOFPPLPLWILFAVDTGLFISTQOQVTFLLKIKRTRK 242
 Db 189 SIADVVDYTYEYRWLQIPLPLVAILFAVDTGLWFTSHKQFESILKIQTGKG 241

RESULT 4

JL0107
 Fc gamma (IgG) receptor III-A precursor (natural killer cell) [validated] - human
 N:Alternate names: CD16 antigen; low affinity IgG Fc receptor type III-2 precursor; surf C:Species: Homo sapiens (man)
 C:Date: 07-Sep-1990 #sequence_revision 02-Aug-1996 #text_change 08-Dec-2000
 C:Accession: JL0107; A60383; A32933; I37627
 R:Ravetch, J.V.; Perussia, B.
 J. Exp. Med. 170, 481-497, 1989
 A:Title: Alternative membrane forms of Fc gamma RIII (CD16) on human natural killer cells

A:Reference number: J010107; MUID:89328325; PMID:2526846
A:Accession: J010107
A:Molecule type: mRNA
A:Residues: 1-254 <RAV>
A:CROSS-references: GB:X52645; GB:M31937; NID:G31323; PIDN:CAA36870.1; PID:G31324
A:Note: the sequence of the receptor from human polymorphonuclear granulocytes, reported 21 residues
R:Tronstine, M.L.; Peltz, G.A.; Yssel, H.; Huizinga, T.W.J.; von dem Borne, A.E.G.K.; S. Int. Immunol. 2, 303-310, 1990
A>Title: Reactivity of cloned, expressed human Fc gamma RIII isoforms with monoclonal anti A:Reference number: A60383; MUID:91120527; PMID:1703781
A:Accession: A60383
A>Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-254 <TRO>
R:Scallion, B.J.; Scigliano, E.; Freedman, V.H.; Miedel, M.C.; Pan, Y.C.E.; Unkeless, J.C. Proc. Natl. Acad. Sci. U.S.A. 86, 5079-5083, 1989
A>Title: A human immunoglobulin G receptor exists in both polypeptide-anchored and phosph A:Reference number: A32933; MUID:89296947; PMID:2525780
A:Accession: A32933
A:Molecule type: mRNA
A:Residues: 31-254 <SCA>
A:CROSS-references: GB:M24853; NID:G14849; PIDN:AAA53506.1; PID:G386806
R:Gesner, J.E.; Grussemeyer, T.; Kolanus, W.; Schmidt, R.E. J. Biol. Chem. 270, 1350-1361, 1995
A>Title: The human low affinity immunoglobulin G Fc receptor III-A and III-B genes. Mole A:Reference number: A55439; MUID:95138131; PMID:7836402
A:Accession: I37627
A:Molecule type: DNA
A:Residues: 1-39 <RES>
A:CROSS-references: EMBL:Z46222; NID:G559445; PIDN:CAA86295.1; PID:G1478198
A:Note: translation has been corrected relative to PID:G871305
C:Comment: This low affinity IGG Fc receptor of natural killer cells, which is the produ c nearly identical, yet this receptor lacks a glycosylphosphatidylinositol anchor and in C:Genetics:
A:Gene: GDB:FCGR3A; FCGR3
A:CROSS-references: GDB:119904; OMIM:146740
A:Map position: 1Q23-1Q23
A:Introns: 14/1; 21/1
A:Note: the list of introns is incomplete
C:Superfamily: Fc gamma receptor III; immunoglobulin homology
C:Keywords: glycoprotein; receptor; transmembrane protein
F:1-17/Domain: signal sequence #status predicted <SIG>
F:18-254/Product: Fc gamma (IGG) receptor III-A #status experimental <MAT>
F:18-208/Domain: extracellular #status predicted <EXT>
F:40-91/Domain: immunoglobulin homology <IMM1>
F:111-174/Domain: immunoglobulin homology <IMM2>
F:209-229/Domain: transmembrane #status predicted <TRZ>
F:230-254/Domain: intracellular #status predicted <CYT>
F:56,63,92,180,187/Binding site: carbohydrate (Asn) (covalent) #status predicted

JU0284
Fc gamma (IGG) receptor III-B precursor (neutrophil) - human
A:Alternate names: FcR III; IGG Fc receptor precursor, type III-1 (polymorphonuclear gra C:Species: Homo sapiens (man)
C:Date: 07-Sep-1990 #sequence, revision 02-Aug-1996 #text_change 28-Jan-2000
A:Accession: JU0284; S00758; I37628; B32933; A31460
R:Ravetch, J.V.; Perussia, B. J. Exp. Med. 170, 481-497, 1989
A>Title: Alternative membrane forms of Fc gamma RIII(CD16) on human natural killer cells A:Reference number: J010107; MUID:89328325; PMID:2526846
A:Accession: JU0284
A:Molecule type: mRNA
A:Residues: 1-201, 'SF', 204-233 <RAV>
A:CROSS-references: GB:J04162
A:Note: the sequence of the receptor from human NK cells, reported in the same paper, di rboxyl end
R:Simmons, D.; Seed, B. Nature 333, 568-570, 1988
A>Title: The Fc-gamma receptor of natural killer cells is a phospholipid-linked membrane A:Reference number: S00758; MUID:88232937; PMID:2967436
A:Accession: S00758
A:Molecule type: mRNA
A:Residues: 1-233 <STM>
A:CROSS-references: EMBL:X07934; NID:G29744; PIDN:CAA30758.1; PID:G29745
R:Gesner, J.E.; Grussemeyer, T.; Kolanus, W.; Schmidt, R.E. J. Biol. Chem. 270, 1350-1361, 1995
A>Title: The human low affinity immunoglobulin G Fc receptor III-A and III-B genes. Mole A:Reference number: A55439; MUID:95138131; PMID:7836402
A:Accession: I37628
A:Molecule type: DNA
A:Residues: 1-72 <RES>
A:CROSS-references: EMBL:Z46223; NID:G559446; PIDN:CAA86296.1; PID:G871306
R:Scallion, B.J.; Scigliano, E.; Freedman, V.H.; Miedel, M.C.; Pan, Y.C.E.; Unkeless, J.C. Proc. Natl. Acad. Sci. U.S.A. 86, 5079-5083, 1989
A>Title: A human immunoglobulin G receptor exists in both polypeptide-anchored and phosph A:Reference number: A32933; MUID:89296947; PMID:2525780
A:Accession: B32933
A:Molecule type: mRNA
A:Residues: 1-121, 'E', 123-150, 'S', 152-233 <SCA>
A:CROSS-references: GB:M24854; NID:G184851; PIDN:AAA53507.1; PID:G306930
R:Peltz, G.A.; Grundy, H.O.; Iebbo, R.V.; Yssel, H.; Barsh, G.S.; Moore, K.W. Proc. Natl. Acad. Sci. U.S.A. 86, 1013-1017, 1989
A>Title: Human Fc-gamma-RIII: cloning, expression, and identification of the chromosomal A:Reference number: A31460; MUID:89128838; PMID:2521732
A:Accession: A31460
A:Molecule type: mRNA
A:Residues: 1-35, 'R', 37-64, 'N', 66-81, 'D', 83-105, 'V', 107-233 <PEL>
A:CROSS-references: GB:J04162; NID:G183036; PIDN:AAA53881.1; PID:G183037
C:Comment: This low affinity IGG Fc receptor of neutrophils, which is the product of the 1, yet this receptor lacks 21 residues at the carboxyl end because of an early stop cod C:Genetics:
A:Gene: GDB:FCGR3B; FCGR3
A:CROSS-references: GDB:128176; OMIM:146740
A:Map position: 1Q23-1Q23
A:Introns: 14/1; 21/1
A:Note: the list of introns is incomplete
C:Superfamily: Fc gamma receptor III; immunoglobulin homology
C:Keywords: blocked carboxyl end; glycoprotein; lipoprotein; phosphatidylinositol linka F:1-18/Domain: signal sequence #status predicted <SIG>
F:19-203/Product: Fc gamma (IGG) receptor III-B #status predicted <MAT>
F:40-91/Domain: immunoglobulin homology <IMM1>
F:111-174/Domain: immunoglobulin homology <IMM2>
F:56,63,92,180,187/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:203/Modified site: GPI-anchor ethanolamine amidated carboxyl end (Ser) (in mature form

Query Match 30.1%; Score 418; DB 1; Length 254;
Best Local Similarity 40.9%; Pred. No. 4.5e-25;
Matches 94; Conservative 34; Mismatches 92; Indels 10; Gaps 3;
QY 10 LLCVALLFPADGVLAVPQPK--VSLNPPNRIKGENVTLTCNGNNFEVSTQWFHN 67
DB 5 LLPTALLLVASG-MRTEDLPKAVVFLEFPQYRVLKDSVTLKCGAYSPEDNSTQWFHN 63
QY 68 GSLSEBTSSNLINNAKFEDESGYKCCQVQVNESEPVYLFVSDWLLQASAVVMGQP 127
DB 64 ESLISSQASSYFIDAATVDDSGEYRCQNLSTLSDPVQLVHIGWLLQAPRVFKEEDP 123
QY 128 LFLRCHGRNDVYKVIYKQGEALKYWEHNHNSINATVEDSGTYCTCKVWQLDYES 187
DB 124 IHLRCHSKWNTALHKVTVLQNGKGRKYPHNSDPIPKATLKDSGYSYFCGLFGSKNVSS 183
QY 188 EPLNTITVIAKPREKYLQFFIP-----LLVILFAVDITGLFTSTQQOV 230
DB 184 ETVNITITGLAVSTISSFFPPGQVSCVCLWVLLFVADITGLYFSVKTNI 233

RESULT 5

QY 68 GSLSEETNSLNIIVNAKFDSEYKCOHQVNESEPVYLEVFSDDLQASAEVVMGQP 127
 Db 64 ESLISSQASSYFIDAATVNDSEYRCQTNLSTLSDPVQLEVHIGWLLQAPRWFKEDP 123
 QY 128 LFLRCHGWRNDVYKVIYKDGKALKYWENHISITNATVEDSGTYCTGKWQLDYES 187
 Db 124 IHLRCHSWNTALHKVYIQLONGKDRKIFHNHSDPHIPKATLKDSGYFCRGLVSGKNVSS 183
 QY 188 EPLNITVIAKPEKXWLOFPFIP-----LLVVLFAVDGTGLFISTQOQV 230
 Db 184 ETWNITITGLAVSTISSPSPGQVQVFCFLVNLVFAVDGTGLYFSVKINI 233

RESULT 6

FC-gamma receptor II - bovine
 C:Species: Bos primigenius taurus (cattle)
 C>Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 23-Jul-1999
 C:Accession: I46021; S40204
 R:Zhang, G.; Young, J.R.; Tregaskes, C.R.; Howard, C.J.
 Immunogenetics 39, 423-427, 1994
 A:Title: Cattle FC gamma RII: molecular cloning and ligand specificity.
 A:Reference number: I46021; MUID:94245284; PMID:8188320
 A:Accession: I46021
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-296 <ZHA>
 A:Cross-references: EMBL:X75671; NID:g437978; PIDN:CAA53367.1; PID:g437979
 C:Superfamily: FC gamma receptor III; immunoglobulin homology
 C:Keywords: immunoglobulin receptor

Query Match 29.1%; Score 405; DB 2; Length 296;
 Best Local Similarity 42.2%; Pred. No. 5.4e-24;
 Matches 79; Conservative 33; Mismatches 71; Indels 4; Gaps 2;
 QY 10 LLVALLFFAPDGVAVPQPKK--VSLNPPNRIKGENVTLTCNGNNFFEVSTKWFHN 67
 Db 29 LLWTLALLFLAP--VSGKPDLPKAVTIQPAWINVLRDHVTLTCQGTFSAGNLITWFEN 86
 QY 68 GSLSEETNSLNIIVNAKFDSEYKCOHQVNESEPVYLEVFSDDLQASAEVVMGQP 127
 Db 87 GSSHTQKQSYSPRAGNSDGSSTRCQRETSLSDPVHLDDVSDWLLQTPSLVFOGEP 146
 QY 128 LFLRCHGWRNDVYKVIYKDGKALKYWENHISITNATVEDSGTYCTGKWQLDYES 187
 Db 147 IMLRCHSWRNOPLNKITFYQDRKSIKFSYQRTNFSIPRANLSHGQVHTAFIGKMLHSS 206
 QY 188 EPLNITV 194
 Db 207 QPWNITV 213

RESULT 7

FC gamma (IgG) receptor I-B splice form 1 precursor - human
 N:Alternate names: CD64
 N:Contains: FC-gamma (IgG) receptor I-B splice form 2
 C:Species: Homo sapiens (man)
 C>Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 21-Jan-2000
 C:Accession: I55577; I70303
 R:Porces, A.J.; Redecha, P.B.; Doebele, R.; Pan, L.C.; Salmon, J.B.; Kimberly, R.P.
 J. Clin. Invest. 90, 2102-2109, 1992
 A:Title: Novel FC gamma receptor I family gene products in human mononuclear cells.
 A:Reference number: I55577; MUID:93055454; PMID:1430234
 A:Accession: I55577
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-280 <RES>
 A:Cross-references: GB:I03419; NID:g182460; PIDN:AAA35825.1; PID:g292023
 A:Note: splice form B1
 A:Accession: I70303
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA

A:Residues: 1-10,103-153,'A',155-280 <RE2>
 A:Cross-references: GB:I03420; NID:g182461; PIDN:AAA35826.1; PID:g292024
 A:Experimental source: mononuclear cells
 A:Note: splice form B2
 C:Comment: This receptor does not bind monomeric IgG with high affinity.
 C:Genetics:
 A:Gene: GDB:FCGR1B; CD64
 A:Cross-references: GDB:135923; OMIM:601502
 A:Map position: lp12-1p12
 C:Superfamily: FC gamma receptor I; immunoglobulin homology
 C:Keywords: alternative splicing; glycoprotein; immunoglobulin receptor; transmembrane p
 F:117-170/Domain: immunoglobulin homology <IMM>

Query Match 29.0%; Score 403; DB 2; Length 280;
 Best Local Similarity 36.1%; Pred. No. 7.3e-24;
 Matches 84; Conservative 50; Mismatches 89; Indels 10; Gaps 4;
 QY 11 LCVALFFAPDGVAVPQPKVSLNPPNRIKGENVTLTCNGNNFFEVSTKWFHNGSL 70
 Db 4 LTTLLWVPVDCQVDT-TKAVITLQPPWVSFQESTVTLHCEVLHLPGSSSTQWFLNGTA 62
 QY 71 SEETNSLNIIVNAKFDSEYKCOHQVNESEPVYLEVFSDDLQASAEVVMGQPFL 130
 Db 63 TQSTPSYRITSASVNDSGEYRCQRLSDPIQLIHRGWLQLQVSRVFMGEPELAL 122
 QY 131 RCHGWRNDVYKVIYKDGKALKYWENHISITNATVEDSGTYCTGKWQLDYES 190
 Db 123 RCHAWKDLVNLVYRNGKAFKPFHWSNLTLKTNISHNGTVHCSG-MGKHRYTSAGI 181
 QY 191 NITVIAKPR--EKYWLQFFIPLLVVLFAVDGTGLFISTQOQVTLTKIKTRK 241
 Db 182 SOYTVKGLQLPFPVHFVLFYLAVGIMFLVNLVMTIRKE-----LKRKKK 228

RESULT 8

S29360
 FC gamma (IgG) receptor alpha - mouse
 C:Species: Mus musculus (house mouse)
 C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 23-Jul-1999
 C:Accession: S29360; S46999
 R:Ravetch, J.V.; Luster, A.D.; Weisshank, R.; Kochan, J.; Pavlovic, A.; Portnoy, D.A.; H
 Science 234, 718-725, 1996
 A:Title: Structural heterogeneity and functional domains of murine immunoglobulin G Fc r
 A:Reference number: S29360; MUID:87042761; PMID:2946078
 A:Accession: S29360
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-261 <RAV>
 A:Cross-references: EMBL:M14215; NID:g193247; PIDN:AAA37604.1; PID:g309228
 R:Feinman, R.; Qiu, W.Q.; Pearce, R.N.; Nikolaiczky, B.S.; Sen, R.; Sheffery, M.; Ravecc
 EMBO J 13, 3852-3860, 1994
 A:Title: PU.1 and an HLH family member contribute to the myeloid-specific transcription
 A:Reference number: S46999; MUID:94349933; PMID:8070412
 A:Accession: S46999
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-22 <FEI>
 C:Superfamily: FC gamma receptor III; immunoglobulin homology
 C:Keywords: immunoglobulin receptor; transmembrane protein
 F:130-183/Domain: immunoglobulin homology <IMM2>

Query Match 28.9%; Score 401.5; DB 2; Length 261;
 Best Local Similarity 35.6%; Pred. No. 8.8e-24;
 Matches 90; Conservative 44; Mismatches 104; Indels 15; Gaps 5;

QY 11 LCVALFFAPDGVAVPQPKVSLNPPNRIKGENVTLTCNGNNFFEVSTKWFHNG-S 69
 Db 16 LTTLLFAFADRSQAAALPKAVVVKLDPPMTQVLKEDMTLMCEGTHNPGNSSQWTFHNGS 75
 QY 70 LSEETNSLNIIVNAKFDSEYKCOHQVNESEPVYLEVFSDDLQASAEVVMGQPFL 129
 Db 76 IRSQVQASVTF-KATVNDSGEYRCQRLSDPIQLIHRGWLQLQVSRVFMGEPEL 134


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QY 130 LRCHGRNDVYKVIYKDGKALKYVYENHNISITNATVEDSGTYICTKQWOLDYSEPL 189
DB 135 LRCHSWRKNLNRISFHNKSVRYHYKGNFSPKANHSHSGDYKCKSLGSGTQHSKP 194
QY 190 LNVITV----IKAPREKYLQFFIPLLVILFAVDTLGLFISTQOQVTFLLKIKETKRGFR- 244
DB 195 VTIIVQDPAITSS-SLVWYHTAFSLVCLLFAVDTLGLFYFVR------NLQTPREYWK 248
QY 245 --LLNPHKPNPK 255
DB 249 SLSIRKHOAPDK 261

RESULT 9
A35902
Fc gamma RIIB-alpha - rat
C:Species: Rattus norvegicus (Norway rat)
C>Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 21-Jan-2000
C:Accession: A35902
R:Farber, D.L.; Sears, D.W.
J. Immunol. 146, 4352-4361, 1991
A:Title: Rat Cd16 is defined by a family of class III Fc-gamma receptors requiring co-ex
A:Reference number: A35902; MUID:91250730; PMID:1710249
A:Accession: A35902
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-267 <RES>
A:Cross-references: GB:M64369; NID:g206674; PIDN:AAA42048.1; PID:g206675
C:Superfamily: Fc gamma receptor III; immunoglobulin homology
F:55-106/Domain: immunoglobulin homology <IMM>

Query Match 28.7%; Score 399; DB 2; Length 267;
Best Local Similarity 37.1%; Pred. No. 1.4e-23;
Matches 83; Conservative 42; Mismatches 95; Indels 4; Gaps 1;

QY 11 LCVALLFPADGVLAVPQKPKVSLNPPNRRIFKGENVTLTGNNPFVSVSTKWFHNGSL 70
DB 22 LTMLLFAFADQTDGLLKAVKRDPEWIOVLKEDTVTLTCEGTHPNGNSSTQWFHNGSS 81
QY 71 SEETNSSLNINAKFEDSGYKCOHQVNESEPVYLEVFSMDLLQLQASAEVVMGQPLEL 130
DB 82 TWGQVQASYTFKATVNDSGEYRCMAHTSLSDPIHLEVISDWLLQTPQLVFEGETITL 141
QY 131 RCHGRNDVYKVIYKDGKALKYVYENHNISITNATVEDSGTYICTKQWOLDYSEPL 190
DB 142 RCHSWKNKQLTKVLLFQNGKRPVRYQSSNFSIPKANHSHSGNYKAYILGRTHMVSKPV 201
QY 191 NITV----IKAPREKYLQFFIPLLVILFAVDTLGLFISTQOQV 230
DB 202 TITVQGSATASSTSLVWFHFAFCLVCLLFAVDTLGLFYFCVRRNL 245

RESULT 10
A35902
Fc gamma (Igg) receptor II (low affinity) alpha precursor - rat
C:Species: Rattus norvegicus (Norway rat)
C>Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 23-Jul-1999
C:Accession: A35902
R:Zeiger, D.L.; Hogarth, P.M.; Sears, D.W.
Proc. Natl. Acad. Sci. U.S.A. 87, 3425-3429, 1990
A:Title: Characterization and expression of an Fc-gamma receptor cDNA cloned from rat na
A:Reference number: A35902; MUID:90239026; PMID:1692135
A:Accession: A35902
A:Molecule type: mRNA
A:Residues: 1-267 <28G>
A:Cross-references: GB:M32062; NID:g204114; PIDN:AAA41148.1; PID:g204115
C:Superfamily: Fc gamma receptor III; immunoglobulin homology
C:Keywords: duplication; glycoprotein; immunoglobulin receptor; transmembrane protein
F:55-106/Domain: immunoglobulin homology <IMM>

Query Match 28.4%; Score 395; DB 2; Length 267;
Best Local Similarity 36.6%; Pred. No. 2.9e-23;
Matches 82; Conservative 42; Mismatches 96; Indels 4; Gaps 1;

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QY 11 LCVALLFPADGVLAVPQKPKVSLNPPNRRIFKGENVTLTGNNPFVSVSTKWFHNGSL 70
DB 22 LTMLLFAFADQTDGLLKAVKRDPEWIOVLKEDTVTLTCEGTHPNGNSSTQWFHNGSS 81
QY 71 SEETNSSLNINAKFEDSGYKCOHQVNESEPVYLEVFSMDLLQLQASAEVVMGQPLEL 130
DB 82 TWGQVQASYTFKATVNDSGEYRCMAHTSLSDPIHLEVISDWLLQTPQLVFEGETITL 141
QY 131 RCHGRNDVYKVIYKDGKALKYVYENHNISITNATVEDSGTYICTKQWOLDYSEPL 190
DB 142 RCHSWKNKQLTKVLLFQNGKRPVRYQSSNFSIPKANHSHSGNYKAYILGRTHMVSKPV 201
QY 191 NITV----IKAPREKYLQFFIPLLVILFAVDTLGLFISTQOQV 230
DB 202 TITVQGSATASSTSLVWFHFAFCLVCLLFAVDTLGLFYFCVRRNL 245

RESULT 11
A34636
Fc gamma receptor II precursor - guinea pig
C:Species: Cavia porcellus (guinea pig)
C>Date: 13-Jul-1990 #sequence_revision 13-Jul-1990 #text_change 16-Jul-1999
C:Accession: A34636
R:Tomisinga, M.; Sakata, A.; Ohmura, T.; Yamashita, T.; Koyama, J.; Onoue, K.
Biochem. Biophys. Res. Commun. 169, 683-689, 1990
A:Title: The structure and expression of the guinea pig Fc receptor for IgG1 and IgG2 (t
A:Reference number: A34636; MUID:90241239; PMID:1692213
A:Accession: A34636
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-270 <TOM>
A:Cross-references: GB:M35272
C:Superfamily: Fc gamma receptor III; immunoglobulin homology
C:Keywords: immunoglobulin receptor
F:37-88/Domain: immunoglobulin homology <IMM>

Query Match 28.1%; Score 390.5; DB 2; Length 270;
Best Local Similarity 36.7%; Pred. No. 6.4e-23;
Matches 86; Conservative 37; Mismatches 108; Indels 7; Gaps 4;

QY 10 LLCVALLFPAP-DGVLAVPQKPKVSLNPPNRRIFKGENVTLTGNNPFVSVSTKWFHNG 68
DB 2 LLMTITVLFLAPVAGTSADPPKAVVRLEPPWIOVLGRDVRTLTCEGAPSGNHSHTQWLHNG 61
QY 69 SLSEETNSSLNINAKFEDSGYKCOHQVNESEPVYLEVFSMDLLQLQASAEVVMGQPL 128
DB 62 RLITQVLPSYRFTAKNGDSGEYRCQAGTSLSDPRLDVISDWLVLTQSLIFQEGGVI 121
QY 129 FLRCHGRNDVYKVIYKDGKALKYVYENHNISITNATVEDSGTYICTKQWOLDYSEPL 188
DB 122 VLCHSWNNWPLAKVTFYHNGVAKYFYSIKNFSIPQANHSHSGAYNCTGLIGRTSH*SP 181
QY 189 PLNITVLIKAPREKYLQFFIPLLVILFAVDTLGLFISTQOQVTFLLKIKETKRGFRLNLP 248
DB 182 PVTITV-QGPKSSD--SSWVVIIVAAVIGIATAIVVA--VVAICLKKKKOPPANLSDP 235

RESULT 12
I72882
Fc gamma receptor - rat
C:Species: Rattus norvegicus (Norway rat)
C>Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 21-Jan-2000
C:Accession: I72882
R:Sears, D.
J. Immunol. 150, 4364-4375, 1993
A:Title: Rat class III Fc gamma receptor isoforms differ in IGG subclass-binding specifi
A:Reference number: I56166; MUID:93246650; PMID:8482840
A:Accession: I72882
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-267 <RES>
A:Cross-references: GB:L08446; NID:g204120; PIDN:AAA41151.1; PID:g204121

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C:Superfamily: Fc gamma receptor III; immunoglobulin homology
C:Keywords: immunoglobulin receptor
F:155-106/Domain: immunoglobulin homology <IMM>

Query Match 27.3%; Score 380; DB 2; Length 267;
Best Local Similarity 36.2%; Pred. No. 4.1e-22;
Matches 81; Conservative 43; Mismatches 96; Indels 4; Gaps 1;
QY 11 LCVALFFAPDGVLAPOKPKVSLNPPNRIKGVNTLTCGNFFVSTKWFHNGSL 70
DB 22 LTMLLFAFADRGDGLLKAVKRDPPWQIQLKDDTVLTCEGTHNPGNSSTQWFHNGSS 81
QY 71 SEETNSSLNINAKFDSGEYKQHQVNESEPVLEFSDWLLLOASAEVWMEGQPLFL 130
DB 82 TWGQVQASYTFKATVNSGECRCMAHTSUSDPVLEVISDWLLQTPQVLFLEGERITL 141
QY 131 RCHGRNWDVYKVIYKDGKALKYWNHNISITNATVDSGTYYCTGKWLQDYSEPL 190
DB 142 RCHGWKSIQLARISFLQNGEPVSPHPYNSYSIGNANSHSGDYCKAYLGRTEHVSKPV 201
QY 191 NITV----IKAPREKYNLQFPIPLVILFAVDTGLFISTQQQV 230
DB 202 TITVQGSATASSTSLVWFHFAFCVLVNCLLFAVDTLGLYFCVRNML 245

RESULT 13
148471
Fc gamma (IgG) receptor high affinity - mouse
C:Species: Mus musculus (house mouse)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 21-Jan-2000
R:Prins, J.B.; Todd, J.A.; Rodriques, N.R.; Ghosh, S.; Hogarth, P.M.; Wicker, L.S.; Gaff
Science 260, 695-698, 1993
A:Title: Linkage on chromosome 3 of autoimmune diabetes and defective Fc receptor for Ig
A:Reference number: 148471; MUID:93242399; PMID:8480181
A:Accession: 148471
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-336 <RES>
A:Cross-references: EMBL:X70980; NID:g311748; PIDN:CAA50311.1; PID:g311749
C:Superfamily: Fc gamma receptor I; immunoglobulin homology
C:Keywords: immunoglobulin receptor
F:126-180/Domain: immunoglobulin homology <IMM>

Query Match 27.3%; Score 379; DB 2; Length 336;
Best Local Similarity 37.8%; Pred. No. 6.3e-22;
Matches 90; Conservative 42; Mismatches 94; Indels 12; Gaps 6;
QY 10 LLCVALFFAPDGVLAPOKPKVSLNPPNRIKGVNTLTCGNFFVSTKWFHNGS 69
DB 12 LTMLLWVPVGGVGNATKAVITLQPPWASIFQKENVTLWCCEGPHLPGDSSTQWFINGT 71
QY 70 LSEETNSSLNINAKFDSGEYKQHQVNESEPVVLEVFSDWLLLOASAEVWMEGQPL 128
DB 72 VVQTSPTSYSISVASFQDSGEYRCQIGSSVPDVPQLOIHKEDWLLLOASRRVLTEGEP 131
QY 129 FLCHGRNWDVYKVIYKDGKALKYWNHNISITNATVDSGTYYCTGKWLQDYSE 188
DB 132 ALRCHGWKKNLVNVPVYFNRNGSKFQFSSGSKIALKTLNLSHSGIYHCSG-MGRHRYTSA 189
QY 189 PLNITVIKAPREKYNLQFPIPL-VVILFAVDTGLFISTQQQVTFLLKIKTRKGRFL 245
DB 190 GVSITVKAPLE----LFTTPVLASVSPFPFEGSLVTLNCTNLLQ----RPLQL 239

RESULT 14
A46480
Fc gamma (IgG) receptor high affinity - mouse
N:Alternate names: high affinity IgG receptor
C:Species: Mus musculus (house mouse)
C:Date: 18-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000
C:Accession: A46480; A43511
R:Osman, N.; Kozak, C.A.; McKenzie, I.F.; Hogarth, P.M.

J. Immunol. 148, 1570-1575, 1992
A:Title: Structure and mapping of the gene encoding mouse high affinity Fc gamma RI and
A:Reference number: A46480; MUID:92166399; PMID:1531670
A:Accession: A46480
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-404 <OSM>
A:Note: sequence extracted from NCBI backbone (NCBI:85205, NCBI:85208, NCBI:85212, NC
R:Sears, D.W.; Osman, N.; Tate, B.; McKenzie, I.F.C.; Hogarth, P.M.
J. Immunol. 144, 371-378, 1990
A:Title: Molecular cloning and expression of the mouse high affinity Fc receptor for IgG
A:Reference number: A43511; MUID:9011035; PMID:2136886
A:Accession: A43511
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-404 <SEA>
A:Cross-references: GB:M31314; NID:g200752; PIDN:AAA40056.1; PID:g200753
C:Superfamily: Fc gamma receptor I; immunoglobulin homology
C:Keywords: immunoglobulin receptor; transmembrane protein
F:127-179/Domain: immunoglobulin homology <IMM>

Query Match 27.3%; Score 379; DB 2; Length 404;
Best Local Similarity 41.6%; Pred. No. 7.8e-22;
Matches 77; Conservative 37; Mismatches 69; Indels 2; Gaps 2;
QY 10 LLCVALFFAPDGVLAPOKPKVSLNPPNRIKGVNTLTCGNFFVSTKWFHNGS 69
DB 12 LTMLLWVPVGGVGNATKAVITLQPPWASIFQKENVTLWCCEGPHLPGDSSTQWFINGT 71
QY 70 LSEETNSSLNINAKFDSGEYKQHQVNESEPVVLEVFSDWLLLOASAEVWMEGQPL 129
DB 72 AVQISTPSYSIPASFDQSGEYRCQIGSSWPDVPQIHNWLLQASRRVLTEGEP 131
QY 130 LRCHGRNWDVYKVIYKDGKALKYWNHNISITNATVDSGTYYCTGKWLQDYSE 189
DB 132 LRCHGWKKNLVNVPVYFNRNGSKFQFSSDSEVALKTLNLSHSGIYHCSG-TGRHRYTSA 189
QY 190 LNTIV 194
DB 190 VSIIV 194

RESULT 15
A41357
Fc gamma (IgG) receptor I (high affinity) form b - human
N:Alternate names: Cp64
C:Species: Homo sapiens (man)
C:Date: 03-Apr-1992 #sequence_revision 03-Apr-1992 #text_change 21-Jan-2000
C:Accession: A41357; S03019
R:Allen, J.M.; Seed, B.
Science 243, 378-381, 1989
A:Title: Isolation and expression of functional high-affinity Fc receptor complementary
A:Reference number: A41357; MUID:89100284; PMID:2911749
A:Accession: A41357
A:Molecule type: mRNA
A:Residues: 1-344 <ALL1>
A:Cross-references: GB:X14355; GB:M21090; NID:g31333; PIDN:CAA32536.1; PID:g31334
R:Allen, J.M.; Seed, B.
Nucleic Acids Res. 16, 11824, 1988
A:Title: Nucleotide sequence of three cDNAs for the human high affinity Fc receptor (FcR
A:Reference number: S03018; MUID:89098339; PMID:2974947
A:Accession: S03019
A:Molecule type: mRNA
A:Residues: 1-344 <ALL2>
A:Cross-references: EMBL:X14355; NID:g31333; PIDN:CAA32536.1; PID:g31334
C:Note: the authors translated the codon ACT for residue 25 as Ala
C:Superfamily: Fc gamma receptor I; immunoglobulin homology
C:Keywords: alternative splicing; immunoglobulin receptor; transmembrane protein
F:117-170/Domain: immunoglobulin homology <IMM>

Query Match 27.1%; Score 376; DB 2; Length 344;
Best Local Similarity 39.7%; Pred. No. 1.1e-21;
Matches 73; Conservative 39; Mismatches 70; Indels 2; Gaps 2;

Tue Oct 12 09:19:26 2004

11	LCVALLFPDGVLAUPOKPKVLSINFPWNI	FKGENVTLTCNGNFFVSSYFKWFHNSGL	70
4	LTLLTLWFVFDGQDT-TKAVITLQPEW	SVFOEETVTLHCEVLLHPDSSSTQWFENGT	62
71	SEETNSSLNIYNAKFEDSGEYKCHQOQVNE	SEPWLEVSFDMILLQASAEVYMEQCPLEL	130
63	TQTSTPSVRITSAWNSDGEYRCORGUSGR	SDPIQLEIHRGWLLOLVSSRVFTEGEPLAL	122
131	RCHGHRNWDVYKVIYKDGALKYTWYBNHN	SITNATVEDSGTYCYTGKXWOLDYESPL	190
123	RCHAWKDKLVYNLVYRNGKAFKPFHNSNL	ITKLTNISHNGTYHCSG-MGKHRYTSAGI	181
191	NTTV	194	
182	SVTV	185	
b			

Search completed: October 6, 2004, 09:23:41
Job time : 16.0781 secs

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OM protein - protein search, using sw model

Run on: October 6, 2004, 08:59:40 ; Search time 40.4371 Seconds
(without alignments)
2005.293 Million cell updates/sec

Title: US-10-763-400-2
Perfect score: 1390
Sequence: 1 MAPAMESPTLLCVALLFFAP.....RTRKGRLLNPHKPNKPN 257

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 segs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL 25: *
1: sp_archaea: *
2: sp_bacteria: *
3: sp_fungi: *
4: sp_human: *
5: sp_invertebrate: *
6: sp_mammal: *
7: sp_nhc: *
8: sp_organelle: *
9: sp_phase: *
10: sp_plant: *
11: sp_rodent: *
12: sp_virus: *
13: sp_vertebrate: *
14: sp_unclassified: *
15: sp_virus: *
16: sp_bacteriaph: *
17: sp_archaeap: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	832.5	59.9	255	Q8MI30	Q8MI30 equus caball
2	800	57.6	260	Q8MJ20	Q8MJ20 ovis aries
3	419	30.1	254	Q8SPW2	Q8SPW2 macaca fasc
4	411	29.6	249	Q9N216	Q9N216 felis silve
5	405.5	29.2	250	Q9N215	Q9N215 felis silve
6	403.5	29.0	256	Q9N222	Q9N222 sus scrofa
7	403	29.0	280	Q92637	Q92637 homo sapien
8	402	28.9	233	Q8UPY7	Q8UPY7 homo sapien
9	401.5	28.9	249	Q8R477	Q8R477 mus musculus
10	395.5	28.7	249	Q8R2R4	Q8R2R4 mus musculus
11	398	28.6	261	Q9ES92	Q9ES92 mus musculus
12	386	27.8	261	Q7TWM9	Q7TWM9 mus musculus
13	383.5	27.6	357	Q8SPW5	Q8SPW5 macaca fasc
14	380.5	27.4	294	Q8SPW3	Q8SPW3 macaca fasc
15	379	27.3	330	Q8R142	Q8R142 mus musculus
16	378.5	27.2	349	Q9MZT0	Q9MZT0 bos taurus

17	376	27.1	374	4	Q92663	Q92663 homo sapien
18	375.5	27.0	375	4	Q92495	Q92495 homo sapien
19	366.5	26.4	372	6	Q7YQUS	Q7YQUS canis famil
20	366	26.3	327	6	Q95N21	Q95N21 sus scrofa
21	355	25.5	318	11	Q8VIQ0	Q8VIQ0 rattus norv
22	352	25.3	310	6	Q8SPW4	Q8SPW4 macaca fasc
23	351	25.3	316	6	Q8SPV8	Q8SPV8 pan troglod
24	341.5	24.6	316	4	Q8WU54	Q8WU54 homo sapien
25	337.5	24.3	316	4	Q8WUN1	Q8WUN1 homo sapien
26	271.5	19.5	515	4	Q96RE0	Q96RE0 homo sapien
27	269.5	19.4	199	4	Q96P27	Q96P27 homo sapien
28	269.5	19.4	639	4	Q96P30	Q96P30 homo sapien
29	268.5	19.3	734	4	Q96P31	Q96P31 homo sapien
30	268.5	19.3	734	4	Q96LA4	Q96LA4 homo sapien
31	268.5	19.3	740	4	Q96P29	Q96P29 homo sapien
32	268.5	19.3	742	4	Q9N6S2	Q9N6S2 homo sapien
33	267.5	19.2	189	4	Q96P28	Q96P28 homo sapien
34	267.5	19.2	515	4	Q96PJ5	Q96PJ5 homo sapien
35	267	19.2	977	4	Q96RD9	Q96RD9 homo sapien
36	257	18.5	582	11	Q80WN2	Q80WN2 mus musculu
37	246	17.7	360	4	Q8N732	Q8N732 homo sapien
38	232.5	16.7	188	4	Q92638	Q92638 homo sapien
39	206	14.8	509	11	Q91YK7	Q91YK7 mus musculu
40	206	14.8	509	11	Q9EQY5	Q9EQY5 mus musculu
41	194.5	14.0	168	6	Q9N1Y3	Q9N1Y3 bos taurus
42	191.5	13.8	130	4	Q8IZV7	Q8IZV7 homo sapien
43	187.5	13.5	365	4	Q8NEW4	Q8NEW4 homo sapien
44	187.5	13.5	376	4	Q8WXH3	Q8WXH3 homo sapien
45	175.5	12.6	352	11	Q920A9	Q920A9 mus musculu

ALIGNMENTS

RESULT 1

Q8MI30 PRELIMINARY; PRT; 255 AA.
ID Q8MI30
AC Q8MI30;
DT 01-OCT-2002 (Tremblrel. 22, Created)
DT 01-OCT-2002 (Tremblrel. 22, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE High affinity immunoglobulin E receptor alpha subunit.
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=1; TISSUE=Bronchoalveolar lavage fluid;
RX MEDLINE=20424522; PubMed=10970105;
RA McAleese S.M., Halliwell R.E.W., Miller H.R.P.;
RT "Cloning and Sequencing of the horse and sheep high-affinity Ige
RT receptor alpha chain cDNA".
RL Immunogenetics 51:878-881(2000).
DR EMBL; Y18204; CAB40387.1; -.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003598; IG_c2.
DR Pfam; PF00847; ig; 2.
DR SMART; SM00409; IG; 2.
DR SMART; SM00408; Igc2; 2.
DR PROSITE; PS00835; IG-LIKE; 2.
KW Immunoglobulin domain; Receptor.
SQ SEQUENCE 255 AA; 29366 MW; A60659700684FBD8 CRC64;

Query Match 59.9%; Score 832.5; DB 6; Length 255;

Best Local Similarity 63.9%; Pred. No. 4.9e-67;

Matches 163; Conservative 31; Mismatches 56; Indels 5; Gaps 2;

QY 1 MAPAMESPTLLCVALLFFAPDGLVAPQPKVSLNPPNRIKFNKGVTLTCNKNPFVFS 60

Db 1 MEAPMGSPALLWITFLFLSLDGVPAIRKSTVSLNPPNRIKFNKGVTLTCNKNKPLKGN 60

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QY 61 STKWFHSLSEETTNSLNINNAKPEDSGEYKQHQVNESEPVYLEVFSWLLQLQASAE 120
DB 61 STEWTYNTTLEVTISSLNITNASHRSSEGEVRCNRNDNLSEAHVLEVFSWLLQLQASAE 120
QY 121 VMEQOPLFLRCHGRNWDVYKVIYKDGKALKYWYENHNISITNATVEDSGTYCTG-- 178
DB 121 EVIEGKALVLRGKWDVFKVIYKDGKPLEYWKYENKNISIESATTENSGTYCEGAF 180
QY 179 --KWQDYSEPLNITVIKAPREK-YWLQFFILPLVILFAVDTGLFISTQQQVTFLLK 235
DB 181 NFKRTSERTSYDNLNITVKKBAQSKRYWLQFIPLVILFAVDTGLFVSTQQQLTLLK 240
QY 236 IKRTRGRKRLNPH 250
DB 241 IKRTRGRKRLMDPH 255

RESULT 2
Q8MJZO Q8MJZO PRELIMINARY; PRT; 260 AA.
AC Q8MJZO;
DT 01-OCT-2002 (TREMELrel. 22, Created)
DT 01-OCT-2002 (TREMELrel. 22, Last sequence update)
DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
DE High affinity immunoglobulin E receptor alpha subunit.
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=1; TISSUE=Bone marrow;
RX MEDLINE=20424522; PubMed=10970105;
RA McAlleese S.M., Halliwell R.E.W., Miller H.R.P.;
RT "Cloning and Sequencing of the horse and sheep high-affinity IgE
receptor alpha chain cDNA.";
RL Immunogenetics 51:878-891(2000).
DR GO; Y18205; CAB40544.1; -
DR EMBL; AF485815; AAL92098.1; -
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003598; IG_C2.
DR Pfam; PF00047; ig; 2.
DR SMART; SM00409; IG; 2.
DR SMART; SM00408; IGC2; 2.
DR PROSITE; PS50835; IG_LIKE; 2.
KW Immunoglobulin domain; Receptor.
SQ SEQUENCE 260 AA; 30047 MW; 67111F2F17D596ED CRC64;

Query Match 57.6%; Score 800; DB 6; Length 260;
Best Local Similarity 60.0%; Pred. No. 4.3e-64;
Matches 153; Conservative 31; Mismatches 69; Indels 2; Gaps 1;

QY 5 MESPTLLCVALLFPADGVLA--VPQKPKVSLNPPNRIKGENVTLTCGNNNFFVSVSTKW 64
DB 6 MGAPALLWIALLLFPDGSAAWKSQVSLNPPNRIKGETVTLTCGNVRSSESVW 65
QY 65 FHNSLSSETNSLNINNAKPEDSGEYKQHQVNESEPVYLEVFSWLLQLQASAEVYME 124
DB 66 IHNGTTLKETSNDVIRVQDSQKQCRIGKFAISEPVYLVNIVSDWLLQLQASAEVYME 125
QY 125 GQPLFLRCHGRNWDVYKVIYKDGKALKYWYENHNISITNATVEDSGTYCTGKWQLD 184
DB 126 GESFLRCHSWNLNAFVIYKDNKRLKYWYENHNISITNATVEDSGTYCTGGRIOQLN 185
QY 185 YESEPLNITVIKAPREK--YWLQFFILPLVILFAVDTGLFISTQQQVTFLLKIKRKG 242
DB 186 YTSNKLKIVKQVTSQNYFWLQFLIPLVILFAVDTGLLSTQQQVTFLLKIKRIRK 245
QY 243 FRLNPHKPNPKNN 257
| : : : : : |

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DB 246 NRFTDPQPKDPDPGN 260

RESULT 3
Q8SPW2 Q8SPW2 PRELIMINARY; PRT; 254 AA.
AC Q8SPW2;
DT 01-JUN-2002 (TREMELrel. 21, Created)
DT 01-JUN-2002 (TREMELrel. 21, Last sequence update)
DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
DE PC gamma receptor IIla.
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
OC Cercopitheidae; Macaca.
OX NCBI_TaxID=9541;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Namenuk A.K., Hong K., Meng Y.G., Shields R.L., Cromwell M.E.M.,
RA Presta L.G.;
RT "Binding of human IIG to cynomolgus FcR.";
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF485815; AAL92098.1; -
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR Pfam; PF00047; ig; 2.
DR SMART; SM00409; IG; 2.
DR PROSITE; PS50835; IG_LIKE; 2.
KW Receptor.
SQ SEQUENCE 254 AA; 29120 MW; 11A4856B3A34AF7B CRC64;

Query Match 30.1%; Score 419; DB 6; Length 254;
Best Local Similarity 40.4%; Pred. No. 1e-29;
Matches 93; Conservative 39; Mismatches 88; Indels 10; Gaps 3;

QY 10 LLCVALLFPADGVLA--VPQKPKVSLNPPNRIKGENVTLTCGNNNFFVSVSTKW 67
DB 5 LLPTALLLVLSAGMRAEDLP-KAVVFLPEQVRYVLEKORVTLKCGAYSPEDNSTRWFHN 63
QY 68 GSLSETNSLNINNAKPEDSGEYKQHQVNESEPVYLEVFSWLLQLQASAEVYMEQOP 127
DB 64 ESLISSQTSYFIAAARVNNSEYRCQTSLSLSPVQLVHIGWLLQLQAPWVFEES 123
QY 128 LFLRCHGRNWDVYKVIYKDGKALKYWYENHNISITNATVEDSGTYCTGKWQLDYES 187
DB 124 IFLRCHSWKNLTLHKVTVLQNGKGRKYPHNSDFYIPKATLKDSGFCRGLGSKNWS 183
QY 188 EPLNITVIKAPREKYWLQFFIP-----LLWVILFAVDTGLFISTQQQV 230
DB 184 EIVNITITQDLAVSSISFFPPFGYQVSLWVLLFAVDTGLYFSMKKSI 233

RESULT 4
Q9N216 Q9N216 PRELIMINARY; PRT; 249 AA.
AC Q9N216;
DT 01-OCT-2000 (TREMELrel. 15, Created)
DT 01-OCT-2000 (TREMELrel. 15, Last sequence update)
DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
DE CD16.
GN CD16.
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX NCBI_TaxID=9685;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20180233; PubMed=10713347;
RA Nishimura Y., Miyazawa T., Ikeda Y., Izumiya Y., Nakamura K., Sato E.,
RA Mikami T., Takahashi E.;
RT "Molecular cloning and sequencing of the cDNA encoding the feline

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RT Fc(gamma)RIIIA (CD16) homologue.;
RL Vet. Immunol. Immunopathol. 73:353-359 (2000).
DR EMBL; AB025314; BAA92347.1; -.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR Pfam; PF00047; IG; 2.
DR SMART; SM00409; IG; 2.
DR PROSITE; PS00835; IG LIKE; 2.
SQ SEQUENCE 249 AA; 27902 MW; 693528C68A7CAB7A CRC64;

Query Match      29.2%; Score 411; DB 6; Length 249;
Best Local Similarity 39.1%; Pred. No. 5.4e-29;
Matches 92; Conservative 33; Mismatches 100; Indels 10; Gaps 2;

QY 7 SPTLLCVALLFPADGVLAVP-QPKVSLNPPNRIKGENVTLCNGNFFEVSSSTKWF 66
Db 6 SPT----ALLLVSAAGTRADLSKAMVLEPEWNRVLVSDGVILKCEGAYPPGDNLSAQWH 61

QY 67 NGSLSSETNSSLINVAKEDSGEYKCOHQVNESEPVYLEVFSDFWLLQLQASAEVVMQ 126
Db 62 NGSVIPHRAPSYSEIARSEDSEYKCOGLSEASDPVQLVHTGMLLLQAPRWVFOEG 121

QY 127 PLELRCHGRNWDVYKVIYKDGKALKYWYENHNISITNATVEDSGTYCTGKWQLDYE 186
Db 122 TIQLRCHSWKNTVQKVFQDGRGKMFPHKNSDFYIPKATSKHSGSYFCRGLIGNKNE 181

QY 187 SEPANITVIKAPREK-----YWLQFFIPLVLVFAVDTLGLFISTQQQVTFLLK 235
Db 182 SEAVNITVQGPVPSTSTPLPHWYQIAFFLVLTALLFVVDTLGLHAVAVQDLSQSVK 236

RESULT 5
Q9N215 PRELIMINARY; PRT; 250 AA.
ID Q9N215
AC Q9N215;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR SMART; SM00409; IG; 2.
DR PROSITE; PS00835; IG LIKE; 2.
SQ SEQUENCE 250 AA; 27973 MW; 161350918A1628EB CRC64;

Query Match      29.2%; Score 405.5; DB 6; Length 250;
Best Local Similarity 39.0%; Pred. No. 1.7e-28;
Matches 92; Conservative 33; Mismatches 100; Indels 11; Gaps 3;

QY 7 SPTLLCVALLFPADGVLAVP-QPKVSLNPPNRIKGENVTLCNGNFFEVSSSTKWF 65
Db 6 SPT----ALLLVSAAGTRADLSKAMVLEPEWNRVLVSDGVILKCEGAYPPGDNLSAQW 61

QY 66 HNGSLSETNSSLINVAKEDSGEYKCOHQVNESEPVYLEVFSDFWLLQLQASAEVVMQ 125
Db 62 HNGSVIPHRAPSYSEIARSEDSEYKCOGLSEASDPVQLVHTGMLLLQAPRWVFOEG 121

QY 126 QPLFLRCHGRNWDVYKVIYKDGKALKYWYENHNISITNATVEDSGTYCTGKWQLDY 185
Db 122 ESIRLCHTWKNITQKQVYFQNGMGKFSHQNFVHFNATLKDGSGSYFCRGIKNYKL 181

QY 186 ESEPLNITVIKAPREKYNLQFFIP-----LLVVLFAVDTLGLFISTQQQVTFLLK 238
Db 182 SSEAVKTVQGSKSPSPILSFLEFPHQIIFLCVMGFLFAVDTLGLYFSVR-----KVLR 234
QY 239 TRK 241
Db 235 SSX 237

Query Match      29.0%; Score 403.5; DB 6; Length 256;
Best Local Similarity 38.3%; Pred. No. 2.7e-28;
Matches 93; Conservative 42; Mismatches 89; Indels 19; Gaps 4;

QY 7 SPTLLCVALLFPADGVLAVP-QPKVSLNPPNRIKGENVTLCNGNFFEVSSSTKWF 65
Db 6 SPT----ALLLVSAAGTHAEDPPKSVVILDPWDRLLEKDSVTLKCGAYPPGDDSTEW 61

QY 66 HNGSLSETNSSLINVAKEDSGEYKCOHQVNESEPVYLEVFSDFWLLQLQASAEVVMQ 125
Db 62 WNGTLISNKASSYSITDATVNGSGEYTCGTLSAQSDPLRLLEVYKGLWLLQAPRWVQEG 121

QY 126 QPLFLRCHGRNWDVYKVIYKDGKALKYWYENHNISITNATVEDSGTYCTGKWQLDY 185
Db 122 ESIRLCHTWKNITQKQVYFQNGMGKFSHQNFVHFNATLKDGSGSYFCRGIKNYKL 181

QY 186 ESEPLNITVIKAPREKYNLQFFIP-----LLVVLFAVDTLGLFISTQQQVTFLLK 238
Db 182 SSEAVKTVQGSKSPSPILSFLEFPHQIIFLCVMGFLFAVDTLGLYFSVR-----KVLR 234
QY 239 TRK 241
Db 235 SSX 237

RESULT 7
Q92637 PRELIMINARY; PRT; 280 AA.
ID Q92637
AC Q92637;
DT 01-FEB-1997 (TrEMBLrel. 02, Created)
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR SMART; SM00409; IG; 2.
DR PROSITE; PS00835; IG LIKE; 2.
SQ SEQUENCE 280 AA; 27973 MW; 161350918A1628EB CRC64;

Query Match      29.2%; Score 405.5; DB 6; Length 250;
Best Local Similarity 39.0%; Pred. No. 1.7e-28;
Matches 92; Conservative 33; Mismatches 100; Indels 11; Gaps 3;

QY 7 SPTLLCVALLFPADGVLAVP-QPKVSLNPPNRIKGENVTLCNGNFFEVSSSTKWF 65
Db 6 SPT----ALLLVSAAGTRADLSKAMVLEPEWNRVLVSDGVILKCEGAYPPGDNLSAQW 61

QY 66 HNGSLSETNSSLINVAKEDSGEYKCOHQVNESEPVYLEVFSDFWLLQLQASAEVVMQ 125
Db 62 HNGSVIPHRAPSYSEIARSEDSEYKCOGLSEASDPVQLVHTGMLLLQAPRWVFOEG 121

QY 126 QPLFLRCHGRNWDVYKVIYKDGKALKYWYENHNISITNATVEDSGTYCTGKWQLDY 185
Db 122 ESIRLCHTWKNITQKQVYFQNGMGKFSHQNFVHFNATLKDGSGSYFCRGIKNYKL 181

QY 186 ESEPLNITVIKAPREKYNLQFFIP-----LLVVLFAVDTLGLFISTQQQVTFLLK 238
Db 182 SSEAVKTVQGSKSPSPILSFLEFPHQIIFLCVMGFLFAVDTLGLYFSVR-----KVLR 234
QY 239 TRK 241
Db 235 SSX 237
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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RX MEDLINE=93055454; PubMed=1430234;
RA Porces A.J., Redecha P.B., Doebele R., Pan L.C., Salmon J.E.,
RA Kimberlin R.P.;
RT "Novel Fc gamma receptor I family gene products in human mononuclear
RT cells.";
RL J. Clin. Invest. 90:2102-2109(1992).
DR EMBL; L03419; AAA35825.1; -.
DR PIR; I55577.
DR GO; GO:0005886; C:plasma membrane; NAS.
DR GO; GO:0003793; F:defense/immunity protein activity; NAS.
DR GO; GO:0016489; F:immunoglobulin receptor activity; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR Pfam; PF00047; ig; 2.
DR SMART; SM00409; IG; 2.
DR PROSITE; PS50835; IG_LIKE; 2.
DR Receptor.
KW Receptor.
SQ SEQUENCE 280 AA; 32232 MW; C6C6C45AE3D345C6 CRC64;

Query Match 29.0%; Score 403; DB 4; Length 280;
Best Local Similarity 36.1%; Pred. No. 3.3e-28;
Matches 84; Conservative 50; Mismatches 89; Indels 10; Gaps 4;

QY 11 LCVALFFAPDGVLAQPKVSNPPNRIKGENVTLCNGNFFVSTKWFHNGSL 70
DB : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 4 LTTLLVVPDGVDT-TKAVITLQPPWVSQFBETVTLCEVLHLPGSSSTQWFLNGTA 62
QY 71 SEETNSSINIVNAKPEDSGEYKCOHQVNESEPVYLEVFDWLLLOQASAEVMEQPLF 130
DB : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 63 TQSTPTRYRTSANDSGEYRCQGLSGRSDPIQIEHIGWLLQVSRVMEGEPLAL 122
QY 131 RCHGWRNMDVYKVIYKDGKALKYVNHNSITNATVEDSGTYCTGKVMQDLYSEPL 190
DB : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 123 RCHAKDKLVNVLVYENGKAFKFFHNSLTILKTNISNGYHCSG-MGKHRYTSAGI 181
QY 191 NITVIKAPR--EKWLOFFPLLVLLFAVDLTGLFISTQOQVFLKIKRTRK 241
DB : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 182 SQYTVKGLQPLTPWFHVLVFLVAVGIMFLVNTVLTWITRKE-----LRRKKK 228

RESULT 8
Q9UPV7 ID Q9UPV7 PRELIMINARY; PRT; 233 AA.
AC Q9UPV7
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE FC-gamma receptor IIIB (CD 16).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RX MEDLINE=20487377; PubMed=11034564;
RA Watanabe Y., Shimada E., Fujiwara K., Niihara H., Shimano K.,
RA Mitsunaga S., Tadokoro K., Juji T.;
RT "Nucleotide sequence of a new Fc gamma receptor IIIB allele that codes
RT for a neutrophil antigen.";
RL Tissue Antigens 56:272-275(2000).
DR EMBL; AB025256; BAA83803.1; -.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR003599; IG.
DR Pfam; PF00047; ig; 2.
DR SMART; SM00409; IG; 2.

Query Match 28.9%; Score 401.5; DB 11; Length 249;
Best Local Similarity 38.9%; Pred. No. 3.9e-28;
Matches 88; Conservative 40; Mismatches 87; Indels 11; Gaps 2;

QY 10 LLCVALLFFAPDGVLAQPKVSNPPNRIKGENVTLCNGNFFVSTKWFHNGS 69
DB : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 5 LLPTALVLTAFSGIQAGLQKAVVNLDPKVRVLEEDSVTLRCQGTSPEDNSIKWFHNS 64
QY 70 LSEETNSSINIVNAKPEDSGEYKCOHQVNESEPVYLEVFDWLLLOQASAEVMEQPLF 129
DB : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 65 LIHQDANVVIQSAVRKDSGMRCTALSTISDPVQLVHMGWLLQTTKWLFOEGDPT 124
QY 130 LRCHGWRNMDVYKVIYKDGKALKYVNHNSITNATVEDSGTYCTGKVMQDLYSEPL 189
DB : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 125 LRCHSWQNRVPRKVTYLONGKKGKYPHENSELPIPKATHNDSSYFCRGLIGHNKSAS 184

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DR PROSITE; PS50835; IG_LIKE; 1.
KW Receptor.
FT VARIANT 54 54 K -> E.
SQ SEQUENCE 233 AA; 26215 MW; 74B51B909272B388 CRC64;

Query Match 28.9%; Score 402; DB 4; Length 233;
Best Local Similarity 40.0%; Pred. No. 3.2e-28;
Matches 92; Conservative 34; Mismatches 94; Indels 10; Gaps 3;

QY 10 LLCVALLFFAPDGVLAQPKV--VSLNPPNRIKGENVTLCNGNFFVSTKWFH 67
DB : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 5 LLPTALLLVLSAG-WRTEDLPRAVFLPQWVSLEKDSVTLKCGAVSPKDNSTQWFHN 63
QY 68 GSLSEETNSSINIVNAKPEDSGEYKCOHQVNESEPVYLEVFDWLLLOQASAEVMEQGP 127
DB : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 64 ESLISSQASSYFIDAATVNDSGEYRCQTNLSTLSDPVQLEVHIGWLLQAPRWVFKEDP 123
QY 128 LFLRCHGWRNMDVYKVIYKDGKALKYVNHNSITNATVEDSGTYCTGKVMQDLYES 187
DB : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 124 IHLRCHSWKNTALHKVTYLONGKORKYFHNSDFHIPKATLKDSGSYFCRGLVSGKNVSS 183
QY 188 EPLNITVIKAPREKYWLQFFIP-----LLVWILFAVDLTGLFISTQOQV 230
DB : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 184 ETWNITITQGLAVSTISSFSPPGYQVSCVWVLLFAVDLTGLYFSVKINI 233

RESULT 9
Q8R477 ID Q8R477 PRELIMINARY; PRT; 249 AA.
AC Q8R477
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Transmembrane receptor CD16-2.
GN FCRL3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL; TISSUE=Liver;
RA Mechetina L.V., Najakshin A.M., Alabyev B.Y., Chikaev N.A.,
RA Taranin A.V.;
RT "Identification of CD16-2, a novel mouse receptor homologous to
RT CD16/FCGR3II."
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF499613; AAM19249.1; -.
DR MGD; MGI:2179523; Fcrl3.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR Pfam; PF00047; ig; 2.
DR SMART; SM00409; IG; 2.
DR PROSITE; PS50835; IG_LIKE; 2.
KW Receptor.
SQ SEQUENCE 249 AA; 28382 MW; 3DEAF3D935BEF5CD CRC64;

Query Match 28.9%; Score 401.5; DB 11; Length 249;
Best Local Similarity 38.9%; Pred. No. 3.9e-28;
Matches 88; Conservative 40; Mismatches 87; Indels 11; Gaps 2;

QY 10 LLCVALLFFAPDGVLAQPKVSNPPNRIKGENVTLCNGNFFVSTKWFHNGS 69
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DB 5 LLPTALVLTAFSGIQAGLQKAVVNLDPKVRVLEEDSVTLRCQGTSPEDNSIKWFHNS 64
QY 70 LSEETNSSINIVNAKPEDSGEYKCOHQVNESEPVYLEVFDWLLLOQASAEVMEQPLF 129
DB : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 65 LIHQDANVVIQSAVRKDSGMRCTALSTISDPVQLVHMGWLLQTTKWLFOEGDPT 124
QY 130 LRCHGWRNMDVYKVIYKDGKALKYVNHNSITNATVEDSGTYCTGKVMQDLYSEPL 189
DB : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 125 LRCHSWQNRVPRKVTYLONGKKGKYPHENSELPIPKATHNDSSYFCRGLIGHNKSAS 184

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QY 190 LNTV-----IKAPREKYLQFFPLLVILFAVDTLGFIHQ 228
DB 185 FRISLGDGPGSPMFPP-----WHQITCLLIGLFAIDTVLYFSVR 226

RESULT 10
Q8R2R4 PRELIMINARY; PRT; 249 AA.
AC Q8R2R4;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
GN FCRL3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC027310; AAH27310.1; -.
DR MGD; MGI:2179523; FCRL3.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; Ig-like.
DR Pfam; PF00047; IG; 2.
DR SMART; SM00409; IG; 2.
DR PROSITE; PS00835; IG_LIKE; 2.
DR Hypothetical protein.
KW Hypothetical protein.
SQ SEQUENCE 249 AA; 28372 MW; 7406B38E1536224 CRC64;

Query Match 28.7%; Score 399.5; DB 11; Length 249;
Best Local Similarity 38.9%; Pred. No. 5.9e-28;
Matches 88; Conservative 40; Mismatches 87; Indels 11; Gaps 2;

QY 10 LLCVALLFPADGVLAQPKKVSINPPNRIKGVNLTGCGNNFREVSTKWFHGS 69
DB 5 LLPTALVLTAFSGIQAGLQKAVNLDPKWVRVLEEDSVTLRCOGTSPDINSIKVPHNS 64

QY 70 LSEETSSNLINAKFEDSGEYKCOHQVNESEPVYLEFSDWLLQLQASAEVMEGQPLF 129
DB 65 LIHQDANYVIOQARVKDSQWYKQALSTISDPVQLEVMHGMWLLQTTKWLFOEGDPTH 124

QY 130 LRCHGWRNDVYKVIYKDGKALKYVENHNISITNATVEDSGTYCTGKVMQWLDYSEP 189
DB 125 LRCHSWQNRVPRKVTYSQNGKGYFHENSELLIPKATHNDSGYSFCRGLIGHNKKSSAS 184

QY 190 LNTV-----IKAPREKYLQFFPLLVILFAVDTLGFIHQ 228
DB 185 FRISLGDGPGSPMFPP-----WHQITCLLIGLFAIDTVLYFSVR 226

RESULT 11
Q9ES92 PRELIMINARY; PRT; 261 AA.
AC Q9ES92;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE FC gamma receptor III.
GN FCGR3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Fossati Jimack L.; Boucrot E.; Izui S.;
RA "Mouse FC gamma RII: identification and characterization of a new
RT allele in C57BL/6 mice.";
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RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Ovary, and Uterus;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium.
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
DR EMBL; AF197930; AAG28520.1; -.
DR EMBL; AK077227; BC36696.1; -.
DR MGD; MGI:95500; FCGR3.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; Ig-like.
DR Pfam; PF00047; IG; 2.
DR SMART; SM00409; IG; 2.
DR PROSITE; PS00835; IG_LIKE; 2.
KW Receptor.
SQ SEQUENCE 261 AA; 30098 MW; 9C8570E032F94730 CRC64;

Query Match 28.6%; Score 398; DB 11; Length 261;
Best Local Similarity 37.8%; Pred. No. 8.5e-28;
Matches 85; Conservative 39; Mismatches 95; Indels 6; Gaps 3;

QY 11 LCVALLFPADGVLAQPKKVSINPPNRIKGVNLTGCGNNFREVSTKWFHNS-GS 69
DB 16 LTILLFAFADRSQAALPKAVKLDPPWQVLKEDMTLMCEGTHNFCNSTQWFHNS 75

QY 70 LSEETSSNLINAKFEDSGEYKCOHQVNESEPVYLEFSDWLLQLQASAEVMEGQPLF 129
DB 76 IRSQVQSSYTF-KATVNDSGEYRCQEQTRLSDVDLGVISDWLLQTPQRFVEGETIT 134

QY 130 LRCHGWRNDVYKVIYKDGKALKYVENHNISITNATVEDSGTYCTGKVMQWLDYSEP 189
DB 135 LRCHSWNRKLNRIISFFHNKSVHYHNSFKANHSKSHSGDYKGLSGTQHQSKP 194

QY 190 LNTV-----IKAPREKYLQFFPLLVILFAVDTLGFIHQ 230
DB 195 VTIIVQDPATTSISLVWYHTAFSLVMCLLFAVDTLGYFYVRNL 239

RESULT 12
Q7TMW9 PRELIMINARY; PRT; 261 AA.
AC Q7TMW9;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Similar to FC gamma receptor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6NCr; TISSUE=Hematopoietic Stem Cell;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L.; Feingold E.A.; Grouse L.H.; Derge J.G.;
RA Klausner R.D.; Collins F.S.; Wagner L.; Shenmen C.M.; Schuler G.D.;
RA Altschul S.F.; Zeeberg B.; Buetow K.H.; Schaefer C.F.; Bhat N.K.;
RA Hopkins R.F.; Jordan H.; Moore T.; Max S.I.; Wang J.; Hsieh F.;
RA Diatchenko L.; Marusina K.; Farmer A.A.; Rubin G.M.; Hong L.;
RA Stapleton M.; Soares M.B.; Bonaldo M.F.; Casavant T.L.; Scheetz T.E.;
RA Brownstein M.J.; Usdin T.B.; Toshiyuki S.; Carninci P.; Prange C.;
RA Raha S.S.; Loquellano N.A.; Peters G.J.; Abramson R.D.; Mullahy S.J.;
RA Bosak S.A.; McEwan P.J.; McKernan K.J.; Malek J.A.; Gunaratne P.H.;
RA Richards S.; Worley K.C.; Hale S.; Garcia A.M.; Gay L.J.; Hulyk S.W.;
RA Villalón D.K.; Muzny D.M.; Sodergren E.J.; Lu X.; Gibbs R.A.;
RA Fahey J.; Helton E.; Kettman M.; Madan A.; Rodrigues S.; Sanchez A.;
RA Whiting M.; Madan A.; Young A.C.; Shevchenko Y.; Bouffard G.G.;
RA Blakesley R.W.; Touchman J.W.; Green E.D.; Dickson M.C.;
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RESULT 14	
Q8SPW3	
ID	Q8SPW3
ID	PRELIMINARY; PRT; 294 AA.
AC	Q8SPW3;
DT	01-JUN-2002 (TrEMBLrel. 21, Created)
DT	01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT	01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE	FC gamma receptor I1b.
OS	Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Euthera; Primates; Catarrhini; Cercopitheciidae;
OC	Cercopitheciinae; Macaca.
OX	NCBI_Taxid=9541;
RN	[1]
RP	SEQUENCE FROM N.A.

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Query Match      27.4%; Score 380.5; DB 6; Length 294;
Best Local Similarity 35.0%; Pred. NO. 3.8e-36;
Matches 86; Conservative 42; Mismatches 99; Indels 19; Gaps 4;

10 LLCVALLAFAP-DGVLAVPQPKVSLNPPWNRILKFGENVLTTCNGNNPFVSTKWFHNG 68
29 LLWTAVFLAPVAGTAAAPKAVLKLEPPWNLVRLDSVLTTCGAHSPDSDSTOWFHNG 88

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Db ||
 257 ANPTNP 262

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RESULT 15
QBR142
ID QBR142 PRELIMINARY;
PRT; 330 AA.

Search completed: October 6, 2004, 09:07:01
Job time : 44.4371 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 10, 2004, 11:14:29 ; Search time 3370.32 Seconds
(without alignments)
9953.801 Million cell updates/sec

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Perfect score: 774
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Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues
Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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3: gb.in.*
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and is derived by analysis of the total score distribution.

SUMMARIES

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2	774	100.0	774	6	AR175482	AR175482 Sequence
3	774	100.0	1068	6	A21606	A21606 human FC.ep
4	774	100.0	1068	6	BD264325	BD264325 Recombina
5	774	100.0	1068	6	AX026808	AX026808 Sequence
6	774	100.0	1081	9	HUMWCIAA	J03605 Human mast
7	774	100.0	1102	9	BC005912	BC005912 Homo sapi
8	774	100.0	1174	6	AR123794	AR123794 Sequence
9	774	100.0	1198	6	AR175479	AR175479 Sequence
10	774	100.0	1198	6	AR175480	AR175480 Sequence
11	774	100.0	1198	6	AX074287	AX074287 Sequence
12	774	100.0	1198	6	AX074289	AX074289 Sequence
13	774	100.0	1198	6	AX101304	AX101304 Sequence
14	774	100.0	1198	6	AX335621	AX335621 Sequence
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27	591	76.4	1983	6	AX074312	AX074312 Sequence
28	591	76.4	1983	6	AX074314	AX074314 Sequence
29	591	76.4	2268	6	AX074303	AX074303 Sequence
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33	528	68.2	528	6	AX274969	AX274969 Sequence
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35	516	66.7	516	6	AR175487	AR175487 Sequence
36	516	66.7	516	6	AX074296	AX074296 Sequence
37	516	66.7	516	6	AX074298	AX074298 Sequence
38	516	66.7	1908	6	AX074315	AX074315 Sequence
39	516	66.7	1908	6	AX074317	AX074317 Sequence
40	516	66.7	2193	6	AX074306	AX074306 Sequence
41	516	66.7	2193	6	AX074308	AX074308 Sequence
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ALIGNMENTS

RESULT 1
AR175481
LOCUS AR175481
DEFINITION Sequence 4 from patent US 6309832.
ACCESSION AR175481
VERSION AR175481.1 GI:17916780
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 774)
AUTHORS Frank,G.R., Porter,J.P., Rushlow,K.E. and Wassom,D.L.
TITLE Method to detect IGE
JOURNAL Patent: US 6309832-A 4 30-OCT-2001;
FEATURES Location/Qualifiers

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Pred. No. is the number of results predicted by chance to have a

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RESULT 2
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LOCUS AR175482 774 bp DNA linear PAT 17-DEC-2001
DEFINITION Sequence 5 from patent US 6309832.
ACCESSION AR175482
VERSION AR175482.1 GI:17916781
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 774)

AUTHORS Frank, G.R., Porter, J.P., Rushlow, K.E. and Wassom, D.L.
TITLE Method to detect IGE
JOURNAL Patent: US 6309832-A 5 30-OCT-2001;
FEATURES Location/Qualifiers
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DB 661 GGATTTATTATCTCAACTCAGCAGCGTCAATTTCTTTGAAGATTAAAGAACCCAGG 720
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DB 721 AAAGCTTCAGACTTCTGAACCCACATCTTAAGCCAAACCCCAAAACAACTGA 774

RESULT 3
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LOCUS A21606 1068 bp DNA linear PAT 21-JUL-1994
DEFINITION human FC epsilon RI1a.
ACCESSION A21606
VERSION A21606.1 GI:579605
KEYWORDS

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SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1068)
AUTHORS HYBRID FC RECEPTOR MOLECULES
TITLE Patent: WO 9106570-A 29 16-MAY-1991;
JOURNAL Location/Qualifiers
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/db_xref="GOA:P12319"
/db_xref="SWISS-PROT:P12319"
/translation="MAPAMESPTLLCVALLFFAPDGLVAFQPKVSLNPPNRIKFG
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PYLEVSFDMILLQASAEVMEQPLFLRCHGWRMDVVKVIYKDGKALKYWNHN
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ORIGIN
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Best Local Similarity 100.0%; Pred. No. 1e-224;
Matches 774; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 ATGGCTCTGCGCATGGAAATCCCTACTCTACTGTGTAGCTTACTGTCTTCTCGCTCCA 60
40 ATGGCTCTGCGCATGGAAATCCCTACTCTACTGTGTAGCTTACTGTCTTCTCGCTCCA 99
51 GATGCGGTGTAGCAGTCCCTCAGAAACCTTAAGTCTCTCTGAAACCTTCATGGAATAGA 120
100 GATGCGGTGTAGCAGTCCCTCAGAAACCTTAAGTCTCTCTGAAACCTTCATGGAATAGA 159
121 ATATTTAAAGGAGAGAGATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGT 180
160 ATATTTAAAGGAGAGAGATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGT 219
181 TCCACCAAAATGGTCCCAATGGCAGCTTTCAGAGAGACAAATTCAGATTGGAATATT 240
220 TCCACCAAAATGGTCCCAATGGCAGCTTTCAGAGAGACAAATTCAGATTGGAATATT 279
241 GTGAATGCCAAATTTGAAGACAGTGGAGATACAAATGTCAGACCAACAAGTTAATGAG 300
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301 AGTGAACCTGTGTACCTGGAAGTCTTCAGTGAAGTGTCTCTCAGGCTCTGCTGAG 360
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BD264325 1068 bp DNA linear PAT 17-JUL-2003
LOCUS Recombinant soluble Fc receptors.
DEFINITION BD264325
ACCESSION BD264325
VERSION 1 GI:33074093
KEYWORDS JP 2002531086-A/8.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1068)
AUTHORS Sondermann, P., Huber, R. and Jakob, U.
TITLE Recombinant soluble Fc receptors
JOURNAL Patent: JP 2002531086-A 8 24-SEP-2002;
COMMENT MAX PLANCK GESELLSCHAFT ZUR FORDERUNG DER WISSENSCHAFTEN EV
OS Homo sapiens (human)
PN JP 2002531086-A/8
PD 24-SEP-2002
PF 03-DEC-1999 JP 2000585398
PR 03-DEC-1998 EP 98122969.3
PI PETER SONDERMANN, ROBERT HUBER, UWE JAKOB
PC C12N15/09, A61K38/00, A61K45/00, A61P19/02, A61P29/00, A61P31/18,
PC A61P35/00,
PC A61P37/02, A61P37/08, C07K14/735, C12N1/21, G01N33/53, G01N33/53//
PC A61P37/02, A61P37/08, C07K14/735, C12N1/21, G01N33/53, G01N33/53//
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FT Location/Qualifiers
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Query Match 100.0%; Score 774; DB 6; Length 1068;
Best Local Similarity 100.0%; Pred. No. 1e-224;
Matches 774; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 ATGGCTCTGCGCATGGAAATCCCTACTCTACTGTGTAGCTTACTGTCTTCTCGCTCCA 60
40 ATGGCTCTGCGCATGGAAATCCCTACTCTACTGTGTAGCTTACTGTCTTCTCGCTCCA 99
51 GATGCGGTGTAGCAGTCCCTCAGAAACCTTAAGTCTCTCTGAAACCTTCATGGAATAGA 120
100 GATGCGGTGTAGCAGTCCCTCAGAAACCTTAAGTCTCTCTGAAACCTTCATGGAATAGA 159
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ORIGIN      Unreported.
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Query Match      100.0%; Score 774; DB 9; Length 1081;
Best Local Similarity 100.0%; Pred. No. 1e-224;
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DB |||||||
QY 61 GATGCGGTGTPAGCAGTCCCTCAGAACCTTAAGGTCTCTTGAACCTCATGGAATAGA 120
DB |||||||
QY 95 GATGCGGTGTPAGCAGTCCCTCAGAACCTTAAGGTCTCTTGAACCTCATGGAATAGA 154
DB |||||||
QY 121 ATATTAAAGAGAGAGATGTGACCTTACATGTAATGGGAACAATTTCTTGAAGTCAGT 180
DB |||||||
QY 155 ATATTAAAGAGAGAGATGTGACCTTACATGTAATGGGAACAATTTCTTGAAGTCAGT 214
DB |||||||
QY 181 TCCACCAATGGTTCACCAATGGCAGCTTTCAGAGAGACAAATTCAGTTTGAATATT 240
DB |||||||
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DB |||||||
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DB |||||||
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DB |||||||
QY 635 AAGTACTGGCTACAAATTTTATCCCAATGTTGGTGTGATCTCTGTTCTGTGGACACA 694
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DB |||||||
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RESULT 7
BC005912      1102 bp      mRNA      linear      PRI 03-OCT-2003
LOCUS      Homo sapiens Fc fragment of IgE, high affinity I, receptor for;
DEFINITION      alpha polypeptide, mRNA (cDNA clone MGC:14507 IMAGE:4294467),
complete cds.
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ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
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REFERENCE
AUTHORS
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BC005912
BC005912.1 GI:13543505
MGC.
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Homo sapiens (human)
Homo sapiens
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
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Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
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Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
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Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, G., Hsieh, F.,
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Diatchenko, K., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
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Scapleze, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
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Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
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Carninci, P., Prance, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
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Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
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Bouffard, G.G., Blakeley, R.W., Touchman, J.W., Green, E.D.,
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Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
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Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smal, D.E.,
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Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
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Generation and initial analysis of more than 15,000 full-length
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human and mouse cDNA sequences
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Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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2 (bases 1 to 1102)
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Strausberg, R.
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Direct Submission
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REFERENCE
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AUTHORS
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JOURNAL
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TITLE
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USA
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NIH-MGC Project URL: http://mgc.nci.nih.gov
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Contact: MGC help desk
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Email: cgapbs@mail.nih.gov
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Tissue Procurement: CLONTECH
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cDNA Library Preparation: CLONTECH Laboratories, Inc.
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DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
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CNA Sequencing by: Sequencing Group at the Stanford Human Genome
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Center, Stanford University School of Medicine, Stanford, CA 94305
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Web site: http://www.shgc.stanford.edu
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Contact: (Dickson, Mark) mcd@paxil.stanford.edu
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Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers,
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R. M.
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Clone distribution: MGC clone distribution information can be found
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through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
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Best Local Similarity 100.0%; Pred. No. 1e-224;
Matches 774; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGCTCTCGCATGGAATCCCTACTCTACTGTGTAGCCTTACTGTCTTGGCTCCA 60
DB 30 ATGGCTCTCGCATGGAATCCCTACTCTACTGTGTAGCCTTACTGTCTTGGCTCCA 89
QY 61 GATGCGGTGTAGCAGTCCCTCAGAAACCTTAGGCTCTCTGAAACCTCCATGGAATAGA 120
DB 90 GATGCGGTGTAGCAGTCCCTCAGAAACCTTAGGCTCTCTGAAACCTCCATGGAATAGA 149
QY 121 ATATTTAAAGAGAGAATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGT 180
DB 150 ATATTTAAAGAGAGAATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGT 209
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DEFINITION Sequence 10 from patent US 6171803.
ACCESSION AR123794
VERSION AR123794.1 GI:14109155
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
AUTHORS 1 (bases 1 to 1174)
TITLE Kinet,J.Pierre.
JOURNAL Isolation, characterization, and use of the human .beta. subunit of
FEATURES the high affinity receptor for immunoglobulin E
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ORIGIN

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RESULT 9

ARI175479

LOCUS ARI175479 1198 bp DNA linear PAT 17-DEC-2001

DEFINITION Sequence 1 from patent US 6309832.

ACCESSION ARI175479

VERSION ARI175479.1 GI:17916778

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 1198)

AUTHORS Frank,G.R., Porter,J.P., Rushlow,K.E. and Wassom,D.L.

TITLE Method to detect IGE

JOURNAL Patent: US 6309832-A 1 30-OCT-2001;

FEATURES

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/mol_type="unassigned DNA"

ORIGIN

Query Match 100.0%; Score 774; DB 6; Length 1198;

Best Local Similarity 100.0%; Pred. No. 1e-224;

Matches 774; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGGCTCTGCTGATGGAATCCCTTACTCTACTGTGTAGCTTCTTCTTCTGCTCA 60

Db 107 ATGGCTCTGCTGATGGAATCCCTTACTCTACTGTGTAGCTTCTTCTTCTGCTCA 166

Qy 61 GATGGCTGTAGCAGTCCCTCAGAAACCTTAAGTCTCTCTTGAACCCCTCATGGAATGA 120

Db 167 GATGGCTGTAGCAGTCCCTCAGAAACCTTAAGTCTCTCTTGAACCCCTCATGGAATGA 226

Qy 121 ATATTTAAAGAGAGAGATGTACTTACATGTAAATGGGAACAAATTTCTTGAAGTCAGT 180

Db 227 ATATTTAAAGAGAGAGATGTACTTACATGTAAATGGGAACAAATTTCTTGAAGTCAGT 286

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Db 647 TGGCAGCTGGAGTATGAGTCTGAGCCCTCAACATTTACTGTATATAAGCTCCGCTGAG 706

Qy 601 AAGTACTGGCTACAAATTTTATCCCAATTTGTTGGTGTGATTTCTTCTGCTGGACACA 660

Db 707 AAGTACTGGCTACAAATTTTATCCCATTTCTTGGTGGTGAATCTGTTTGTGTGGACACA 766

Qy 661 GGATTATTATCTCAACTCAGCAGGTCACATTTCTCTTGAAGATTAAAGAACACAGG 720

Db 767 GGATTATTATCTCAACTCAGCAGGTCACATTTCTCTTGAAGATTAAAGAACACAGG 826

Qy 721 AAAGGCTCAGACTCTTGAACCCACATCTTAAGCCAAACCCCAAAACAACTGA 774

Db 827 AAAGGCTCAGACTCTTGAACCCACATCTTAAGCCAAACCCCAAAACAACTGA 880

RESULT 10

ARI175480/c

LOCUS ARI175480 1198 bp DNA linear PAT 17-DEC-2001

DEFINITION Sequence 3 from patent US 6309832.

ACCESSION ARI175480

VERSION ARI175480.1 GI:17916779

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 1198)

AUTHORS Frank,G.R., Porter,J.P., Rushlow,K.E. and Wassom,D.L.

TITLE Method to detect IGE

JOURNAL Patent: US 6309832-A 3 30-OCT-2001;

FEATURES

source 1. 1198

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ORIGIN

Query Match 100.0%; Score 774; DB 6; Length 1198;

Best Local Similarity 100.0%; Pred. No. 1e-224;

Matches 774; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGGCTCTGCTGATGGAATCCCTTACTCTACTGTGTAGCTTCTTCTTCTGCTCA 60

Db 1092 ATGGCTCTGCTGATGGAATCCCTTACTCTACTGTGTAGCTTCTTCTTCTGCTCA 1033

Qy 61 GATGGCTGTAGCAGTCCCTCAGAAACCTTAAGTCTCTCTTGAACCCCTCATGGAATGA 120

Db 1032 GATGGCTGTAGCAGTCCCTCAGAAACCTTAAGTCTCTCTTGAACCCCTCATGGAATGA 973

Qy 121 ATATTTAAAGAGAGAGATGTACTTACATGTAAATGGGAACAAATTTCTTGAAGTCAGT 180

Db 972 ATATTTAAAGAGAGAGATGTACTTACATGTAAATGGGAACAAATTTCTTGAAGTCAGT 913

Qy 181 TCCACCAAAATGGTTCACAAATGGCAGCCTTTCAGAAAGAGACAAATTCAGATTTGAATAT 240

Db 912 TCCACCAAAATGGTTCACAAATGGCAGCCTTTCAGAAAGAGACAAATTCAGATTTGAATAT 853

Qy 241 GTGAATCCCAAAATTTGAAGAGAGATGTACTTACATGTAAATGGGAACAAATTTCTTGAAGTCAGT 300

Db 852 GTGAATCCCAAAATTTGAAGAGAGATGTACTTACATGTAAATGGGAACAAATTTCTTGAAGTCAGT 793

Qy 301 AGTGAACCTGTGTACCTGGAAGTCTTCAGTGACTGGCTGCTCCTTCAGGCTCTGCTGAG 360

Db 792 AGTGAACCTGTGTACCTGGAAGTCTTCAGTGACTGGCTGCTCCTTCAGGCTCTGCTGAG 733

Qy 361 GTGGTATGGAGGCGCAGCCCTCTTCTCAGTGCCATGGTTGGAGGAACTGGGATGTG 420

Db 732 GTGGTATGGAGGCGCAGCCCTCTTCTCAGTGCCATGGTTGGAGGAACTGGGATGTG 673

Qy 421 TACAAGGTGATCTATTATAAGGATGTGAAGTCTCAAGTACTGTGTATGAGAACCAAC 480

Db 672 TACAAGGTGATCTATTATAAGGATGTGAAGTCTCAAGTACTGTGTATGAGAACCAAC 613

Qy 481 ATCTCCATTACAATGCGACAGTTGAAGAGAGATGTGAAGTCTCAAGTACTGTGTATGAGAACCAAGTG 540

Db 612 ATCTCCATTACAATGCGACAGTTGAAGAGAGATGTGAAGTCTCAAGTACTGTGTATGAGAACCAAGTG 553

Qy 541 TGGCAGCTGGAGTATGAGTCTGAGCCCTCAACATTTACTGTATATAAGCTCCGCTGAG 600

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Db      552 TGGAGCTGGACTAGTCTGAGGCCCTCAACATTACTGTATAAAAGCTCCCGGTGAG 493
QY      601 AAGTACTGGCTACAAATTTTATCCCATTTGTTGGTGGTGAATCTGTTTGGCTGTGGACACA 660
Db      492 AAGTACTGGCTACAAATTTTATCCCATTTGTTGGTGGTGAATCTGTTTGGCTGTGGACACA 433
QY      661 GGATTTATTACTCAACTCAGCAGCAGTCACTTCTTTGAAGATTAAAGAACAGG 720
Db      432 GGATTTATTATCTCAACTCAGCAGCAGTCACTTCTTTGAAGATTAAAGAACAGG 373
QY      721 AAAGCTTTCAGACTTCTGAACCCACATCTTAAGCCAAACCCCAAAACCACTGA 774
Db      372 AAAGCTTTCAGACTTCTGAACCCACATCTTAAGCCAAACCCCAAAACCACTGA 319

RESULT 11
AX074287
LOCUS      AX074287      1198 bp      DNA      linear      PAT 06-FEB-2001
DEFINITION Sequence 1 from Patent WO0104310.
ACCESSION AX074287
VERSION    AX074287.1 GI:12710474
KEYWORDS
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1
AUTHORS    Weber,E.R., Wood,K.V. and Hall,M.P.
TITLE      Fc epsilon receptor-luminescence inducing protein chimeric nucleic
            acid molecules, fusion proteins and uses thereof
JOURNAL    Patent: WO 0104310-A 1 18-JAN-2001;
            Heska Corporation (US) ; PROMEGA CORPORATION (US)
FEATURES   Location/Qualifiers
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                        107..1880
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ORIGIN
Query Match      100.0%; Score 774; DB 6; Length 1198;
Best Local Similarity 100.0%; Pred. No. 1e-224;
Matches 774; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  ATGCTCTCCGATGGATCCCTACTCTACTGTGTAGCCCTTACTGTTCTCGTCCA 60
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QY      61  GATGGCGTGTAGCAGTCCCTCAGAACCTTAAGGTCTCTTGAACCTCCATGGATAGA 120
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QY      121 ATATTTAAAGGAGAGATGTGACTCTTACATGTATGGGAAACAATTTCTTTGAAGTCAGT 180
Db      227 ATATTTAAAGGAGAGATGTGACTCTTACATGTATGGGAAACAATTTCTTTGAAGTCAGT 286

QY      181 TCCACCAAAATGGTTCCACAATGSCGCCCTTTCAGAGAGACAAATTCAGTTTGAATATT 240
Db      287 TCCACCAAAATGGTTCCACAATGSCGCCCTTTCAGAGAGACAAATTCAGTTTGAATATT 346

QY      241 GTGAATGCCAAATTTGAAGACAGTGGAGAAATCAAAATGTGACACCAACAAAGTTAATGAG 300
Db      347 GTGAATGCCAAATTTGAAGACAGTGGAGAAATCAAAATGTGACACCAACAAAGTTAATGAG 406

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QY      301 AGTGAACCTGTGTACTGGAAGTCTTTCAGTGAAGTGGCTGCTCTTTCAGGSCCTCTGCTGAG 360
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QY      361 GTGGTGAATGAGGGGCGAGCCCTCTTTCCTCAGTCCCATGTTGGAGAACTGGGATGTG 420
Db      467 GTGGTGAATGAGGGGCGAGCCCTCTTTCCTCAGTCCCATGTTGGAGAACTGGGATGTG 526

QY      421 TACAAGTGTATCTATTATTAAGGATGCTGAAGCTCTCAAGTACTCTGATGATGAGAACCAAC 480
Db      527 TACAAGTGTATCTATTATTAAGGATGCTGAAGCTCTCAAGTACTCTGATGATGAGAACCAAC 586

QY      481 ATCTCATTACAAATGCCACAGTTTGAAGACAGTGAACCTACTACTGTACGGGCAAAAGTG 540
Db      587 ATCTCATTACAAATGCCACAGTTTGAAGACAGTGAACCTACTACTGTACGGGCAAAAGTG 646

QY      541 TGGCAGCTGGACTATGAGTCTGAGCCCTCAACATTACTGTATAAAGCTCCGGGTGAG 600
Db      647 TGGCAGCTGGACTATGAGTCTGAGCCCTCAACATTACTGTATAAAGCTCCGGGTGAG 706

QY      601 AAGTACTGGCTACAAATTTTATCCCATTTGTTGGTGGTGAATCTGTTTCTGCTGTGACACA 660
Db      707 AAGTACTGGCTACAAATTTTATCCCATTTGTTGGTGGTGAATCTGTTTCTGCTGTGACACA 766

QY      661 GGATTTATTATCTCAACTCAGCAGCAGTCACTTCTTCTTGAAGATTAAAGAACCCAGG 720
Db      767 GGATTTATTATCTCAACTCAGCAGCAGTCACTTCTTCTTGAAGATTAAAGAACCCAGG 826

QY      721 AAAGCTTTCAGACTTCTGAACCCACATCTTAAGCCAAACCCCAAAACCACTGA 774
Db      827 AAAGCTTTCAGACTTCTGAACCCACATCTTAAGCCAAACCCCAAAACCACTGA 880

RESULT 12
AX074289/c
LOCUS      AX074289      1198 bp      DNA      linear      PAT 06-FEB-2001
DEFINITION Sequence 3 from Patent WO0104310.
ACCESSION AX074289
VERSION    AX074289.1 GI:12710476
KEYWORDS
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1
AUTHORS    Weber,E.R., Wood,K.V. and Hall,M.P.
TITLE      Fc epsilon receptor-luminescence inducing protein chimeric nucleic
            acid molecules, fusion proteins and uses thereof
JOURNAL    Patent: WO 0104310-A 3 18-JAN-2001;
            Heska Corporation (US) ; PROMEGA CORPORATION (US)
FEATURES   Location/Qualifiers
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ORIGIN
Query Match      100.0%; Score 774; DB 6; Length 1198;
Best Local Similarity 100.0%; Pred. No. 1e-224;
Matches 774; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  ATGCTCTCTCCGATGGAAATCCCTACTCTACTGTGTAGCCCTTACTGTTCTTCGTTCCA 60
Db      1092 ATGCTCTCTCCGATGGAAATCCCTACTCTACTGTGTAGCCCTTACTGTTCTTCGTTCCA 1033

QY      61  GATGGCGTGTAGCAGTCCCTCAGAACCTTAAGGTCTCTTGAACCTCCATGGATAGA 120
Db      1032 GATGGCGTGTAGCAGTCCCTCAGAACCTTAAGGTCTCTTGAACCTCCATGGATAGA 973

QY      121 ATATTTAAAGGAGAGATGTGACTCTTACATGTATGGGAAACAATTTCTTTGAAGTCAGT 180
Db      972 ATATTTAAAGGAGAGATGTGACTCTTACATGTATGGGAAACAATTTCTTTGAAGTCAGT 913

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QY 181 TCACCAAAATGTTCCAAATGGAGCCCTTTTCAGAGAGACAAATTCAGTTTGAATATT 240
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QY 241 GTGAATGCCAAATTTGAAGACAGTGGAGAAATCAAAATGTCAGCAACCAAGTTAATGAG 300
Db 852 GTGAATGCCAAATTTGAAGACAGTGGAGAAATCAAAATGTCAGCAACCAAGTTAATGAG 793
QY 301 AGTGAACCTGTGTACCTGGAAATCTTCAGTGTGCTGCTCTCTTCAGGCTCTCTCTGAG 360
Db 792 AGTGAACCTGTGTACCTGGAAATCTTCAGTGTGCTGCTCTCTTCAGGCTCTCTCTGAG 733
QY 361 GTGCTGATGGAGGGCCAGCCCTCTTCCTCAGTGGCCATGTTGGAGAACTGGGATGTG 420
Db 732 GTGCTGATGGAGGGCCAGCCCTCTTCCTCAGTGGCCATGTTGGAGAACTGGGATGTG 673
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Db 672 TACAAGGTGATCTATTATTAAGAGTGTGAAGTCTCAAGTACTGTGATGAGAACCAAC 613
QY 481 ATCTCCATTACAAATGCCACAGTTGAAGACAGTGGAACTTACTACTGTACGGGCAAGTG 540
Db 612 ATCTCCATTACAAATGCCACAGTTGAAGACAGTGGAACTTACTACTGTACGGGCAAGTG 553
QY 541 TGGCAGCTGACTATGAGTCTGAGCCCTCAACATTACTGTATTAAGTCTCGGCTGAG 600
Db 552 TGGCAGCTGACTATGAGTCTGAGCCCTCAACATTACTGTATTAAGTCTCGGCTGAG 493
QY 601 AAGTACTGGCTACAAATTTTATPCCATTGTTGGTGGTGAATCTGTTCTGTGGACACA 660
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Db 432 GGAATATTATCTCACTCAGCAGCAGGTCACATTTCTCTGAAAGATTAAAGAACCCAGG 373
QY 721 AAAGGCTTCAGACTTCTGAACCCACATCTCTAAGCCAAACCCCAAAACCAACTGA 774
Db 372 AAAGGCTTCAGACTTCTGAACCCACATCTCTAAGCCAAACCCCAAAACCAACTGA 319

RESULT 13
AX101304
LOCUS
DEFINITION
Sequence 7 from Patent WO0121816.
ACCESSION
AX101304
VERSION
AX101304.1 GI:13620094
KEYWORDS
Homo sapiens (human)
SOURCE
Homo sapiens
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 Kinet,J.P., Donnadieu,E., Jouvin,M.H., Cookson,W. and Moffatt,M.F.
AUTHORS
Modulation of lge receptor cell surface expression
TITLE
Patent: WO 0121816-A 7 29-MAR-2001;
JOURNAL
ISIS INNOVATION LIMITED (GB) ; Beth Israel Deaconess Medical
Center, Inc. (US)
FEATURES
Location/Qualifiers
1..1198
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Query Match 100.0%; Score 774; DB 6; Length 1198;
Best Local Similarity 100.0%; Pred. No. 1e-224;
Matches 774; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGGCTCTCGCATGGAAATCCCTACTCTACTGTGTGAGCTTACTGTCTTCTGCTCCA 60
Db 107 ATGGCTCTCGCATGGAAATCCCTACTCTACTGTGTGAGCTTACTGTCTTCTGCTCCA 166

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Db 167 GATGGCGTGTAGCAGTCCCTCAGAACTTAAGTCTCTCTTGAACCCCTCCATGAATAGA 226
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Db 227 ATATTTAAAGGAGAGAAATGTGACTCTTTACATGTAATGGGAACAATTTCTTTGAAGTCAGT 286
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Db 347 GTGAATGCCAAATTTGAAGACAGTGGAGAAATCAAAATGTCAGCAACCAAGTTAATGAG 406
QY 301 AGTGAACCTGTGTACCTGGAAATCTTCAGTGTGCTGCTCTCTTCAGGCTCTCTCTGAG 360
Db 407 AGTGAACCTGTGTACCTGGAAATCTTCAGTGTGCTGCTCTCTTCAGGCTCTCTCTGAG 466
QY 361 GTGCTGATGGAGGGCCAGCCCTCTTCCTCAGTGGCCATGTTGGAGAACTGGGATGTG 420
Db 467 GTGCTGATGGAGGGCCAGCCCTCTTCCTCAGTGGCCATGTTGGAGAACTGGGATGTG 526
QY 421 TACAAGGTGATCTATTATTAAGAGTGTGAAGTCTCAAGTACTGTGATGAGAACCAAC 480
Db 527 TACAAGGTGATCTATTATTAAGAGTGTGAAGTCTCAAGTACTGTGATGAGAACCAAC 586
QY 481 ATCTCCATTACAAATGCCACAGTTGAAGACAGTGGAACTTACTACTGTACGGGCAAGTG 540
Db 587 ATCTCCATTACAAATGCCACAGTTGAAGACAGTGGAACTTACTACTGTACGGGCAAGTG 646
QY 541 TGGCAGCTGGAATGATGAGTCTGAGCCCTCAACATTACTGTATTAAGTCTCCGCTGAG 600
Db 647 TGGCAGCTGGAATGATGAGTCTGAGCCCTCAACATTACTGTATTAAGTCTCCGCTGAG 706
QY 601 AAGTACTGGCTACAAATTTTATPCCATTGTTGGTGGTGAATCTGTTCTGTGGACACA 660
Db 707 AAGTACTGGCTACAAATTTTATCCATTGTTGGTGGTGAATCTGTTCTGTGGACACA 766
QY 661 GGAATATTATCTCACTCAGCAGCAGGTCACATTTCTCTTGAAGATTAAAGAACCCAGG 720
Db 767 GGAATATTATCTCACTCAGCAGCAGGTCACATTTCTCTTGAAGATTAAAGAACCCAGG 826
QY 721 AAAGGCTTCAGACTTCTGAACCCACATCTCTAAGCCAAACCCCAAAACCAACTGA 774
Db 827 AAAGGCTTCAGACTTCTGAACCCACATCTCTAAGCCAAACCCCAAAACCAACTGA 880

RESULT 14
AX335621
LOCUS
DEFINITION
Sequence 6130 from Patent WO0194629.
ACCESSION
AX335621
VERSION
AX335621.1 GI:18126340
KEYWORDS
Homo sapiens (human)
SOURCE
Homo sapiens
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 Young,P.E., Augustus,M., Carter,K.C., Ebner,R., Endress,G.,
AUTHORS
Horrigan,S., Soppet,D.R. and Weaver,Z.
TITLE
Cancer gene determination and therapeutic screening using signature
JOURNAL
Patent: WO 0194629-A 6130 13-DEC-2001;
FEATURES
Avalon Pharmaceuticals (US)
Location/Qualifiers
1..1198
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Query Match 100.0%; Score 774; DB 6; Length 1198;									
Best Local Similarity 100.0%; Pred. No. 1e-224;									
Matches 774; Conservative 0; Mismatches 0; Indels 0; Gaps 0;									
QY	1	ATGGCTCTCGCATGAATCCCTACTCTACTCTGTGTGTAGCTTACTTCTCGCTCCA	60						
Db	107	ATGGCTCTCGCATGAATCCCTACTCTACTGTGTGTAGCTTACTTCTCGCTCCA	166						
QY	61	GATGGCTGTAGCAGTCCCTCAGAACCTAAGCTCTCTTGAACCCCTCCATGAATAGA	120						
Db	167	GATGGCTGTAGCAGTCCCTCAGAACCTAAGCTCTCTTGAACCCCTCCATGAATAGA	226						
QY	121	ATATTTAAAGGAGAGATGTGACTCTTACATGTAAATGGGACAAATTTCTTTGAAGTCAGT	180						
Db	227	ATATTTAAAGGAGAGATGTGACTCTTACATGTAAATGGGACAAATTTCTTTGAAGTCAGT	286						
QY	181	TCCACCAATGTTCCCAATGGCAGCTTTTCAAGAGACAAATTTCAAGTTTGAATATT	240						
Db	287	TCCACCAATGTTCCCAATGGCAGCTTTTCAAGAGACAAATTTCAAGTTTGAATATT	346						
QY	241	GTGAATGCCAAATTTGAAGCAGTGGGAGATACAAATGTTCAGACCAACCAAGTTAATGAG	300						
Db	347	GTGAATGCCAAATTTGAAGCAGTGGGAGATACAAATGTTCAGACCAACCAAGTTAATGAG	406						
QY	301	AGTGAACCTGTACTTGGAGCTTTCAGTGTACTGGCTCTCTTCAAGGCTCTGCTGAG	360						
Db	407	AGTGAACCTGTACTTGGAGCTTTCAGTGTACTGGCTCTCTTCAAGGCTCTGCTGAG	466						
QY	361	GTGGTGTATGGAGGGCCAGCCCTCTTCTCAGTGTCCATGGTGGAGAACTGGGATGTG	420						
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QY	421	TACAAGGTGATCTATTATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCAAC	480						
Db	527	TACAAGGTGATCTATTATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCAAC	586						
QY	481	ATCTCCATTACAATGCCAGTTGAAGACAGTGGAACTTACTGTAGGGCAAGTG	540						
Db	587	ATCTCCATTACAATGCCAGTTGAAGACAGTGGAACTTACTGTAGGGCAAGTG	646						
QY	541	TGGCAGCTGGACTATGAGTCTGAGCCCTCAACATTACTGTAAATGAGTCTCGCGTGAG	600						
Db	647	TGGCAGCTGGACTATGAGTCTGAGCCCTCAACATTACTGTAAATGAGTCTCGCGTGAG	706						
QY	601	AAGTACTGGCTACAAATTTTATCCCATTTGTGGTGTGATTCGTGTGTGGACACA	660						
Db	707	AAGTACTGGCTACAAATTTTATCCCATTTGTGGTGTGATTCGTGTGTGGACACA	766						
QY	661	GGATTATTATCTCAACTCAGCAGCTCACATTTCTTGAAGATTAAAGAACCCAGG	720						
Db	767	GGATTATTATCTCAACTCAGCAGCTCACATTTCTTGAAGATTAAAGAACCCAGG	826						
QY	721	AAAGGCTTCAGACTTCTGAACCCACATCTTCAAGCCAAACCCCAAAACCACTGA	774						
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LOCUS Human mRNA for high affinity IGE receptor alpha-subunit (FcERI).									
DEFINITION X06948									
ACCESSION X06948.1 GI:31317									
VERSION FcERI gene; IGE receptor alpha-subunit.									
KEYWORDS Homo sapiens (human)									
SOURCE Homo sapiens									
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;									
REFERENCE Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.									
1 (bases 1 to 1198)									
AUTHORS Kochan.J., Pettine.L.F., Hakimi.J., Kishi.K. and Kinet,J.P.									
TITLE Isolation of the gene coding for the alpha subunit of the human									

high affinity IGE receptor
Nucleic Acids Res. 16 (8), 3584 (1988)
88233953
2967464
REFERENCE 2 (bases 1 to 1198)
Kochan.J.P.
AUTHORS Direct Submission
JOURNAL Submitted (24-FEB-1988) Kochan J. P., Hoffman-La Roche, Dept
Molecular Genetics, 340 Kingsland, Nutley, New Jersey 07110
*source cell line=KUB12; library=lambdta 5tll cDNA.
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/clone="pLJ587 & pLJ563"
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misc_feature
ORIGIN
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Best Local Similarity 100.0%; Pred. No. 1e-224;
Matches 774; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGGCTCTCGCATGAATCCCTACTCTACTGTGTGTAGCTTACTTCTCGCTCCA 60
Db 107 ATGGCTCTCGCATGAATCCCTACTCTACTGTGTGTAGCTTACTTCTCGCTCCA 166
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QY 301 AGTGAACCTGTACTTGGAGCTTTCAGTGTACTGGCTCTCTTCAAGGCTCTGCTGAG 360
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QY 361 GTGGTGTATGGAGGGCCAGCCCTCTTCTCAGTGTCCATGGTGGAGAACTGGGATGTG 420
Db 467 GTGGTGTATGGAGGGCCAGCCCTCTTCTCAGTGTCCATGGTGGAGAACTGGGATGTG 526
QY 421 TACAAGGTGATCTATTATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCAAC 480

Db	527	TACAAGGTGATCTATTATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCAAC	586
Qy	481	ATCTCCATTACAAATGCCACAGTTGAAGACAGTGAACCTACTACTGTACGGGCAAGTG	540
Db	587	ATCTCCATTACAAATGCCACAGTTGAAGACAGTGAACCTACTACTGTACGGGCAAGTG	646
Qy	541	TGGCAGCTGGACTATGAGTCTGAGCCCTCAACATTACTGTAAATAAAAGCTCCGCGTGAG	600
Db	647	TGGCAGCTGGACTATGAGTCTGAGCCCTCAACATTACTGTAAATAAAAGCTCCGCGTGAG	706
Qy	601	AAGTACTGGCTACAAATTTTATCCANTGTTGGTGGTGATCTCTGTTGCTGTGGACACA	660
Db	707	AAGTACTGGCTACAAATTTTATCCANTGTTGGTGGTGATCTCTGTTGCTGTGGACACA	766
Qy	661	GGATTATTTATCTCAACTCAGCAGCAGGTCAATTTCTTGAAGATTAAAGAGAACCCAGG	720
Db	767	GGATTATTTATCTCAACTCAGCAGCAGGTCAATTTCTTGAAGATTAAAGAGAACCCAGG	826
Qy	721	AAAGGCTTCAGACTTCTGAACCCACATCCTAAGCCAAACCCCAAAACAACTGA	774
Db	827	AAAGGCTTCAGACTTCTGAACCCACATCCTAAGCCAAACCCCAAAACAACTGA	880

Search completed: October 10, 2004, 16:11:54
Job time : 3370.32 secs

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CC a position corresponding to nucleotide 530. (I) can be used in gene
 CC therapy. (I) is useful for therapeutic purposes. A polypeptide (II)
 CC encoded by (I) is useful in drug screening assays and in assays to
 CC measure the binding affinity of one or more candidate drugs targeting
 CC (II). An antibody (III) to (II) is useful to immunoprecipitate (II) from
 CC solution and also reacts with (II) on Western or immunoblots of
 CC polyacrylamide gels on membrane supports or substrates. (III) is also
 CC useful in immunoassays to detect (II) in biological samples. AAF97965 to
 CC AAF98096 represent IGRA allele specific oligonucleotide probes; AAF98097
 CC to AAF98140 represent IGRA gene polymorphism detection primers; and
 CC AAF98141 to AAF98180 represent IGRA gene PCR primers which are used in
 CC the exemplification of the present invention. The present sequence
 CC encodes the human IGRA protein used in the present invention
 XX
 SQ Sequence 774 BP; 221 A; 172 C; 177 G; 204 T; 0 U; 0 Other;
 Query Match 100.0%; Score 774; DB 4; Length 774;
 Best Local Similarity 100.0%; Pred. No. 2.4e-223;
 Matches 774; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ATGGCTCTGCGATGGAAATCCCTACTCTACTGTGTGTAGCTTACTGTCTTCGCTCCA 60
 DB 1 ATGGCTCTGCGATGGAAATCCCTACTCTACTGTGTGTAGCTTACTGTCTTCGCTCCA 60
 QY 61 GATGGCGTGTAGCAGTCCCTCAGAAACCTAAGTCTCTTGAACCTCCATGGAATAGA 120
 DB 61 GATGGCGTGTAGCAGTCCCTCAGAAACCTAAGTCTCTTGAACCTCCATGGAATAGA 120
 QY 121 ATATTAAAGAGAGAAATGTGACTCTTACATGTAATGGGAACAAATTTCTTTGAAGTCAGT 180
 DB 121 ATATTAAAGAGAGAAATGTGACTCTTACATGTAATGGGAACAAATTTCTTTGAAGTCAGT 180
 QY 181 TCCACCAATGGTTCACAAATGGCAGCTTTCAGAGAGACAAATTCAGTTTGAATATT 240
 DB 181 TCCACCAATGGTTCACAAATGGCAGCTTTCAGAGAGACAAATTCAGTTTGAATATT 240
 QY 241 GTGAATGCCAAATTTGAAGACAGTGGGAAATACAAATGTGAGCAACCAAGTTAATGAG 300
 DB 241 GTGAATGCCAAATTTGAAGACAGTGGGAAATACAAATGTGAGCAACCAAGTTAATGAG 300
 QY 301 AGTGAACCTGTACCTGGAGTCTTCAAGTACCTGGCTGCTCTTCAAGCTTCTGCTGAG 360
 DB 301 AGTGAACCTGTACCTGGAGTCTTCAAGTACCTGGCTGCTCTTCAAGCTTCTGCTGAG 360
 QY 361 GTGTGTATGGAGGCCAGCCCTCTTCTCAGGTGCTGATGGTGGAGAACTGGGATGTG 420
 DB 361 GTGTGTATGGAGGCCAGCCCTCTTCTCAGGTGCTGATGGTGGAGAACTGGGATGTG 420
 QY 421 TAGAAGTGATCTATTATAGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCAAC 480
 DB 421 TACAAGTGATCTATTATAGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCAAC 480
 QY 481 ATCTCCATTACAAATGCCAGTGAAGACAGTGGAACTTACTACTGTAGGGCAAGTG 540
 DB 481 ATCTCCATTACAAATGCCAGTGAAGACAGTGGAACTTACTACTGTAGGGCAAGTG 540
 QY 541 TGGCAGCTGGAATATGATCTGAGCCCTCAACATTACTGTATATAAAGCTCCGCTGAG 600
 DB 541 TGGCAGCTGGAATATGATCTGAGCCCTCAACATTACTGTATATAAAGCTCCGCTGAG 600
 QY 601 AAGTACTGGCTACAATTTTATCCATGTTGCTGCTGATCTGTTGCTGTGGACACA 660
 DB 601 AAGTACTGGCTACAATTTTATCCCATTTGCTGCTGATCTGTTGCTGTGGACACA 660
 QY 661 GGATTAATTTATCTCAACTCAGCAGCGGTGACATTTCTCTTGAAGATTAAAGAACCCAGG 720
 DB 661 GGATTAATTTATCTCAACTCAGCAGCGGTGACATTTCTCTTGAAGATTAAAGAACCCAGG 720
 QY 721 AAGGGCTTCAGACTTCTGACACCCACATCTTAAGCCAAACCCCAAAACCACTGA 774
 DB 721 AAGGGCTTCAGACTTCTGACACCCACATCTTAAGCCAAACCCCAAAACCACTGA 774

RESULT 2
 AAA27470
 ID AAA27470 standard; cDNA; 1068 BP.
 XX
 AC AAA27470;
 XX
 DT 11-SEP-2000 (first entry)
 XX
 DE Human Fc receptor, FcpsilonRIa, coding sequence.
 XX
 KW Human; Fc receptor; FcpsilonRIa; immunoglobulin; infection;
 KW immune response; HIV; IGF; immunosuppressive; antirheumatic;
 KW antiinflammatory; AIDS; SLE; multiple myeloma; rheumatoid arthritis;
 KW systemic lupus erythematosus; tumour; ss.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 31..813
 FT /tag=a
 FT /product="FcpsilonRIa"
 XX
 PN BP1006183-A1.
 XX
 PD 07-JUN-2000.
 XX
 PP 03-DEC-1998; 98EP-00122969.
 XX
 PR 03-DEC-1998; 98EP-00122969.
 XX
 PA (PLAC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
 XX
 DR WPI: 2000-367568/32.
 DR P-PSDB; AAY96230.
 XX
 PT Novel Fc receptor lacking transmembrane domains, a signal peptide, and
 PT glycosylation, useful for diagnosing and treating immune disorders and
 PT cancer.
 XX
 PS Disclosure; Page 17; 60pp; English.
 XX
 CC The present sequence is the human Fc receptor, FcpsilonRIa, coding
 CC sequence. Fc receptors play a key role in defending the body against
 CC infections. First, pathogens are opsonised by serum immunoglobulins. The
 CC resulting complex then binds to cells expressing Fc receptors. Upon Fc
 CC receptor activation, immune effector pathways are activated, leading to
 CC immune response. The present sequence may be modified to produce
 CC recombinant versions. The recombinant Fc receptor consist only of the
 CC extracellular portion of the receptor and are not glycosylated i.e. they
 CC do not have transmembrane domains or signal peptides. The recombinant
 CC proteins may be used in immunoassays to determine the immune status of
 CC patients with chronic diseases of the immune system, e.g. AIDS, systemic
 CC lupus erythematosus (SLE), multiple myeloma (MM), or rheumatoid
 CC arthritis. In addition, pharmaceutical compositions containing
 CC recombinant proteins may be used to treat or prevent autoimmune diseases,
 CC allergies or tumours, especially AIDS, rheumatoid arthritis or MM
 XX
 SQ Sequence 1068 BP; 330 A; 215 C; 229 G; 294 T; 0 U; 0 Other;
 Query Match 100.0%; Score 774; DB 3; Length 1068;
 Best Local Similarity 100.0%; Pred. No. 2.8e-223;
 Matches 774; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ATGGCTCTGCGATGGAAATCCCTACTCTACTGTGTGTAGCTTACTGTCTTCGCTCCA 60
 DB 40 ATGGCTCTGCGATGGAAATCCCTACTCTACTGTGTGTAGCTTACTGTCTTCGCTCCA 99
 QY 61 GATGGCGTGTAGCAGTCCCTCAGAAACCTAAGTCTCTTGAACCTCCATGGAATAGA 120
 DB 100 GATGGCGTGTAGCAGTCCCTCAGAAACCTAAGTCTCTTGAACCTCCATGGAATAGA 159
 QY 121 ATATTAAAGAGAGAAATGTGACTCTTACATGTAATGGGAACAAATTTCTTTGAAGTCAGT 180

Db 160 ATATTAAAGAGAGAAATGTGACTCTTACATGTAAATGGGAACAATTTCTTTGAAGTCAGT 219
QY 181 TCCACCAAAATGGTTCCCAAAATGGAGCCCTTTTCAAGAGAGACAAATTCAGTTTGAATATT 240
Db 220 TCCACCAAAATGGTTCCCAAAATGGAGCCCTTTTCAAGAGAGACAAATTCAGTTTGAATATT 279
QY 241 GTGAATGCCAAATTTTGAAGACAGTGGAGATACAAATGTGAGCAACCAAAAGTTAATGAG 300
Db 280 GTGAATGCCAAATTTTGAAGACAGTGGAGATACAAATGTGAGCAACCAAAAGTTAATGAG 339
QY 301 AGTGAACCTGTGTACTGTGAAGTCTTTCAGTGTGAGTGGCTGCTCTTTCAGGCGCTTGTGAG 360
Db 340 AGTGAACCTGTGTACTGTGAAGTCTTTCAGTGTGAGTGGCTGCTCTTTCAGGCGCTTGTGAG 399
QY 361 GTGGTGTAGAGGGCCAGCCCTTCTTCTCAGGTGCCATGTTTGAAGAACTGGATGTG 420
Db 400 GTGGTGTAGAGGGCCAGCCCTTCTTCTCAGGTGCCATGTTTGAAGAACTGGATGTG 459
QY 421 TACAAGTGTATCTATTATTAAGATGGTGAAGCTCTCAAGTACTGTGTATGAGAACCAAC 480
Db 460 TACAAGTGTATCTATTATTAAGATGGTGAAGCTCTCAAGTACTGTGTATGAGAACCAAC 519
QY 481 ATCTCCATTACAAATGCCACAGTTGAAGACAGTGGAACTTACTACTGTACGGGCAAGTG 540
Db 520 ATCTCCATTACAAATGCCACAGTTGAAGACAGTGGAACTTACTACTGTACGGGCAAGTG 579
QY 541 TGGCAGCTGAGTATGAGTCTGAGCCCTCAACATTTACTGTAAATAAAAGCTCCGGTGAG 600
Db 580 TGGCAGCTGAGTATGAGTCTGAGCCCTCAACATTTACTGTAAATAAAAGCTCCGGTGAG 639
QY 601 AAGTACTGGCTACAAATTTTATCCCATTTGTTGGTGGTGAATCTGTGTTGCTGTGACACA 660
Db 640 AAGTACTGGCTACAAATTTTATCCCATTTGTTGGTGGTGAATCTGTGTTGCTGTGACACA 699
QY 661 GGAATTTATCTCAACTCAGCAGCAGGTGCATTTCTTCTTGAAGATTAAGAAACCCAGG 720
Db 700 GGAATTTATCTCAACTCAGCAGCAGGTGCATTTCTTCTTGAAGATTAAGAAACCCAGG 759
QY 721 AAAGGCTTCAGACTTCTGAACCCACATCTCTAAGCCAAACCCCAAAACCAACTGA 774
Db 760 AAAGGCTTCAGACTTCTGAACCCACATCTCTAAGCCAAACCCCAAAACCAACTGA 813

RESULT 3
AAN90126
ID AAN90126 standard; cDNA; 1088 BP.
XX AC AAN90126;
XX 24-OCT-2003 (revised)
DT 25-MAR-2003 (revised)
DT 01-NOV-1989 (first entry)
XX cDNA encoding human mast cell IgE receptor alpha subunit.
DE cDNA; immunoglobulin E receptor alpha subunit; treats allergies;
XX design non-peptide drugs; human.
XX Homo sapiens; (Human); mast cell line.
OS KU812.
XX Key Location/Qualifiers
FH 35..805
FT CDS /*tag= a
FT FT
XX WO8905352-A.
XX 15-JUN-1989.
PD 29-NOV-1988; 88WO-US004255.
XX 29-NOV-1988;
PR 01-DEC-1987; 87US-00127214.
XX

PA (HARD) HARVARD COLLEGE.
PA (USSH) NAT INST OF HEALTH.
XX Leder P, Benfey P;
XX WPI; 1989-192698/26.
DR P-PSDB; AAP90385.
XX cDNA encoding IGE receptor alpha-sub-unit - used to treat allergies.
XX Disclosure; Fig 4; 17pp; English.
PS cDNA sequence encoding immunoglobulin E receptor alpha subunit of human
XX mast cell IGE surface receptor (see corresp. AAP90385). Used to produce
CC antibodies which can diagnose IGE receptor levels, measure and treat
CC allergies, and design non-peptide drugs. (Updated on 25-MAR-2003 to
CC correct PA field.) (Updated on 24-OCT-2003 to standardise OS field)
XX
SQ Sequence 1088 BP; 347 A; 216 C; 229 G; 296 T; 0 U; 0 Other;
Query Match 100.0%; Score 774; DB 1; Length 1088;
Best Local Similarity 100.0%; Pred. No. 2.8e-223;
Matches 774; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGGCTCTGCGCATGGAAATCCCTTACTCTACTGTGTAGCCTTACTGTTCTTCGCTCCA 60
Db 35 ATGGCTCTGCGCATGGAAATCCCTTACTCTACTGTGTAGCCTTACTGTTCTTCGCTCCA 94
QY 61 GATGCGGTGTAGCAGTCCCTCAGAAACCTTAAGTCTCTTGAACCCCTCCATGCAATAGA 120
Db 95 GATGCGGTGTAGCAGTCCCTCAGAAACCTTAAGTCTCTTGAACCCCTCCATGCAATAGA 154
QY 121 ATATTTAAAGAGAGAAATGTGACTTTTACATGTAATGGGAACAATTTCTTTGAAGTCAGT 180
Db 155 ATATTTAAAGAGAGAAATGTGACTTTTACATGTAATGGGAACAATTTCTTTGAAGTCAGT 214
QY 181 TCCACCAAAATGGTTCCCAAAATGGAGCCCTTTTCAAGAGAGACAAATTCAGTTTGAATATT 240
Db 215 TCCACCAAAATGGTTCCCAAAATGGAGCCCTTTTCAAGAGAGACAAATTCAGTTTGAATATT 274
QY 241 GTGAATGCCAAATTTTGAAGACAGTGGAGAAATACAATGTGAGCAACCAAGTTTAATGAG 300
Db 275 GTGAATGCCAAATTTTGAAGACAGTGGAGAAATACAATGTGAGCAACCAAGTTTAATGAG 334
QY 301 AGTGAACCTGTGTACTGTGAAGTCTTCAAGTACTGGCTGCTCTTTCAGGCGCTTGTGAG 360
Db 335 AGTGAACCTGTGTACTGTGAAGTCTTCAAGTACTGGCTGCTCTTTCAGGCGCTTGTGAG 394
QY 361 GTGTGTATGGAGGCGCCAGCCCTCTTCTCAAGTGGCATGGTTGGAGGAATGGGATGTG 420
Db 395 GTGTGTATGGAGGCGCCAGCCCTCTTCTCAAGTGGCATGGTTGGAGGAATGGGATGTG 454
QY 421 TACAAGTGTATCTATTATTAAGATGGTGAAGTCTTCAAGTACTGTGTATGAGAACCAAC 480
Db 455 TACAAGTGTATCTATTATTAAGATGGTGAAGTCTTCAAGTACTGTGTATGAGAACCAAC 514
QY 481 ATCTCCATTACAAATGCCACAGTTTGAAGACAGTGGAACTTACTACTGTACGGGCAAGTG 540
Db 515 ATCTCCATTACAAATGCCACAGTTTGAAGACAGTGGAACTTACTACTGTACGGGCAAGTG 574
QY 541 TGGCAGCTGAGTATGAGTCTGAGCCCTCAACATTTACTGTAAATAAAAGCTCCGCTGAG 600
Db 575 TGGCAGCTGAGTATGAGTCTGAGCCCTCAACATTTACTGTAAATAAAAGCTCCGCTGAG 634
QY 601 AAGTACTGGCTACAAATTTTATCCCATTTGTTGGTGGTGAATCTGTGTTGCTGTGACACA 660
Db 635 AAGTACTGGCTACAAATTTTATCCCATTTGTTGGTGGTGAATCTGTGTTGCTGTGACACA 694
QY 661 GGATTTATTTATCTCAACTCAGCAGCAGGTGCATTTCTTCTTGAAGATTAAGAAACCCAGG 720
Db 695 GGATTTATTTATCTCAACTCAGCAGCAGGTGCATTTCTTCTTGAAGATTAAGAAACCCAGG 754
QY 721 AAAGGCTTCAGACTTCTGAACCCACATCTCTAAGCCAAACCCCAAAACCAACTGA 774

QY 61 GATGGCTGTAGCAGTCCCTCAGAAACCTAAGGTCTCTTGAACCCCTCCATGGAATAGA 120
 Db |||||
 QY 167 GATGGCTGTAGCAGTCCCTCAGAAACCTAAGGTCTCTTGAACCCCTCCATGGAATAGA 226
 Db |||||
 QY 121 ATATTTAAAGAGAGAAATGTGACTCTTACATGTAAATGGGAAACAATTTCTTTGAAAGTCAGT 180
 Db |||||
 QY 227 ATATTTAAAGAGAGAAATGTGACTCTTACATGTAAATGGGAAACAATTTCTTTGAAAGTCAGT 286
 Db |||||
 QY 181 TCCACAAATGTTCCCAATGGCAGCCTTTTCAGAGAGACAAATTCAGTTTCAATATT 240
 Db |||||
 QY 287 TCCACAAATGTTCCCAATGGCAGCCTTTTCAGAGAGACAAATTCAGTTTCAATATT 346
 Db |||||
 QY 241 GTGAATGCCAAATTTGAAGACAGTGGAGAAATACAAATGTACAGCCCAACAAAGTTAATGAG 300
 Db |||||
 QY 347 GTGAATGCCAAATTTGAAGACAGTGGAGAAATACAAATGTACAGCCCAACAAAGTTAATGAG 406
 Db |||||
 QY 301 AGTGAACTGTGTACCTGGAAGTCTTTCAGTCACTGGCTCTCTTCAGGCTCTGCTGAG 360
 Db |||||
 QY 407 AGTGAACTGTGTACCTGGAAGTCTTTCAGTCACTGGCTCTCTTCAGGCTCTGCTGAG 466
 Db |||||
 QY 361 GTGGTGTAGGAGGGCCAGCCCTCTTCTCAGGTGCCATGGTTGGAGAACTGGGATGTG 420
 Db |||||
 QY 467 GTGGTGTAGGAGGGCCAGCCCTCTTCTCAGGTGCCATGGTTGGAGAACTGGGATGTG 526
 Db |||||
 QY 421 TACAAGTGTATCTATTATAGAGTGGTGAAGCTCTCAGTACTGGTATGTAGAACCAAC 480
 Db |||||
 QY 527 TACAAGTGTATCTATTATAGAGTGGTGAAGCTCTCAGTACTGGTATGTAGAACCAAC 586
 Db |||||
 QY 481 ATCTCCATTACAATGCCACAGTTGAAGACAGTGGAACTTACTTCTAGGGCAAGTG 540
 Db |||||
 QY 587 ATCTCCATTACAATGCCACAGTTGAAGACAGTGGAACTTACTTCTAGGGCAAGTG 646
 Db |||||
 QY 541 TGGCAGTGGACTATGACTCTGAGCCCTCAACATTTACTGTATAAAGTCTCCGCTGAG 600
 Db |||||
 QY 647 TGGCAGTGGACTATGACTCTGAGCCCTCAACATTTACTGTATAAAGTCTCCGCTGAG 706
 Db |||||
 QY 601 AAGTACTGGCTACAAATTTTATCCCATTTGTTGGTGGTATCTGTTGCTGTGGACACA 660
 Db |||||
 QY 707 AAGTACTGGCTACAAATTTTATCCCATTTGTTGGTGGTATCTGTTGCTGTGGACACA 766
 Db |||||
 QY 661 GGATTATTTACTCAACTCAGCAGCAGTCAATTTCTTTGAAGATTGAAGAACCCAGG 720
 Db |||||
 QY 767 GGATTATTTACTCAACTCAGCAGCAGTCAATTTCTTTGAAGATTGAAGAACCCAGG 826
 Db |||||
 QY 721 AAAGGCTTCAGACTTCTGAACCCACATCTTAAGCCAAACCCCAAAACCACTGA 774
 Db |||||
 QY 827 AAAGGCTTCAGACTTCTGAACCCACATCTTAAGCCAAACCCCAAAACCACTGA 880
 Db |||||
 RESULT 7
 ID AAA34813
 XX AAA34813 standard; DNA; 1198 BP.
 AC AAA34813;
 XX
 DT 28-JUL-2000 (first entry)
 XX
 DE Human adenosine receptor related polynucleotide SEQ ID NO:2502.
 XX
 KW Human; adenosine receptor; low adenosine anti-sense oligonucleotide;
 KW phosphothioate; impaired respiration; inflammation; allergy;
 KW allergic disease; bronchoconstriction; inhibitor; anti-inflammatory;
 KW antiallergic; antiasthmatic; cytosolic; analgesic; impaired airway;
 KW lung disease; ischemic condition; pulmonary vasoconstriction; asthma;
 KW respiratory distress syndrome; pain; cystic fibrosis; emphysema;
 KW pulmonary hypertension; chronic obstructive pulmonary disease; COPD;
 KW cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.
 XX
 OS Homo sapiens.
 XX
 PN W0200009525-A2.
 XX

PD 24-FEB-2000.
 XX
 PF 03-AUG-1999; 99WO-US017712.
 XX
 PR 03-AUG-1998; 98US-0095212P.
 XX
 PA (UYEC-) UNIV EAST CAROLINA.
 XX
 PI Nyce JW;
 XX
 DR WPI; 2000-205971/18.
 XX
 PT New antisense oligonucleotides useful for treating e.g. pulmonary
 PT vasoconstriction, inflammation, allergies, asthma, hypertension,
 PT bronchitis, emphysema, respiratory distress syndrome, ischemia or
 PT cancers.
 XX
 PS Disclosure; Page 655; 1343pp; English.
 XX
 CC The present invention describes a new composition comprising an antisense
 CC oligonucleotide (ON) with low adenosine (up to 15%), which targets
 CC nucleic acids involved in bronchoconstriction, allergies, and/or
 CC inflammation. The ON can have anti-inflammatory, antiallergic,
 CC antiasthmatic, cytostatic and analgesic activities. The compositions are
 CC useful for the treatment of diseases associated with inflammation,
 CC impaired airways, including lung disease and diseases whose secondary
 CC effects afflict the lungs of a subject. They can be used for treating
 CC e.g. ischemic conditions, pulmonary vasoconstriction, allergies, asthma,
 CC impaired respiration, respiratory distress syndrome, pain, cystic
 CC fibrosis, pulmonary hypertension, emphysema, chronic obstructive
 CC pulmonary disease (COPD), and cancers such as leukaemias, lymphomas,
 CC carcinomas, and cancers which may metastasize to the lungs, including
 CC breast and prostate cancer. The reduction of the adenosine content of
 CC the A-containing ONs reduces side effects. The A-containing ONs break down with the
 CC release of deoxyadenosine which activates adenosine receptors causing
 CC bronchoconstriction and inflammation. AAA32313 to AAA35312 represent the
 CC nucleotide sequences given in the sequence listing from the present
 CC invention, which correspond to SEQ ID NO:1 to 2815, and then the last 185
 CC sequences are also called SEQ ID NO:1 to 185, but the sequences differ
 CC from the previously named sequences. SEQ ID NO:11 to 1680 (AAA32323 to
 CC AAA33992) are specifically claimed ONs from the present invention. N.B.
 CC Sequences given in the disclosure of the present invention do not match
 CC up with their corresponding SEQ ID NO: sequences given in the sequence
 CC listing
 XX
 SQ Sequence 1198 BP; 389 A; 243 C; 245 G; 321 T; 0 U; 0 Other;
 Query Match 100.0%; Score 774; DB 3; Length 1198;
 Best Local Similarity 100.0%; Pred. No. 3e-223;
 Matches 774; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ATGGCTCTGCGCATGGAAATCCCTACTCTACTGTGTAGCTTACTGTCTTCTGCTCCA 60
 Db |||||
 QY 107 ATGGCTCTGCGCATGGAAATCCCTACTCTACTGTGTAGCTTACTGTCTTCTGCTCCA 166
 Db |||||
 QY 61 GATGGCTGTAGCAGTCCCTCAGAAACCTAAGGTCTCTTGAACCCCTCCATGGAATAGA 120
 Db |||||
 QY 167 GATGGCTGTAGCAGTCCCTCAGAAACCTAAGGTCTCTTGAACCCCTCCATGGAATAGA 226
 Db |||||
 QY 121 ATATTTAAAGAGAGAAATGTGACTCTTACATGTAAATGGGAAACAATTTCTTTGAAAGTCAGT 180
 Db |||||
 QY 227 ATATTTAAAGAGAGAAATGTGACTCTTACATGTAAATGGGAAACAATTTCTTTGAAAGTCAGT 286
 Db |||||
 QY 181 TCCACAAATGTTCCCAATGGCAGCCTTTTCAGAGAGACAAATTCAGTTTCAATATT 240
 Db |||||
 QY 287 TCCACAAATGTTCCCAATGGCAGCCTTTTCAGAGAGACAAATTCAGTTTCAATATT 346
 Db |||||
 QY 241 GTGAATGCCAAATTTGAAGACAGTGGAGAAATACAAATGTACAGCCCAACAAAGTTAATGAG 300
 Db |||||
 QY 347 GTGAATGCCAAATTTGAAGACAGTGGAGAAATACAAATGTACAGCCCAACAAAGTTAATGAG 406
 Db |||||
 QY 301 AGTGAACTGTGTACCTGGAAGTCTTTCAGTCACTGGCTCTCTTCAGGCTCTGCTGAG 360
 Db |||||

Db 407 AGTGAACCTGTGTACCTGGAACTCTTCAGTGAAGTGTCTCTCAGGCTCTGTGTAG 466
 QY 361 GTGGTGTATGGAGGCGCCCTCTCTCTCAGGTGCCATGGTTGGAGCAACTGGGATGTG 420
 Db 467 GTGGTGTATGGAGGCGCCCTCTCTCTCAGGTGCCATGGTTGGAGCAACTGGGATGTG 526
 QY 421 TACAAGGTGATCTATTATAGGATGGTGAAGCTCTCAAGTACTGGTATGAGACCAAC 480
 Db 527 TACAAGGTGATCTATTATAGGATGGTGAAGCTCTCAAGTACTGGTATGAGACCAAC 586
 QY 481 ATCTCCATTACAATGCGCACAGTTGAAGACAGTGGAACTTACTGTACGGGCAAAAGTG 540
 Db 587 ATCTCCATTACAATGCGCACAGTTGAAGACAGTGGAACTTACTGTACGGGCAAAAGTG 646
 QY 541 TGGAGCTGGTACTAGCTTCAGCCCTTCAACATTAAGTCTTAATAAGCTTCGGGTGAG 600
 Db 647 TGGAGCTGGTACTAGCTTCAGCCCTTCAACATTAAGTCTTAATAAGCTTCGGGTGAG 706
 QY 601 AAGTACTGGTACTCAATTTTATCCCATTTGTGTGTGTGTTCTTGTGGACACA 660
 Db 707 AAGTACTGGTACTCAATTTTATCCCATTTGTGTGTGTGTTCTTGTGGACACA 766
 QY 661 GGATTATTATCTCACTCAGCAGAGTCAATTTCTTGAAGTATGAGAAACAGG 720
 Db 767 GGATTATTATCTCACTCAGCAGAGTCAATTTCTTGAAGTATGAGAAACAGG 826
 QY 721 AAAGCTTCAGACTTCTGAACCCACATCTTAAGCCAAACCCCAAACTCA 774
 Db 827 AAAGCTTCAGACTTCTGAACCCACATCTTAAGCCAAACCCCAAACTCA 880

RESULT 8

AAF20935
 ID AAF20935 standard; DNA; 1198 BP.

AC AAF20935;

DI 14-MAR-2001 (first entry)

DE Human high affinity IgE receptor polynucleotide fragment #2502.

KW Low adenosine antisense oligonucleotide; phosphorothioate; allergy;
 KW human; airway disorder; bronchoconstriction; lung inflammation;
 KW surfactant depletion; respiratory; bronchodilator; antiinflammatory;
 KW immunosuppressive; antilastmatic; analgesic; hypotensive; cytostatic;
 KW respiratory obstruction; pulmonary obstruction; impeded respiration;
 KW surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;
 KW respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;
 KW pulmonary hypertension; emphysema; pulmonary transplantation rejection;
 KW chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
 KW cancer; ss.

OS Homo sapiens.

XX WO200062736-A2.

PN 26-OCT-2000.

XX 24-MAR-2000; 2000WO-US008020.

PF 06-APR-1999; 99US-0127958P.

XX (UYEC-) UNIV EAST CAROLINA.

PA (NYCE/) NYCE J W.

XX Nyce JW;

PI WPI; 2000-679539/66.

DR Low adenosine (A) content antisense oligonucleotides which do not trigger
 PT adenosine receptors during metabolism, useful e.g. for treating cancers
 PT and respiratory obstructions.

XX

PS Disclosure; Page 138; 1592pp; English.

XX The present invention describes low adenosine (A) content antisense
 CC oligonucleotides and compositions (I) comprising them. In the antisense
 CC oligonucleotides the A is replaced by a 'universal' or alternative base.
 CC (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,
 CC immunosuppressive, antilastmatic, hypotensive and cytostatic activities.
 CC The antisense oligonucleotides and (I) can be used to down-regulate the
 CC expression and/or activity of target polypeptides associated with the
 CC lung/respiratory disorders and malignancies, such as stimulating and
 CC activating peptide factors and transmitters, transcription factors,
 CC immunoglobulins and antibodies, antibody receptors, cytokines and
 CC chemokines, endogenously produced specific and non-specific enzymes,
 CC binding proteins, adhesion molecules and their receptors, cytokine and
 CC chemokine receptors, adenosine receptors, bradykinin receptors, central
 CC nervous system (CNS) and peripheral nervous and non-nervous system
 CC receptors, CNS and peripheral nervous and non-nervous system peptide
 CC transmitters, defensins, growth factors, vasoactive peptides and
 CC receptors, binding proteins and malignancy associated proteins. The
 CC antisense oligonucleotides may be used in this way to treat disorders
 CC including respiratory obstruction (especially pulmonary obstruction
 CC and/or bronchoconstriction) and/or lung inflammation, allergy(ies) and/or
 CC surfactant hypoproduction which are associated with a disease or
 CC condition selected from pulmonary vasoconstriction, inflammation,
 CC allergies, asthma, impeded respiration, respiratory distress syndrome
 CC (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary
 CC hypertension, emphysema, chronic obstructive pulmonary disease (COPD),
 CC pulmonary transplantation rejection, pulmonary infections, bronchitis,
 CC and/or cancer. AAF18434 to AAF21543 represent human polynucleotide
 CC fragments and antisense oligonucleotides used in the exemplification of
 CC the present invention

XX SQ Sequence 1198 BP; 389 A; 243 C; 245 G; 321 T; 0 U; 0 Other;

Query Match 100.0%; Score 774; DB 3; Length 1198;

Best Local Similarity 100.0%; Pred. No. 3e-223;

Matches 774; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGCTCTGCTCCATGGAAATCCCTTACTCTACTGTGTAGCTTACTGTTCGTCCA 60
 Db 107 ATGCTCTGCTCCATGGAAATCCCTTACTCTACTGTGTAGCTTACTGTTCGTCCA 166
 QY 61 GATCGCTGTAGCAGTCCCTCAGAACCTTAAGCTCTCTTGAACTCCATCGAATAGA 120
 Db 167 GATCGCTGTAGCAGTCCCTCAGAACCTTAAGCTCTCTTGAACTCCATCGAATAGA 226
 QY 121 ATATTTAAAGGAGAGAAATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCA 180
 Db 227 ATATTTAAAGGAGAGAAATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCA 286
 QY 181 TCCACCAATGGTTCCCAATGGCAGCTTTCAGAGAGACAAATTCAGTTTGAATATT 240
 Db 287 TCCACCAATGGTTCCCAATGGCAGCTTTCAGAGAGACAAATTCAGTTTGAATATT 346
 QY 241 GTGAATGCCAAATTTGAAGACAGTGGAGAAATACAAATGTGAGCAACCAAGTTAATGAG 300
 Db 347 GTGAATGCCAAATTTGAAGACAGTGGAGAAATACAAATGTGAGCAACCAAGTTAATGAG 406
 QY 301 AGTGAACCTGTGTACTGGAGTCTTCAGTCACTGGCTGCTCTTCAGGCTCTGTGTAG 360
 Db 407 AGTGAACCTGTGTACTGGAGTCTTCAGTCACTGGCTGCTCTTCAGGCTCTGTGTAG 466
 QY 361 GTGCTGATGGAGGCCAGCCCTCTTCTCAGTGCATGGTTGGAGGAACCTGGGATGTG 420
 Db 467 GTGCTGATGGAGGCCAGCCCTCTTCTCAGTGCATGGTTGGAGGAACCTGGGATGTG 526
 QY 421 TAGAAGTGTATCTATTATAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCAAC 480
 Db 527 TACAAGTGTATCTATTATAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCAAC 586
 QY 481 ATCTCCATTACAATGCGCACAGTTGAAGACAGTGGAACTTACTGTACGGGCAAAAGTG 540
 Db 587 ATCTCCATTACAATGCGCACAGTTGAAGACAGTGGAACTTACTGTACGGGCAAAAGTG 646

QY 541 TGGCAGCTGACTATGAGTCTCAGCCCTCAACATTACTGTATAAAGCTCCGGTGAG 600
 Db 647 TGGCAGCTGACTATGAGTCTCAGCCCTCAACATTACTGTATAAAGCTCCGGTGAG 706
 QY 601 AAGTACTGGCTACAAATTTTATCCCATGTTGGTGGTGAATCTGTTGCTGTGGACACA 660
 Db 707 AAGTACTGGCTACAAATTTTATCCCATGTTGGTGGTGAATCTGTTGCTGTGGACACA 766
 QY 661 GGATTATTATCTCAACTCAGCAGCAGCTCACTTCTCTTGAAGATTGAAGAACCCAGG 720
 Db 767 GGATTATTATCTCAACTCAGCAGCAGCTCACTTCTCTTGAAGATTGAAGAACCCAGG 826
 QY 721 AAAGCTTCAGACTTCTGAACCCACATCTTAAGCCAAACCCCAAAAACAACCTGA 774
 Db 827 AAAGCTTCAGACTTCTGAACCCACATCTTAAGCCAAACCCCAAAAACAACCTGA 880

RESULT 9

AAF77692

ID AAF77692 standard; cDNA; 1198 BP.

XX AC

AAF77692;

XX DT

29-MAY-2001 (first entry)

XX XX

Human wild-type Fc epsilonRIalpha chain coding sequence.

XX DE

Human; Fc epsilonRIbeta chain; immunoglobulin E; allergy; atopy;

XX KW

conjunctivitis; rhinitis; anaphylaxis; urticaria; angioedema; ss.

XX KW

Homo sapiens.

XX OS

WO200121816-A1.

XX FN

29-MAR-2001.

XX PD

21-SEP-2000; 2000WO-US025877.

XX PF

21-SEP-1999; 99US-0154924P.

XX PR

(ISIS-) ISIS INNOVATION LTD.

XX PA

(BETH-) BETH ISRAEL DEACONESS MEDICAL CENT.

XX PA

Kinet J, Donnadiu E, Jouvin M, Cookson W, Moffatt MF;

XX PI

WPI; 2001-266077/27.

XX DR

Inhibiting expression of high affinity receptors for immunoglobulin (Ig)

XX PT

E, in cell or in subject to treat atopy; anaphylaxis mediated by IGE, by

XX PT

contacting cell or administering to subject, a Fc epsilon chain variant.

XX PS

Disclosure; Page 52; 55pp; English.

XX PS

The present invention describes a method of inhibiting the expression of

XX CC

the Fc epsilonRI receptor by contacting a cell expressing it with an

XX CC

Fc epsilonRIbeta chain variant. The Fc epsilon receptor is a high affinity

XX CC

receptor for immunoglobulin E. The method is useful in the treatment of

XX CC

allergic conditions such as rhinitis, conjunctivitis, atopy, anaphylaxis,

XX CC

urticaria and angioedema. The present sequence is the wild-type human

XX CC

Fc epsilonRIalpha chain coding sequence

XX CC

Sequence 1198 BP; 389 A; 243 C; 245 G; 321 T; 0 U; 0 Other;

XX SQ

Db 167 GATGGCGTGTAGCAGTCCCTCAGAACCTAAGGTCCTCTTGAACCTCCATGGAATAGA 226
 QY 121 ATATTTAAAGGAGAGAAATGTGACTCTTACATGTAATGGGAAACAATTTCTTTGAAGTCAGT 180
 Db 227 ATATTTAAAGGAGAGAAATGTGACTCTTACATGTAATGGGAAACAATTTCTTTGAAGTCAGT 286
 QY 181 TCACCAAAATGTTCCACAATGGCAGCTTTTCAAGAGAGACAAATCAAGTTGAATATT 240
 Db 287 TCACCAAAATGTTCCACAATGGCAGCTTTTCAAGAGAGACAAATCAAGTTGAATATT 346
 QY 241 GTGAATGCCAAATTTGAAGACAGTGGAGAATAACAATGTGACACACAACAAGTTAATGAG 300
 Db 347 GTGAATGCCAAATTTGAAGACAGTGGAGAATAACAATGTGACACACAACAAGTTAATGAG 406
 QY 301 AGTGAACCTGTGTACTTGGAACTCTTCACTGACTGGCTCTCTTTCAGGCTCTGCTGAG 360
 Db 407 AGTGAACCTGTGTACTTGGAACTCTTCACTGACTGGCTCTCTTTCAGGCTCTGCTGAG 466
 QY 361 GTGGTGTATGGAGGGCCAGCCCTCTTCTCAGTGGCCATGTTGGAGGAACCTGGATGTG 420
 Db 467 GTGGTGTATGGAGGGCCAGCCCTCTTCTCAGTGGCCATGTTGGAGGAACCTGGATGTG 526
 QY 421 TACAAGGTGATCTATTATAAGGATGGTGAAGCTCTCAAGTACTTGTATGAGAACCAAC 480
 Db 527 TACAAGGTGATCTATTATAAGGATGGTGAAGCTCTCAAGTACTTGTATGAGAACCAAC 586
 QY 481 ATCTCCATTAACAATGCCACAGTTGAAGACAGTGGAACTACTACTGTACGGGAAAGTG 540
 Db 587 ATCTCCATTAACAATGCCACAGTTGAAGACAGTGGAACTACTACTGTACGGGAAAGTG 646
 QY 541 TGGCAGCTGAGTATGAGTCTGAGCCCTCAACATTACTGTATAAAGCTCCCGGTGAG 600
 Db 647 TGGCAGCTGAGTATGAGTCTGAGCCCTCAACATTACTGTATAAAGCTCCCGGTGAG 706
 QY 601 AAGTACTGGCTACAAATTTTATCCCATGTTGGTGGTGAATCTGTTGCTGTGGACACA 660
 Db 707 AAGTACTGGCTACAAATTTTATCCCATGTTGGTGGTGAATCTGTTGCTGTGGACACA 766
 QY 661 GGATTATTATCTCAACTCAGCAGCAGTCACTTTCTTGAAGATTGAAGAACCCAGG 720
 Db 767 GGATTATTATCTCAACTCAGCAGCAGTCACTTTCTTGAAGATTGAAGAACCCAGG 826
 QY 721 AAAGCTTCAGACTTCTGAACCCACATCTTAAGCCAAACCCCAAAAACAACCTGA 774
 Db 827 AAAGCTTCAGACTTCTGAACCCACATCTTAAGCCAAACCCCAAAAACAACCTGA 880

RESULT 10

AAF24912/c

ID AAF24912 standard; DNA; 1198 BP.

XX XX

AC AAF24912;

XX XX

DT 30-APR-2001 (first entry)

XX XX

Complement sequence of a human Fc epsilon receptor alpha-chain gene.

XX DE

Fc epsilon receptor; Fc epsilonR; immunoglobulin E; IGE; atopic disease; luminescence inducing protein; allergy; hyper IGE syndrome; internal parasite infection; B cell neoplasia; ss.

XX KW

Homo sapiens.

XX OS

WO200104310-A1.

XX FN

18-JAN-2001.

XX PD

13-JUL-2000; 2000WO-US019070.

XX PF

13-JUL-1999; 99US-0143612P.

XX XX

02-MAR-2000; 2000US-0186412P.

XX PR

XX XX

Query Match 100.0%; Score 774; DB 4; Length 1198;

Best Local Similarity 100.0%; Pred. No. 3e-223;

Matches 774; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGCTTCCTGCCATGAATCCCTACTCTACTGTGTAGCCTTACTGTCTTCGCTCCA 60

Db 107 ATGGCTTCCTGCCATGAATCCCTACTCTACTGTGTAGCCTTACTGTCTTCGCTCCA 166

QY 61 GATGGCGTGTAGCAGTCCCTCAGAACCTAAGGTCCTCTTGAACCTCCATGGAATAGA 120

601 AAGTACTGGCTACAAATTTTATCCCATTTGTTGGTGGTATTTCTTGTCTGGACACA 660
492 AAGTACTGGCTACAAATTTTATCCCATTTGTTGGTGGTATTTCTTGTCTGGACACA 433
661 GGATTATTATCTCACTCAGCAGCAGTCCACATTTCTTGAAGATTAAAGAGAACAGG 720
432 GGATTATTATCTCACTCAGCAGCAGTCCACATTTCTTGAAGATTAAAGAGAACAGG 373
721 AAAGGCTTCAGATTTCTGAACCCACATCTTAAGCCAAACCCCAAAACAACACTGA 774
372 AAAGGCTTCAGATTTCTGAACCCACATCTTAAGCCAAACCCCAAAACAACACTGA 319

RESULT 11
AAF24911
ID AAF24911 standard; DNA; 1198 BP.
XX
AC AAF24911;
XX
DT 30-APR-2001 (first entry)
XX
DE Nucleotide sequence of a human Fc epsilon receptor alpha-chain.
XX
KW Fc epsilon receptor; Fc epsilonR; immunoglobulin E; IgE; atopic disease;
KW luminescence inducing protein; allergy; hyper IgE syndrome;
KW internal parasite infection; B cell neoplasia; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 107..880
FT /*tag= a
FT /product= "Fc epsilon receptor alpha-chain"
XX
PN WO200104310-A1.
XX
PD 18-JAN-2001.
XX
PF 13-JUL-2000; 2000WO-US019070.
XX
PR 13-JUL-1999; 99US-0143612P.
PR 02-MAR-2000; 2000US-0186412P.
XX
PA (HESK-) HESKA CORP.
XX
PI Weber ER, Wood KV, Hall MP;
XX
DR WPI; 2001-103082/11.
XX
PT A fusion protein, comprising an Fc epsilon receptor domain and a
PT luminescence inducing protein domain that induces a LP substrate to emit
PT light when contacted with the LP domain, useful for detecting
XX immunoglobulin (Ig) E.
PS Claim 17; Page 58-59; 105pp; English.
XX
CC The present sequence encodes a human Fc epsilon receptor (FcepsilonR)
CC alpha-chain protein, that binds to immunoglobulin (Ig) E. The FcepsilonR
CC domain is used to produce a fusion protein, which also comprises a
CC luminescence inducing protein domain that induces a substrate to emit
CC light when contacted with the luminescence inducing protein domain. The
CC fusion protein may be used to detect IgE. It may also be used to identify
CC a compound capable of inhibiting FcepsilonR protein activity. IgE
CC antibody production is indicative of diseases such as allergies, atopic
CC disease, hyper IgE syndrome, internal parasite infections and B cell
CC neoplasia. Detection of IgE production in an animal following therapy is
CC indicative of the efficacy of the treatment, for example when using
XX treatments intended to disrupt IgE production
XX
SQ Sequence 1198 BP; 389 A; 243 C; 245 G; 321 T; 0 U; 0 Other;

PA (HESK-) HESKA CORP.
PA (PROM-) PROMEGA CORP.
XX
PI Weber ER, Wood KV, Hall MP;
XX
DR WPI; 2001-103082/11.
XX
PT A fusion protein, comprising an Fc epsilon receptor domain and a
PT luminescence inducing protein domain that induces a LP substrate to emit
PT light when contacted with the LP domain, useful for detecting
XX immunoglobulin (Ig) E.
XX
PS Example; Page 61; 105pp; English.
XX
CC The present sequence represents the complement of a human Fc epsilon
CC receptor (FcepsilonR) alpha-chain protein, that binds to immunoglobulin
CC (Ig) E. The FcepsilonR domain is used to produce a fusion protein, which
CC also comprises a luminescence inducing protein domain that induces a
CC substrate to emit light when contacted with the luminescence inducing
CC protein domain. The fusion protein may be used to detect IgE. It may also
CC be used to identify a compound capable of inhibiting FcepsilonR protein
CC activity. IgE antibody production is indicative of diseases such as
CC allergies, atopic disease, hyper IgE syndrome, internal parasite
CC infections and B cell neoplasia. Detection of IgE production in an animal
CC following therapy is indicative of the efficacy of the treatment, for
CC example when using treatments intended to disrupt IgE production
XX
SQ Sequence 1198 BP; 321 A; 245 C; 243 G; 389 T; 0 U; 0 Other;

Query Match 100.0%; Score 774; DB 5; Length 1198;
Best Local Similarity 100.0%; Pred. No. 3e-223;
Matches 774; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 ATGGCTCTCCGATGAATCCCTACTCTACTGTGTAGCTTACTGTCTTCTCGTCCA 60
1092 ATGGCTCTCCGATGAATCCCTACTCTACTGTGTAGCTTACTGTCTTCTCGTCCA 1033
61 GATGGCGTTAGCAGTCCCTCAGAAACCTTAAGTCTCTTGAACCTCCATGGAATAGA 120
1032 GATGGCGTTAGCAGTCCCTCAGAAACCTTAAGTCTCTTGAACCTCCATGGAATAGA 973
121 ATATTAAAGGAGAGATGACTCTTACATGTAATGGAACAAATTTCTTGAAGTCAGT 180
972 ATATTAAAGGAGAGATGACTCTTACATGTAATGGAACAAATTTCTTGAAGTCAGT 913
181 TCCACCAATATGGTTCCAAATGGCAGCCTTTCAGAAGAGACAAATTCAGTTGAATATT 240
912 TCCACCAATATGGTTCCAAATGGCAGCCTTTCAGAAGAGACAAATTCAGTTGAATATT 853
241 GTGAATCCCAATTTGAAGACAGTGGAGATACAAATGTGAGCAACCAACCAAGTTAATGAG 300
852 GTGAATCCCAATTTGAAGACAGTGGAGATACAAATGTGAGCAACCAACCAAGTTAATGAG 793
301 AGTGAACCTGTGTACCTGGAAGTCTTCAAGTCACTGGCTGCTCTTCAAGGCTCTGCTGAG 360
792 AGTGAACCTGTGTACCTGGAAGTCTTCAAGTCACTGGCTGCTCTTCAAGGCTCTGCTGAG 733
361 GTGCTGATGAGGCGCCAGCCCTCTTCTCAGTGCCATGGTGGAGGAATCGGATG 420
732 GTGCTGATGAGGCGCCAGCCCTCTTCTCAGTGCCATGGTGGAGGAATCGGATG 673
421 TACAGGTGATCTATTATAGGATGGTGAAGTCTCAAGTACTGTTGATGAGAACCAAC 480
672 TACAGGTGATCTATTATAGGATGGTGAAGTCTCAAGTACTGTTGATGAGAACCAAC 613
481 ATCTCCATTACAAATGGCACAGTTGAAGACAGTGGAACTTACTACTACGGGCAAGTG 540
612 ATCTCCATTACAAATGGCACAGTTGAAGACAGTGGAACTTACTACTACGGGCAAGTG 553
541 TGGCAGCTGGACATGAGTCTGAGCCCTCAGCACTTACTGTAATAAAGCTCCGCGTGA 600
552 TGGCAGCTGGACATGAGTCTGAGCCCTCAGCACTTACTGTAATAAAGCTCCGCGTGA 493

Query Match 100.0%; Score 774; DB 5; Length 1198;
Best Local Similarity 100.0%; Pred. No. 3e-223;
Matches 774; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGCTCTGCGCATGGAATCCCTACTCTACTGTGTGTAGCTTACTGTCTTCTCGCTCCA 60
DB 107 ATGGCTCTGCGCATGGAATCCCTACTCTACTGTGTGTAGCTTACTGTCTTCTCGCTCCA 166

QY 61 GATGCGGTGTAGAGTCCCTCAGAAACCTAAGTCTCTTGAACCTCCATGGAATAGA 120
DB 167 GATGCGGTGTAGAGTCCCTCAGAAACCTAAGTCTCTTGAACCTCCATGGAATAGA 226

QY 121 ATATTAAAGAGAGAGAGTGTGACTCTTACATGTATGGAACAAATTTCTTGAAGTCAGT 180
DB 227 ATATTAAAGAGAGAGAGTGTGACTCTTACATGTATGGAACAAATTTCTTGAAGTCAGT 286

QY 181 TCCACCAATGGTTCCCAATGGGAGGCTTTTCAGAGAGACAAATTCAGTTTGAATATT 240
DB 287 TCCACCAATGGTTCCCAATGGGAGGCTTTTCAGAGAGACAAATTCAGTTTGAATATT 346

QY 241 GTGAATGCCAATTTGAGACAGTGGAGATACAAATGTGAGCAACCAAGTTAATGAG 300
DB 347 GTGAATGCCAATTTGAGACAGTGGAGATACAAATGTGAGCAACCAAGTTAATGAG 406

QY 301 AGTGAACCTGTGTACCTGGAGTCTTCAAGTGTGCTGCTCTTCAAGGCTCTGCTGAG 360
DB 407 AGTGAACCTGTGTACCTGGAGTCTTCAAGTGTGCTGCTCTTCAAGGCTCTGCTGAG 466

QY 361 GTGTGTATGAGGCGGAGCCCTCTTCTCAGTGTGCTGCTGCTGCTGCTGCTGCTG 420
DB 467 GTGTGTATGAGGCGGAGCCCTCTTCTCAGTGTGCTGCTGCTGCTGCTGCTGCTG 526

QY 421 TACAAGTGTATCTATTATAGATGTGTGAAGTCTTCAAGTGTGCTGCTGCTGCTGCTG 480
DB 527 TACAAGTGTATCTATTATAGATGTGTGAAGTCTTCAAGTGTGCTGCTGCTGCTGCTG 586

QY 481 ATCTCCATTCAGATGAGTGTGAAGTGTGAAGTGTGAAGTGTGAAGTGTGAAGTGTG 540
DB 587 ATCTCCATTCAGATGAGTGTGAAGTGTGAAGTGTGAAGTGTGAAGTGTGAAGTGTG 646

QY 541 TGGCAGCTGGAATGATGCTGAGCCCTCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTG 600
DB 647 TGGCAGCTGGAATGATGCTGAGCCCTCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTG 706

QY 601 AAGTACTGGCTACAAATTTTATCCCATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 660
DB 707 AAGTACTGGCTACAAATTTTATCCCATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 766

QY 661 GGATTTATTTATCTCACTGAGCAGCAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 720
DB 767 GGATTTATTTATCTCACTGAGCAGCAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 826

QY 721 AAAGGCTTCAGATCTTCTGAACCCACATCTTCAAGCCAAACCCCAAAACCACTGA 774
DB 827 AAAGGCTTCAGATCTTCTGAACCCACATCTTCAAGCCAAACCCCAAAACCACTGA 880

RESULT 12

ABL67793

XX ABL67793 standard; DNA; 1198 BP.

XX AC ABL67793;

XX AC ABL67793;

XX DT 15-MAY-2002 (first entry)

XX DE Oesophagus cancer related gene sequence SEQ ID NO:6130.

XX DE Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;

XX DE stomach; lung; prostate; pancreas; cacinoma; antitumour; cancerous;

XX DE cytostatic; gene therapy; antineoplastic; Wilms tumour; adenocarcinoma;

XX DE gene; ds.

XX DE Homo sapiens.

XX OS

XX
PN
XX
XX
PD
XX
XX
PF
XX
30-MAY-2001; 2001WO-US010838.
05-JUN-2000; 2000US-0209473P.
05-JUN-2000; 2000US-0209531P.
18-SEP-2000; 2000US-0233133P.
18-SEP-2000; 2000US-0233617P.
20-SEP-2000; 2000US-0234009P.
20-SEP-2000; 2000US-0234034P.
20-SEP-2000; 2000US-0234052P.
22-SEP-2000; 2000US-0234509P.
22-SEP-2000; 2000US-0234567P.
25-SEP-2000; 2000US-0234923P.
25-SEP-2000; 2000US-0234924P.
25-SEP-2000; 2000US-0235077P.
25-SEP-2000; 2000US-0235082P.
25-SEP-2000; 2000US-0235134P.
25-SEP-2000; 2000US-0235280P.
26-SEP-2000; 2000US-0235637P.
26-SEP-2000; 2000US-0235638P.
27-SEP-2000; 2000US-0235711P.
27-SEP-2000; 2000US-0235720P.
27-SEP-2000; 2000US-0235840P.
27-SEP-2000; 2000US-0235863P.
28-SEP-2000; 2000US-0236028P.
28-SEP-2000; 2000US-0236032P.
28-SEP-2000; 2000US-0236033P.
28-SEP-2000; 2000US-0236034P.
28-SEP-2000; 2000US-0236109P.
28-SEP-2000; 2000US-0236111P.
29-SEP-2000; 2000US-0236842P.
29-SEP-2000; 2000US-0236891P.
02-OCT-2000; 2000US-0237173P.
02-OCT-2000; 2000US-0237278P.
02-OCT-2000; 2000US-0237294P.
02-OCT-2000; 2000US-0237295P.
02-OCT-2000; 2000US-0237316P.
03-OCT-2000; 2000US-0237425P.
03-OCT-2000; 2000US-0237598P.
03-OCT-2000; 2000US-0237604P.
03-OCT-2000; 2000US-0237606P.
03-OCT-2000; 2000US-0237608P.
01-NOV-2000; 2000US-0244867P.
01-NOV-2000; 2000US-0245084P.

(AVAL-) AVALON PHARM.

Young PE, Augustus M, Carter KC, Ebner R, Endress G, Horrigan S;
Soppet DR, Weaver Z;
WPI; 2002-188264/24.

Screening for anti-neoplastic agent involves exposing cells to a chemical agent to be tested for anti-neoplastic activity, and determining a change in expression of a gene of a signature gene set.

Claim 1; SEQ ID NO 6130; 44pp; English.

The present invention describes a method (M1) for screening for an anti-neoplastic agent. The method involves exposing cells to a chemical agent to be tested for anti-neoplastic activity, determining a change in expression of at least one gene (I) of a signature gene set, where (I) comprises a sequence (S) selected from 847 sequences (given in ABL6166 to ABL70110), or is at least 95% identical to (S), where a change in expression is indicative of anti-neoplastic activity. (I) has cytostatic activity and can be used in gene therapy. M1 can be used for screening an anti-neoplastic agent, and can be used for producing a product which is the data collected with respect to the anti-neoplastic agent as a result

of MI, and the data is sufficient to convey the chemical structure and/or properties of the agent. MI can be used in the treatment of cancer such as colon, breast, stomach, lung, thyroid, esophageal, ovarian, kidney, prostate or pancreatic cancer, adenocarcinoma, carcinoma, clear cell cancer, infiltrating ductal cancer, infiltrating lobular cancer, squamous cell carcinoma, neuroendocrine carcinoma, papillary carcinoma and Wilms' tumor

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Query Match      100.0%; Score 774; DB 6; Length 1198;
Best Local Similarity 100.0%; Pred. No. 3e-23;
Matches 774; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

Qy	1	ATGGCTCTCGGCATGGAAATCCCTTACTCTACTGTGTAGCCTTACTGTCTTCGTCCTCA	60
Db	107	ATGGCTCTCGGCATGGAAATCCCTTACTCTACTGTGTAGCCTTACTGTCTTCGTCCTCA	166
Qy	61	GATGGCGTGTATAGCAGTCCTCAGAAACCTTAAGTCTCCCTTGAACCCCTCCATGGAAATAGA	120
Db	167	GATGGCGTGTATAGCAGTCCTCAGAAACCTTAAGTCTCCCTTGAACCCCTCCATGGAAATAGA	226
Qy	121	ATATTTTAAAGGAGAGAAATGTGACTCTTACATGTAAATGGGAACAATTTCTTTGAAGTCAGT	180
Db	227	ATATTTTAAAGGAGAGAAATGTGACTCTTACATGTAAATGGGAACAATTTCTTTGAAGTCAGT	286
Qy	181	TCCACCAAAATGGTTCCAAATGGCAGCCCTTTCAGAAGAGACAAATTCAGTTTGAATATT	240
Db	287	TCCACCAAAATGGTTCCAAATGGCAGCCCTTTCAGAAGAGACAAATTCAGTTTGAATATT	346
Qy	241	GTCAATGCCAAATTTTCAGACAGTGGAGAAATACAAATGTGAGCACCAACAAGTTAATGAG	300
Db	347	GTGAAATGCCAAATTTTGAAGCAGTGGAGAAATACAAATGTGAGCACCAACAAGTTAATGAG	406
Qy	301	AGTGAACCTGTGTACCTGGAAGTCTTCAGTGACTGGTGTCTCTTCAGGCGCTCTGCTGAG	360
Db	407	AGTGAACCTGTGTACCTGGAAGTCTTCAGTGACTGGTGTCTCTTCAGGCGCTCTGCTGAG	466
Qy	361	GTGGTATGAGGGCCAGCCCTCTCTCTCAGTGCATGGTTCGAGGAACTGGGATGTC	420
Db	467	GTGGTATGAGGGCCAGCCCTCTCTCTCAGTGCATGGTTCGAGGAACTGGGATGTC	526
Qy	421	TACAAGTGATCTATTATTAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCAAC	480
Db	527	TACAAGTGATCTATTATTAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCAAC	586
Qy	481	ATCTCCATTAACAAATGCCACAGTTGAGACAGTGGAACTACTACTCTAGCGGCAAGTGC	540
Db	587	ATCTCCATTAACAAATGCCACAGTTGAGACAGTGGAACTACTACTCTAGCGGCAAGTGC	646
Qy	541	TGGCAGCTGGACTATCAGTCTGAGCCCTCAACATTACTGTAAATAAAGCTCCGCGTGAG	600
Db	647	TGGCAGCTGGACTATCAGTCTGAGCCCTCAACATTACTGTAAATAAAGCTCCGCGTGAG	706
Qy	601	AAGTACTGGGTACAATTTTTTATCCCATTTGTTGGTGTGATCTGTGTTGCTGTGGACACA	660
Db	707	AAGTACTGGGTACAATTTTTTATCCCATTTGTTGGTGTGATCTGTGTTGCTGTGGACACA	766
Qy	661	GGATTAATTTATCTCACTCAGCAGCAGGTGCATNTTCTCTTGAAGATTAAGAGAACCCAGG	720
Db	767	GGATTAATTTATCTCACTCAGCAGCAGGTGCATNTTCTCTTGAAGATTAAGAGAACCCAGG	826
Qy	721	AAAGGCTTCAGACTTCTTGAAACCCACATCTCTTAAGCCAAACCCCAAAAACACTGA	774
Db	827	AAAGGCTTCAGACTTCTTGAAACCCACATCTCTTAAGCCAAACCCCAAAAACACTGA	880

RESULT 13

ABZ96629

ID ABZ96629 standard; DNA; 1198 BP.

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AC ABZ96629;
yy

17-OCT-2003 (first entry)

Human high affinity IgE receptor oligonucleotide fragment.

Human, antisense; lung dysfunction; nasal airway dysfunction; antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic; antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy; antisense gene therapy; respiratory; lung; adenosine sensitivity; adenosine receptor; bronchodilation; bronchoconstriction; lung allergy; lung inflammation; respiratory disease; ds.

Homo sapiens.

WO200285308-A2.

31-OCT-2002.

23-APR-2002; 2002WO-US013135.

24-APR-2001; 2001US-0286137P.

(EPIG-) EPIGENESIS PHARM INC.

Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D; Miller S, Tang L, Shahabuddin S;

WPI; 2003-229219/22.

Pharmaceutical composition for treating ailments associated with impaired respiration, has oligo(s) antisense to specific gene(s) or its corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or ubiquinone.

Disclosure; SEQ ID NO 11871; 872bp; English.

The invention relates to a novel pharmaceutical composition, which has a first active agent comprising an oligonucleotide antisense to the initiation codon, coding region, 5' or 3' end genomic flanking regions, 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of junctions of genes encoding a polypeptide associated with lung and/or nasal airway dysfunction and a second active agent comprising an antiinflammatory steroid and ubiquinone. A composition of the invention has antiinflammatory, antiallergic, antiasthmatic, hypotensive, immunosuppressive, and cytostatic activity. The composition may have a use in antisense gene therapy. The composition is useful for treating or preventing a respiratory, lung or malignant disease or condition, also for enhancing the prophylactic or therapeutic respiratory effect of an antiinflammatory steroid in a subject, for reducing or depleting levels of, or reducing sensitivity to adenosine, reducing levels of adenosine receptor, producing bronchodilation, increasing levels of ubiquinone or lung surfactant in a subject's tissue, or treating bronchoconstriction, lung inflammation, lung allergies, or a respiratory disease or condition.

Note: the sequence data for this patent is not represented in the printed specification, but was obtained in electronic format directly from WIPO at http://wipo.int/pub/published_pct_sequences

Sequence 1198 BP; 389 A; 243 C; 245 G; 321 T; 0 U; 0 Other;

	Query Match	100.0%	Score 774	DB 7	Length 1198
	Best Local Similarity	100.0%	Prod. No. 3e-223		
	Matches 774	Conservative 0	Mismatches 0	Indels 0	Gaps 0
QY	1	ATGGCTCTGCGCATGGGAATCCCTTACTCTACTGTGTGTAGCCTTACTGTGTTCTTCGCTCCA	60		
DB	107	ATGGCTCTGCGCATGGGAATCCCTTACTCTACTGTGTGTAGCCTTACTGTGTTCTTCGCTCCA	166		
QY	61	GATGGCGGTGTAGCAGTCCCTCAGAAACCTAAGTCTCCTTGAACCTCCATGGAATAGA	120		
DB	167	GATGGCGGTGTAGCAGTCCCTCAGAAACCTAAGTCTCCTTGAACCTCCATGGAATAGA	226		
QY	121	ATATTAAAGGAGAGAAATGTGACTCTTACATGTAATGGACAAATTTCTTTGAAGTCAGT	180		
DB	227	ATATTAAAGGAGAGAAATGTGACTCTTACATGTAATGGACAAATTTCTTTGAAGTCAGT	286		

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QY 181 TCACCAAAATGGTTCCCAATGGCGAGCCCTTTGAGAGAGACAAAATTCAGTTTGAATATT 240
Db 287 TCACCAAAATGGTTCCCAATGGCGAGCCCTTTGAGAGAGACAAAATTCAGTTTGAATATT 346
QY 241 GTGAATGCCAAATTTGAAGACAGTGGAGAAATACAAATGTCAGCACCACCAAGTTAATGAG 300
Db 347 GTGAATGCCAAATTTGAAGACAGTGGAGAAATACAAATGTCAGCACCACCAAGTTAATGAG 406
QY 301 AGTGAACCTGTGTACTGGAAGTCTTTCAGTGACTGGCTGCTCCTTCAGGCTCTGCTGAG 360
Db 407 AGTGAACCTGTGTACTGGAAGTCTTTCAGTGACTGGCTGCTCCTTCAGGCTCTGCTGAG 466
QY 361 GTGTGTATGGAGGGCCAGCCCTCTTCTCAGGTGCCATGTTGGAGAACTGGGATGTG 420
Db 467 GTGTGTATGGAGGGCCAGCCCTCTTCTCAGGTGCCATGTTGGAGAACTGGGATGTG 526
QY 421 TACAGGTGATCTATTATTAAGGATGGTGAAGTCTCTCAAGTACTGATGAGAACCAAC 480
Db 527 TACAGGTGATCTATTATTAAGGATGGTGAAGTCTCTCAAGTACTGATGAGAACCAAC 586
QY 481 ATCTCCATTACAAATGCCACAGTTTGAAGACAGTGGAACTTACTACTGTACGGGCAAGTG 540
Db 587 ATCTCCATTACAAATGCCACAGTTTGAAGACAGTGGAACTTACTACTGTACGGGCAAGTG 646
QY 541 TGGCAGCTGGACTATGAGTCTGAGCCCTCAACATTTACTGTAATAAAGTCTCGGTGAG 600
Db 647 TGGCAGCTGGACTATGAGTCTGAGCCCTCAACATTTACTGTAATAAAGTCTCGGTGAG 706
QY 601 AAGTACTGGCTACAAATTTTATCCCATTTGTTGGTGGTATCTTGTGTGGACACA 660
Db 707 AAGTACTGGCTACAAATTTTATCCCATTTGTTGGTGGTATCTTGTGTGGACACA 766
QY 767 GGATTATTATCTCAACTCAGCAGGTGCATTTCTTCTTGAAGATTAAAGAACCCAGG 826
Db 827 AAAGGCTTCAGACTTCTGAACCCACATCTTAAGCCAAACCCCAAAACCAACTGA 880

RESULT 14
ID ADB85535
XX ADB85535 standard; cDNA; 1198 BP.
AC ADB85535;
DT 04-DEC-2003 (first entry)
XX Homo sapiens.
Human immunoglobulin E high affinity receptor (FcERI) alpha subunit cDNA.
alpha subunit; high affinity receptor for immunoglobulin E; FcERI;
mast cell; basophil; histamine; serotonin; allergic condition;
antiallergic; allergic response; drug screening assay; immunoglobulin E;
human; Gere; ss.
OS Homo sapiens.
Key Location/Qualifiers
CDS 107..880
/*tag= a
/product= "Human FcERI receptor"
/transl_except= (767..769, aa:Glu)
/transl_except= (863..865, aa:Asp)
XX US6602983-B1.
XX 05-AUG-2003.
XX 22-SEP-1994; 94US-00310902.
XX 24-FEB-1988; 88US-00160457.

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PR 30-OCT-1991; 91US-00785127.
PR 29-MAY-1993; 93US-00066640.
XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX Kinet JP, Kochan JP;
XX WPI; 2003-669612/63.
XX P-PSDB; ADB85536.
XX
PR New alpha subunit of the human high affinity receptor for immunoglobulin
PR E polypeptides, useful as antagonists to prevent allergic response, as
PR reagents in drug screening assays, or for monitoring immunoglobulin E
PR levels in patients.
XX Claim 1; Fig 1; 9pp; English.
XX
CC This invention relates to a novel purified polypeptide corresponding to
CC the alpha subunit of the human high affinity receptor for immunoglobulin
CC E (FcERI) and the DNA sequence which encodes it. The receptor of the
CC invention is found exclusively on mast cells, basophils and related
CC cells. Activation of the receptor triggers the release of preformed
CC mediators such as histamine and serotonin which may result in allergic
CC conditions. Compounds which modulate FcERI activity may have antiallergic
CC activity. The polypeptide of the invention may be useful as an antagonist
CC for preventing allergic response, as a reagent in drug screening assays,
CC as a therapeutic or for monitoring immunoglobulin E levels in patients.
CC The DNA sequences may be useful for producing the polypeptide or for
CC synthesizing cDNA sequences to construct DNA probes used in diagnostic
CC assays. The present sequence is the cDNA sequence encoding the alpha
CC subunit of the human FcERI receptor of the invention.
XX
SQ Sequence 1198 BP; 389 A; 243 C; 245 G; 321 T; 0 U; 0 Other;
Query Match 100.0%; Score 774; DB 9; Length 1198;
Best Local Similarity 100.0%; Pred. No. 3e-223;
Matches 774; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGGCTCTGCGCATGGAAATCCCTTACTCTACTGTGTAGCCTTACTGTTCGCTCCA 60
Db 107 ATGGCTCTGCGCATGGAAATCCCTTACTCTACTGTGTAGCCTTACTGTTCGCTCCA 166
QY 61 GATGGCGTGTAGCAGTCCCTCAGAAACCTTAAGGTCTCTTGAACCTCCATGGAATAGA 120
Db 167 GATGGCGTGTAGCAGTCCCTCAGAAACCTTAAGGTCTCTTGAACCTCCATGGAATAGA 226
QY 121 ATATTTAAAGGAGAGAAATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGT 180
Db 227 ATATTTAAAGGAGAGAAATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGT 286
QY 181 TCCACCAAAATGGTTCCCAATGGCGAGCCCTTTGAGAGAGACAAAATTCAGTTTGAATATT 240
Db 287 TCCACCAAAATGGTTCCCAATGGCGAGCCCTTTGAGAGAGACAAAATTCAGTTTGAATATT 346
QY 241 GTGAATGCCAAATTTGAAGACAGTGGAGAAATACAAATGTCAGCACCACCAAGTTAATGAG 300
Db 347 GTGAATGCCAAATTTGAAGACAGTGGAGAAATACAAATGTCAGCACCACCAAGTTAATGAG 406
QY 301 AGTGAACCTGTGTACTGGAAGTCTTTCAGTGACTGGCTGCTCCTTCAGGCTCTGCTGAG 360
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QY 361 GTGTGTATGGAGGGCCAGCCCTCTTCTCAGGTGCCATGTTGGAGAACTGGGATGTG 420
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QY 421 TACAGGTGATCTATTATTAAGGATGGTGAAGTCTCTCAAGTACTGATGAGAACCAAC 480
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QY 541 TGGCAGCTGGACTATGACTGCTGAGCCCTCACATTACTGTAAATAAAGCTCCGCTGAG 600
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 QY 601 AAGTACTGGCTACAATTTTATCCCAATGTTGGTGGTGAATCTGTTGCTGTGGACACA 660
 Db 707 AAGTACTGGCTACAATTTTATCCCAATGTTGGTGGTGAATCTGTTGCTGTGGACACA 766
 QY 661 GGATTATTATCTCAACTCAGCAGGCTCACATTTCTCTTGAAGATTAAAGAACCCAGG 720
 Db 767 GGATTATTATCTCAACTCAGCAGGCTCACATTTCTCTTGAAGATTAAAGAACCCAGG 826

QY 721 AAAGGCTTCAGACTTCTGAACCCACATCTTAAGCCAAACCCCAAAACCAACTGA 774

Db 827 AAAGGCTTCAGACTTCTGAACCCACATCTTAAGCCAAACCCCAAAACCAACTGA 880

RESULT 15

AAA34816
 ID AAA34816 standard; DNA; 21742 BP.

XX
 AC AAA34816;

XX 28-JUL-2000 (first entry)

DE Human adenosine receptor related polynucleotide SEQ ID NO:2505.

XX Human; adenosine receptor; low adenosine antisense oligonucleotide;
 KW phosphorothioate; impaired respiration; inflammation; allergy;
 KW allergic disease; bronchoconstriction; inhibitor; antiinflammatory;
 KW antiallergic; antiasthmatic; cytostatic; analgesic; impaired airway;
 KW lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;
 KW respiratory distress syndrome; pain; cystic fibrosis; emphysema;
 KW pulmonary hypertension; chronic obstructive pulmonary disease; COPD;
 KW cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.

XX Homo sapiens.

OS WO200009525-A2.

XX 24-FEB-2000.

XX 03-AUG-1999; 99WO-US017712.

XX 03-AUG-1998; 98US-0095212P.

XX (UYEC-) UNIV EAST CAROLINA.

XX Nyce JW;

XX WPI; 2000-205971/18.

XX New antisense oligonucleotides useful for treating e.g. pulmonary
 PT vasoconstriction, inflammation, allergies, asthma, hypertension,
 PT bronchitis, emphysema, respiratory distress syndrome, ischemia or
 PT cancers.

PS Disclosure; Page 658-664; 1343pp; English.

XX The present invention describes a new composition comprising an antisense
 CC oligonucleotide (ON) with low adenosine (up to 15%), which targets
 CC nucleic acids involved in bronchoconstriction, allergies, and/or
 CC inflammation. The ON can have antiinflammatory, antiallergic,
 CC antiasthmatic, cytostatic and analgesic activities. The compositions are
 CC useful for the treatment of diseases associated with inflammation,
 CC impaired airways, including lung disease and diseases whose secondary
 CC effects afflict the lungs of a subject. They can be used for treating
 CC e.g. ischaemic conditions, pulmonary vasoconstriction, allergies, asthma,
 CC impaired respiration, respiratory distress syndrome, pain, cystic
 CC fibrosis, pulmonary hypertension, emphysema, chronic obstructive
 CC pulmonary disease (COPD), and cancers such as leukaemias, lymphomas,
 CC carcinomas, and cancers which may metastasize to the lungs, including

CC breast and prostate cancer. The reduction of the adenosine content of the
 CC ONs reduces side effects. The A-containing ONs break down with the
 CC release of deoxyadenosine which activates adenosine receptors causing
 CC bronchoconstriction and inflammation. AAA32313 to AAA35312 represent the
 CC nucleotide sequences given in the sequence listing from the present
 CC invention, which correspond to SEQ ID NO:1 to 2815, and then the last 185
 CC sequences are also called SEQ ID NO:1 to 185, but the sequences differ
 CC from the previously named sequences. SEQ ID NO:11 to 1680 (AAA32323 to
 CC AAA33992) are specifically claimed ONs from the present invention. N.B.
 CC Sequences given in the disclosure of the present invention do not match
 CC up with their corresponding SEQ ID NO: sequences given in the sequence
 CC listing

XX
 SQ Sequence 21742 BP; 6598 A; 4107 C; 4408 G; 6612 T; 0 U; 17 Other;

Query Match 100.0%; Score 774; DB 3; Length 21742;

Best Local Similarity 100.0%; Pred. No. 1.3e-222;

Matches 774; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGCTCTGCGCATGGAAATCCCTACTCTACTGTGTAGCCTTACTTCTTCGTCTCCA 60

Db 8459 ATGGCTCTGCGCATGGAAATCCCTACTCTACTGTGTAGCCTTACTTCTTCGTCTCCA 8518

QY 61 GATGCGGTGTAGCAGTCCCTCAGAAACCTTAAGTCTCTTGAACCTTCATCGAATAGA 120

Db 8519 GATGCGGTGTAGCAGTCCCTCAGAAACCTTAAGTCTCTTGAACCTTCATCGAATAGA 8578

QY 121 ATATTAAAGGAGAGAATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGT 180

Db 8579 ATATTAAAGGAGAGAATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGT 8638

QY 181 TCCACCAATGGTTCACAAATGGCAGCTTTCAGAGAGACAATTCAGTTTGAATATT 240

Db 8639 TCCACCAATGGTTCACAAATGGCAGCTTTCAGAGAGACAATTCAGTTTGAATATT 8698

QY 241 GTGAATGCCAAATTTGAAGACAGTGGAGAATACAAATGTTCAGACCAACCAAGTTAATGAG 300

Db 8699 GTGAATGCCAAATTTGAAGACAGTGGAGAATACAAATGTTCAGACCAACCAAGTTAATGAG 8758

QY 301 AGTGAACCTGTGTACTTGGAAAGTCTTCAGTACTGGTGTCTCTTCAGGCTCTGCTGAG 360

Db 8759 AGTGAACCTGTGTACTTGGAAAGTCTTCAGTACTGGTGTCTCTTCAGGCTCTGCTGAG 8818

QY 361 GTGGTGTAGTGGAGGGCCAGCCCTCTTCTCCTCAGTGGCATGTTGGAGGAACCTGGGATGTG 420

Db 8819 GTGGTGTAGTGGAGGGCCAGCCCTCTTCTCCTCAGTGGCATGTTGGAGGAACCTGGGATGTG 8878

QY 421 TACAAGTGTATCTATTATAGGATGTGAAGCTCTCAAGTACTGTATGAGAACCAAC 480

Db 8879 TACAAGTGTATCTATTATAGGATGTGAAGCTCTCAAGTACTGTATGAGAACCAAC 8938

QY 481 ATCTCCATTACAAATGCCACAGTTGAAGACAGTGGAAACCTTACTTCTGACGGCAAGTG 540

Db 8939 ATCTCCATTACAAATGCCACAGTTGAAGACAGTGGAAACCTTACTTCTGACGGCAAGTG 8998

QY 541 TGGCAGCTGGACTATGACTGCTGAGCCCTCACATTACTGTAAATAAAGCTCCGCTGAG 600

Db 8999 TGGCAGCTGGACTATGACTGCTGAGCCCTCACATTACTGTAAATAAAGCTCCGCTGAG 9058

QY 601 AAGTACTGGCTACAATTTTATCCCAATGTTGGTGGTGAATCTGTTGCTGTGGACACA 660

Db 9059 AAGTACTGGCTACAATTTTATCCCAATGTTGGTGGTGAATCTGTTGCTGTGGACACA 9118

QY 661 GGATTATTATCTCAACTCAGCAGGCTCACATTTCTCTTGAAGATTAAAGAACCCAGG 720

Db 9119 GGATTATTATCTCAACTCAGCAGGCTCACATTTCTCTTGAAGATTAAAGAACCCAGG 9178

QY 721 AAAGGCTTCAGACTTCTGAACCCACATCTTAAGCCAAACCCCAAAACCAACTGA 774

Db 9179 AAAGGCTTCAGACTTCTGAACCCACATCTTAAGCCAAACCCCAAAACCAACTGA 9232

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Tue Oct 12 09:19:26 2004

us-10-763-400-4.rng

Page 14

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

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Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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5: /cgn2_6/ptodata/2/ina/PCOTS COMB.seq.*
6: /cgn2_6/ptodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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5	774	100.0	774	4	US-09-944-277A-4
6	774	100.0	774	4	US-09-944-277A-5
7	774	100.0	1174	1	US-07-859-933-10
8	774	100.0	1174	3	US-09-103-663-10
9	774	100.0	1198	2	US-08-756-387B-1
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16	699	90.3	699	2	US-08-756-387B-7
17	699	90.3	699	4	US-09-285-873-7
18	699	90.3	699	4	US-09-944-277A-7
19	611	78.9	2955	4	US-08-897-956A-4
20	591	76.4	591	2	US-08-756-387B-10
21	591	76.4	591	4	US-09-285-873-10
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25	516	66.7	516	2	US-08-756-387B-12
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28 438.4 56.6 1015 3 US-09-015-734-1
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c 31 438.4 56.6 1015 4 US-09-515-311-3
32 435 56.2 765 3 US-09-015-734-4
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36 403.8 52.2 708 3 US-09-015-734-6
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c 39 403.8 52.2 708 4 US-09-515-311-8
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ALIGNMENTS

RESULT 1
US-08-756-387B-4
; Sequence 4, Application US/08756387B
; Patent No. 5945294
; GENERAL INFORMATION:
; APPLICANT: Frank, Glenn R.
; APPLICANT: Porter, James P.
; APPLICANT: Rushlow, Keith E.
; APPLICANT: Wasson, Donald L.
; TITLE OF INVENTION: Method to Detect IGE
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carol Talkington Verser, Ph.D.
; STREET: 1825 Sharp Point Drive
; CITY: Fort Collins
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80525
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: Windows 95
; SOFTWARE: WordPerfect for Windows, Version 7.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/756,387B
; FILING DATE: No. 5945294ember 26, 1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Verser, Carol Talkington
; REGISTRATION NUMBER: 37,459
; REFERENCE/DOCKET NUMBER: DI-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 970/493-7272
; TELEFAX: 970/484-9505
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 774 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..774
US-08-756-387B-4

Query Match 100.0%; Score 774; DB 2; Length 774;
Best Local Similarity 100.0%; Pred. No. 5.2e-246;
Matches 774; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Sequence 1, Appli
Sequence 3, Appli
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Sequence 1, Appli
Sequence 3, Appli

1 ATGGCTCTGCGATGGAATCCCTACTCTACTGTGTGTAGCTTACTGTCTTCCGCTCCA 60
Db
1 ATGGCTCTGCGATGGAATCCCTACTCTACTGTGTGTAGCTTACTGTCTTCCGCTCCA 60
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Db 121 ATATTAAAGGAGAGAAATGTGACTCTTACATGTATGGAACAAATTTCTTTGAAGTCAGT 180
QY 181 TCCACCAATGGTTCCCAANTGGGAGCCTTTCAGAGAGACAAATTCGAATTTGAATATT 240
Db 181 TCCACCAATGGTTCCCAANTGGGAGCCTTTCAGAGAGACAAATTCGAATTTGAATATT 240
QY 241 GTGAATGCCAAATTTGAAGACAGTGGAGAAATACAAATGTTCAGACCAACCAAGTTAATGAG 300
Db 241 GTGAATGCCAAATTTGAAGACAGTGGAGAAATACAAATGTTCAGACCAACCAAGTTAATGAG 300
QY 301 AGTGAACCTGTGTACTCTGGAAGTCTTTCAGTGAATCTTCTTCAAGGCTCTGTCTGAG 360
Db 301 AGTGAACCTGTGTACTCTGGAAGTCTTTCAGTGAATCTTCTTCAAGGCTCTGTCTGAG 360
QY 361 GTGGTGATGGAGGGCCAGCCCTCTTCTCAGGTGCCATGGTGGAGGAACCTGGATGTG 420
Db 361 GTGGTGATGGAGGGCCAGCCCTCTTCTCAGGTGCCATGGTGGAGGAACCTGGATGTG 420
QY 421 TACAAGGTGATCTATTATAAGGATGGTGAAGCTCTCAAGTACTGTATGAGAACCAAC 480
Db 421 TACAAGGTGATCTATTATAAGGATGGTGAAGCTCTCAAGTACTGTATGAGAACCAAC 480
QY 481 ATCTCCATTACAAATGCCACAGTTGAAGACAGTGGAACTTACTACTGTAGGGCAAGTG 540
Db 481 ATCTCCATTACAAATGCCACAGTTGAAGACAGTGGAACTTACTACTGTAGGGCAAGTG 540
QY 541 TGGCAGCTGGACTATGAGTCTGAGCCCTCAACATTTACTGTATTAAGGCTCCGCGTGAG 600
Db 541 TGGCAGCTGGACTATGAGTCTGAGCCCTCAACATTTACTGTATTAAGGCTCCGCGTGAG 600
QY 601 AAGTACTGGCTACAAATTTTATCCATTTCCATTTGTTGTGTGATCTGTGTGAGACACA 660
Db 601 AAGTACTGGCTACAAATTTTATCCATTTGTTGTGTGATCTGTGTGAGACACA 660
QY 661 GGATTTATTATCTCAACTCAGCAGCAGTCACTTCTCTTGAAGATTAAGAGAACCCAGG 720
Db 661 GGATTTATTATCTCAACTCAGCAGCAGTCACTTCTCTTGAAGATTAAGAGAACCCAGG 720
QY 721 AAAGGCTTCAGACTTCTGAACCCACATCTTAAGCCAAACCCCAAAACAACTGA 774
Db 721 AAAGGCTTCAGACTTCTGAACCCACATCTTAAGCCAAACCCCAAAACAACTGA 774

RESULT 2

US-08-756-387B-5/c
; Sequence 5, Application US/08756387B
; Patent No. 5945294
; GENERAL INFORMATION:
; APPLICANT: Frank, Glenn R.
; APPLICANT: Porter, James P.
; APPLICANT: Rushlow, Keith E.
; APPLICANT: Wassom, Donald L.
; TITLE OF INVENTION: Method to Detect Ige
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carol Talkington Verser, Ph.D.
; ADDRESSEE: Heskia Corporation
; STREET: 1825 Sharp Point Drive
; CITY: Fort Collins
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80525

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: WordPerfect for Windows, Version 7.0

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/756,387B
FILING DATE: No. 5945294ember 26, 1996
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
NAME: Verser, Carol Talkington
REGISTRATION NUMBER: 37,459
REFERENCE/DOCKET NUMBER: DI-1
TELECOMMUNICATION INFORMATION:

TELEPHONE: 970/493-7272

TELEFAX: 970/494-9505

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 774 nucleotides

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cdna

US-08-756-387B-5

Query Match 100.0%; Score 774; DB 2; Length 774;

Best Local Similarity 100.0%; Pred. No. 5.2e-246; Indels 0; Gaps 0;

Matches 774; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGCTCTGCGATGGAATCCCTACTCTACTGTGTGTAGCTTACTGTCTTCCGCTCCA 60
Db 774 ATGGCTCTGCGATGGAATCCCTACTCTACTGTGTGTAGCTTACTGTCTTCCGCTCCA 715
QY 61 GATGGCGTTAGCAGTCCCTCAGAAACCTTAAGTCTCTTGAACCTTCCATGGAATAGA 120
Db 714 GATGGCGTTAGCAGTCCCTCAGAAACCTTAAGTCTCTTGAACCTTCCATGGAATAGA 655
QY 121 ATATTAAAGGAGAGAAATGTGACTCTTACATGTATGGAACAAATTTCTTTGAAGTCAGT 180
Db 654 ATATTAAAGGAGAGAAATGTGACTCTTACATGTATGGAACAAATTTCTTTGAAGTCAGT 595
QY 181 TCCACCAATGGTTCCCAANTGGGAGCCTTTCAGAGAGACAAATTCGAATTTGAATATT 240
Db 594 TCCACCAATGGTTCCCAANTGGGAGCCTTTCAGAGAGACAAATTCGAATTTGAATATT 535
QY 241 GTGAATGCCAAATTTGAAGACAGTGGAGAAATACAAATGTTCAGACCAACCAAGTTAATGAG 300
Db 534 GTGAATGCCAAATTTGAAGACAGTGGAGAAATACAAATGTTCAGACCAACCAAGTTAATGAG 475
QY 301 AGTGAACCTGTGTACTCTGGAAGTCTTCAAGTACTGTGTGCTCTTCAAGGCTCTGTCTGAG 360
Db 474 AGTGAACCTGTGTACTCTGGAAGTCTTCAAGTACTGTGTGCTCTTCAAGGCTCTGTCTGAG 415
QY 361 GTGGTGATGGAGGGCCAGCCCTCTTCTCAGGTGCCATGGTGGAGGAACCTGGATGTG 420
Db 414 GTGGTGATGGAGGGCCAGCCCTCTTCTCAGGTGCCATGGTGGAGGAACCTGGATGTG 355
QY 421 TACAAGGTGATCTATTATAAGGATGGTGAAGCTCTCAAGTACTGTATGAGAACCAAC 480
Db 354 TACAAGGTGATCTATTATAAGGATGGTGAAGCTCTCAAGTACTGTATGAGAACCAAC 295
QY 481 ATCTCCATTACAAATGCCACAGTTGAAGACAGTGGAACTTACTACTGTAGGGCAAGTG 540
Db 294 ATCTCCATTACAAATGCCACAGTTGAAGACAGTGGAACTTACTACTGTAGGGCAAGTG 235
QY 541 TGGCAGCTGGACTATGAGTCTGAGCCCTCAACATTTACTGTATTAAGGCTCCGCGTGAG 600
Db 234 TGGCAGCTGGACTATGAGTCTGAGCCCTCAACATTTACTGTATTAAGGCTCCGCGTGAG 175
QY 601 AAGTACTGGCTACAAATTTTATCCATTTGTTGTGTGATCTGTGTGAGACACA 660
Db 174 AAGTACTGGCTACAAATTTTATCCATTTGTTGTGTGATCTGTGTGAGACACA 115

QY 661 GGATTATTATCTCAACTCAGCAGCAGTCACTTCTTGAAGATTAGAACACAG 720
DB 114 GGATTATTATCTCACTCAGCAGCAGTCACTTCTTGAAGATTAGAACACAG 55
QY 721 AAAGCTTCAGACTTCTGAACCCACATCTTAAGCCAAACCCAAACAACTGA 774
DB 54 AAAGCTTCAGACTTCTGAACCCACATCTTAAGCCAAACCCAAACAACTGA 1

RESULT 3

US-09-285-873-4
; Sequence 4, Application US/09285873
; Patent No. 6309832
; GENERAL INFORMATION:
; APPLICANT: Frank, Glenn R.
; APPLICANT: Porter, James P.
; APPLICANT: Rushlow, Keith E.
; APPLICANT: Wassom, Donald L.
; TITLE OF INVENTION: Method to Detect Ige
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carol Talkington Verser, Ph.D.
; ADDRESS: Heskia Corporation
; STREET: 1825 Sharp Point Drive
; CITY: Fort Collins
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80525
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: Windows 95
; SOFTWARE: WordPerfect for Windows, Version 7.0
; CURRENT APPLICATION DATA: US/09/285,873
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/756,387
; FILING DATE: No. 6309832, September 26, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Verser, Carol Talkington
; REGISTRATION NUMBER: 37,459
; REFERENCE/DOCKET NUMBER: DI-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 970/493-7272
; TELEFAX: 970/484-9505
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 774 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..774
US-09-285-873-4
Query Match 100.0%; Score 774; DB 4; Length 774;
Best Local Similarity 100.0%; Pred. No. 5.2e-246;
Matches 774; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGCTCTGCGATGGATCCCTACTCTACTGTGTAGCCTTACTGTCTTCTGCTCA 60
DB 1 ATGGCTCTGCGATGGATCCCTACTCTACTGTGTAGCCTTACTGTCTTCTGCTCA 60
QY 61 GATGCGGTGTAGCAGTCCCTCAGAACCTTAAGGTCTCTTGAACCCCTCATGGAATAGA 120
DB 61 GATGCGGTGTAGCAGTCCCTCAGAACCTTAAGGTCTCTTGAACCCCTCATGGAATAGA 120
QY 121 ATATTAAAGAGAGAGATGACTCTTACATGATCGGAACATTTCTTTGAAGTCAGT 180

DB 121 ATATTAAAGAGAGATGACTCTTACATGATCGGAACATTTCTTTGAAGTCAGT 180
QY 181 TCCACCAAAATGGTTCACAAATGAGAGCCCTTTCAGAGAGACAAATTCAGTTTGAATAT 240
DB 181 TCCACCAAAATGGTTCACAAATGAGAGCCCTTTCAGAGAGACAAATTCAGTTTGAATAT 240
QY 241 GTGAATGCCAAATTTGAAGACAGTGGAGAAATACAAATGTGACACCAACAAAGTTAATGAG 300
DB 241 GTGAATGCCAAATTTGAAGACAGTGGAGAAATACAAATGTGACACCAACAAAGTTAATGAG 300
QY 301 AGTGAACCTGTGTACTTGGAAAGTCTTTCAGTACTGCTGCTCTTTCAGGCTTCTGCTGAG 360
DB 301 AGTGAACCTGTGTACTTGGAAAGTCTTTCAGTACTGCTGCTCTTTCAGGCTTCTGCTGAG 360
QY 361 GTGGTGTATGAGAGGCCAGCCCTCTTCTCAGGTGCTTGGTTGGAGAACTTGGGATGTG 420
DB 361 GTGGTGTATGAGAGGCCAGCCCTCTTCTCAGGTGCTTGGTTGGAGAACTTGGGATGTG 420
QY 421 TACAAGGTGATCTATTATATAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCAAC 480
DB 421 TACAAGGTGATCTATTATATAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCAAC 480
QY 481 ATCTCCATTACAAATGCCAGTTGAAGACAGTGGAACTTACTTCTGTACGGGCAAGTG 540
DB 481 ATCTCCATTACAAATGCCAGTTGAAGACAGTGGAACTTACTTCTGTACGGGCAAGTG 540
QY 541 TGGCAGCTGACTATGAGTCTGAGCCCTCAACATTTACTGTATATAAAGCTCCGCTGAG 600
DB 541 TGGCAGCTGACTATGAGTCTGAGCCCTCAACATTTACTGTATATAAAGCTCCGCTGAG 600
QY 601 AAGTACTGGCTACAAATTTTATCCCATTTGGTGGTGAATCTGTTTCTGTGGACACA 660
DB 601 AAGTACTGGCTACAAATTTTATCCCATTTGGTGGTGAATCTGTTTCTGTGGACACA 660
QY 661 GGATTATTATCTCAACTCAGCAGCAGTCACTTCTTCTTGAAGATTAGAACACAGG 720
DB 661 GGATTATTATCTCAACTCAGCAGCAGTCACTTCTTCTTGAAGATTAGAACACAGG 720
QY 721 AAAGCTTCAGACTTCTGAAACCCACATCTTAAGCCAAACCCAAACAACTGA 774
DB 721 AAAGCTTCAGACTTCTGAAACCCACATCTTAAGCCAAACCCAAACAACTGA 774

RESULT 4

US-09-285-873-5/c
; Sequence 5, Application US/09285873
; Patent No. 6309832
; GENERAL INFORMATION:
; APPLICANT: Frank, Glenn R.
; APPLICANT: Porter, James P.
; APPLICANT: Rushlow, Keith E.
; APPLICANT: Wassom, Donald L.
; TITLE OF INVENTION: Method to Detect Ige
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carol Talkington Verser, Ph.D.
; ADDRESS: Heskia Corporation
; STREET: 1825 Sharp Point Drive
; CITY: Fort Collins
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80525
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: Windows 95
; SOFTWARE: WordPerfect for Windows, Version 7.0
; CURRENT APPLICATION DATA: US/09/285,873
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA: US/08/756,387

FILING DATE: NO. 6309832ember 26, 1996

ATTORNEY/AGENT INFORMATION:

NAME: Verser, Carol Talkington

REGISTRATION NUMBER: 37,459

REFERENCE/DOCKET NUMBER: DI-1

TELECOMMUNICATION INFORMATION:

TELEPHONE: 970/493-7272

TELEFAX: 970/484-9505

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 774 nucleotides

TYPE: nucleic acid

STRADEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cdna

US-09-285-873-5

Query Match 100.0%; Score 774; DB 4; Length 774;
Best Local Similarity 100.0%; Pred. No. 5.2e-246;
Matches 774; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 ATGGCTCTGCCATGAATCCCTACTCTACTGTGTGTAGCTTACTGTCTTCGCTCCA 60
Db 774 ATGGCTCTGCCATGAATCCCTACTCTACTGTGTGTAGCTTACTGTCTTCGCTCCA 715

QY 61 GATGCGGTGTAGCAGTCCCTCAGAACTTAAGTCTCCTTGAACCCCTCCATGAATAGA 120
Db 714 GATGCGGTGTAGCAGTCCCTCAGAACTTAAGTCTCCTTGAACCCCTCCATGAATAGA 655

QY 121 ATATTAAAGAGAGAGATGTGACTCTTACATGTATATGGAACTTCTTTTGAAGTCAGT 180
Db 654 ATATTAAAGAGAGAGATGTGACTCTTACATGTATATGGAACTTCTTTTGAAGTCAGT 595

QY 181 TCCACCAAAATGGTTCACAAATGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 240
Db 594 TCCACCAAAATGGTTCACAAATGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 535

QY 241 GTGAATGCCAAATTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 300
Db 534 GTGAATGCCAAATTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 475

QY 301 AGTGAACCTGTGTACCTGGAAGTCTTCAAGTGTGCTCTTCAAGGCTCTGCTGAG 360
Db 474 AGTGAACCTGTGTACCTGGAAGTCTTCAAGTGTGCTCTTCAAGGCTCTGCTGAG 415

QY 361 GTGTGTATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 420
Db 414 GTGTGTATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 355

QY 421 TACAAGGTGATCTATTATAGGATGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 480
Db 354 TACAAGGTGATCTATTATAGGATGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 295

QY 481 ATCTCCATTAACAATGCCAGTGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540
Db 294 ATCTCCATTAACAATGCCAGTGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 235

QY 541 TGGCAGCTGAGCTATGAGTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 600
Db 234 TGGCAGCTGAGCTATGAGTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 175

QY 601 AAGTACTGGCTACAAATTTTATATCCATTTTGTGGTGTGATCTGTGTTGCTGTGACACA 660
Db 174 AAGTACTGGCTACAAATTTTATATCCATTTTGTGGTGTGATCTGTGTTGCTGTGACACA 115

QY 661 GGATTTATTTATCTCAACTCAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 720
Db 114 GGATTTATTTATCTCAACTCAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 55

QY 721 AAGGCTTCAGACTTCTGAACCCCAATCTTAAGCCCAACCCCAACCCCAACCCCAACCTGA 774
Db 54 AAGGCTTCAGACTTCTGAACCCCAATCTTAAGCCCAACCCCAACCCCAACCCCAACCTGA 1
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RESULT 5

US-09-944-277A-4

Sequence 4, Application US/09944277A

Patent No. 6682894

GENERAL INFORMATION:

APPLICANT: Frank, Glenn R.

Porter, James P.

Rushlow, Keith E.

Wassom, Donald L.

TITLE OF INVENTION: Method to Detect Ige

NUMBER OF SEQUENCES: 13

CORRESPONDENCE ADDRESS:

ADDRESSES: Carol Talkington Verser, Ph.D.

Heska Corporation

STREET: 1825 Sharp Point Drive

CITY: Fort Collins

STATE: Colorado

COUNTRY: USA

ZIP: 80525

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: Windows 95

SOFTWARE: WordPerfect for Windows, Version 7.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/944,277A

FILING DATE: 30-Aug-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/285,873

FILING DATE: 1999-03-31

ATTORNEY/AGENT INFORMATION:

NAME: Verser, Carol Talkington

REGISTRATION NUMBER: 37,459

REFERENCE/DOCKET NUMBER: DI-1

TELECOMMUNICATION INFORMATION:

TELEPHONE: 970/493-7272

TELEFAX: 970/484-9505

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 774 nucleotides

TYPE: nucleic acid

STRADEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cdna

FEATURE:

NAME/KEY: CDS

LOCATION: 1..774

SEQUENCE DESCRIPTION: SEQ ID NO: 4:

US-09-944-277A-4

Query Match

Best Local Similarity 100.0%; Score 774; DB 4; Length 774;

Matches 774; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 ATGGCTCTGCCATGAATCCCTACTCTACTGTGTGTAGCTTACTGTGTAGCTTACTGTCTTCGCTCCA 60
Db 1 ATGGCTCTGCCATGAATCCCTACTCTACTGTGTGTAGCTTACTGTGTAGCTTACTGTCTTCGCTCCA 60

QY 61 GATGCGGTGTAGCAGTCCCTCAGAACTTAAGTCTCCTTGAACCCCTCCATGAATAGA 120
Db 61 GATGCGGTGTAGCAGTCCCTCAGAACTTAAGTCTCCTTGAACCCCTCCATGAATAGA 120

QY 121 ATATTAAAGAGAGAGATGTGACTCTTACATGTATATGGAACTTCTTTTGAAGTCAGT 180
Db 121 ATATTAAAGAGAGAGATGTGACTCTTACATGTATATGGAACTTCTTTTGAAGTCAGT 180

QY 181 TCCACCAAAATGGTTCACAAATGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 240
Db 181 TCCACCAAAATGGTTCACAAATGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 240

QY 241 GTGAATGCCAAATTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 300
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Db 241 GTGAATGCAAAATTTGAAGACAGTGGAGAAATACAAATGTGAGCAACCAAGTAAATGAG 300
Qy 301 AGTGAACCTGTGACCTGGAAGTCTTTCAGTGACCTGGCTGCTCTTCAGGCTCTGCTGAG 360
Db 301 AGTGAACCTGTGACCTGGAAGTCTTTCAGTGACCTGGCTGCTCTTCAGGCTCTGCTGAG 360
Qy 361 GTGGTGTGAGGGCCAGCCCTCTTCTCAGGTGCCATGGTTGGAGAACTGGGATGTG 420
Db 361 GTGGTGTGAGGGCCAGCCCTCTTCTCAGGTGCCATGGTTGGAGAACTGGGATGTG 420
Qy 421 TACAGAGTGATCTATTATAGGAGTGGAGCTCTCAAGTACTGATGAGACCAAC 480
Db 421 TACAGAGTGATCTATTATAGGAGTGGAGCTCTCAAGTACTGATGAGACCAAC 480
Qy 481 ATCTCCATTACAAATGGCCACAGTTTGAAGACAGTGGAACTTACTGTACGGGCAAGTG 540
Db 481 ATCTCCATTACAAATGGCCACAGTTTGAAGACAGTGGAACTTACTGTACGGGCAAGTG 540
Qy 541 TGGCAGCTGACTATGCTGAGCCCTCAACATTTACTGATTAATAAGCTCCGCTGAG 600
Db 541 TGGCAGCTGACTATGCTGAGCCCTCAACATTTACTGATTAATAAGCTCCGCTGAG 600
Qy 601 AAGTACTGGCTACAAATTTTTTATCCCATTTGTTGGTGGTGAATCTGTTTGTGTGACACA 660
Db 601 AAGTACTGGCTACAAATTTTTTATCCCATTTGTTGGTGGTGAATCTGTTTGTGTGACACA 660
Qy 661 GGATATTATCTCAACTCAGCAGCTGACATTTCTTCTGAGATTAAGAGAACGAG 720
Db 661 GGATATTATCTCAACTCAGCAGCTGACATTTCTTCTGAGATTAAGAGAACGAG 720
Qy 721 AAAGGCTTCAGACTTCTGAACCCACATCTTAAGCCAAACCCCAACCAACTGA 774
Db 721 AAAGGCTTCAGACTTCTGAACCCACATCTTAAGCCAAACCCCAACCAACTGA 774

RESULT 6

US-09-944-277A-5/c
; Sequence 5, Application US/09944277A
; Patent No. 6682894
; GENERAL INFORMATION:

APPLICANT: Frank, Glenn R.
Porter, James P.
Rushlow, Keith E.
Wasson, Donald L.
TITLE OF INVENTION: Method to Detect Ige
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Carol Talkington Verser, Ph.D.
Heska Corporation
STREET: 1825 Sharp Point Drive
CITY: Fort Collins
STATE: Colorado
COUNTRY: USA
ZIP: 80525

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: WordPerfect for Windows, Version 7.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/944,277A
FILING DATE: 30-Aug-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/285,873
FILING DATE: 1999-03-31
ATTORNEY/AGENT INFORMATION:
NAME: Verser, Carol Talkington
REGISTRATION NUMBER: 37,459
REFERENCE/DOCKET NUMBER: DI-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 970/493-7272

TELEFAX: 970/484-9505
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 774 nucleotides
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-944-277A-5
Query Match 100.0%; Score 774; DB 4; Length 774;
Best Local Similarity 100.0%; Pred. No. 5.2e-246; Indels 0; Gaps 0;
Matches 774; Conservative 0; Mismatches 0;
Qy 1 ATGGCTCTCTGCCATGGAAATCCCTTACTTACTGTGTGTAGCCCTTACTTCTTTCGCTCCA 60
Db 774 ATGGCTCTCTGCCATGGAAATCCCTTACTTACTGTGTGTAGCCCTTACTTCTTTCGCTCCA 715
Qy 61 GATGGCTGTGTAGCAGTCCCTCAGAAACCTTAAGGTCTCCTTGAACCTCCATGGAATAGA 120
Db 714 GATGGCTGTGTAGCAGTCCCTCAGAAACCTTAAGGTCTCCTTGAACCTCCATGGAATAGA 655
Qy 121 ATATTTAAAGGAGAGAAATGTGACTCTTACATGTAAATGGGAAACAAATTTCTTTGAAGTCAGT 180
Db 654 ATATTTAAAGGAGAGAAATGTGACTCTTACATGTAAATGGGAAACAAATTTCTTTGAAGTCAGT 595
Qy 181 TCCACCAATATGGTTCACATGAGCAGCTTTCAGAGAGACACAAATTCAGATTTGATATT 240
Db 594 TCCACCAATATGGTTCACATGAGCAGCTTTCAGAGAGACACAAATTCAGATTTGATATT 535
Qy 241 GTGAATGCCAAATTTGAAGACAGTGGAGAAATACAAATGTGAGCAACCAACAAATTAATGAG 300
Db 534 GTGAATGCCAAATTTGAAGACAGTGGAGAAATACAAATGTGAGCAACCAACAAATTAATGAG 475
Qy 301 AGTGAACCTGTGTACTGGAAATCTTTCAGTACTGCTGCTCTTTCAGGCTCTTCTGCTGAG 360
Db 474 AGTGAACCTGTGTACTGGAAATCTTTCAGTACTGCTGCTCTTTCAGGCTCTTCTGCTGAG 415
Qy 361 GTGGTGTGAGGGGCCAGCCCTCTTCTCAGTGTGCTGCTGGAGGAACTGGGATGTG 420
Db 414 GTGGTGTGAGGGGCCAGCCCTCTTCTCAGTGTGCTGCTGGAGGAACTGGGATGTG 355
Qy 421 TACAGGTGATCTATTATAGGATGGTGAAGCTCTCAAGTACTGTGTATGAGAACCAAC 480
Db 354 TACAGGTGATCTATTATAGGATGGTGAAGCTCTCAAGTACTGTGTATGAGAACCAAC 295
Qy 481 ATCTCCATTACAAATGCCACAGTTGAAGACAGTGGAAACCTTACTGTACGGGCAAGTG 540
Db 294 ATCTCCATTACAAATGCCACAGTTGAAGACAGTGGAAACCTTACTGTACGGGCAAGTG 235
Qy 541 TGGCAGCTGACTATGAGTCTGAGCCCTCAACATTTACTGTATATAAAGCTCCGCTGAG 600
Db 234 TGGCAGCTGACTATGAGTCTGAGCCCTCAACATTTACTGTATAAAGCTCCGCTGAG 175
Qy 601 AAGTACTGGCTACAAATTTTATCCCATTTGTTGGTGGTGAATCTGTTTCTGTGACACA 660
Db 174 AAGTACTGGCTACAAATTTTATCCCATTTGTTGGTGGTGAATCTGTTTCTGTGACACA 115
Qy 661 GGATATTATCTCAACTCAGCAGCTGAGTCAATTTCTTCTTGAAGATTAAGAGAACGAG 720
Db 114 GGATATTATCTCAACTCAGCAGCTGAGTCAATTTCTTCTTGAAGATTAAGAGAACGAG 55
Qy 721 AAAGGCTTCAGACTTCTGAACCCACATCTTAAGCCAAACCCCAACCAACTGA 774
Db 54 AAAGGCTTCAGACTTCTGAACCCACATCTTAAGCCAAACCCCAACCAACTGA 1

RESULT 7

US-07-869-933-10
; Sequence 10, Application US/07869933
; Patent No. 5770396
; GENERAL INFORMATION:


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QY 301 AGTGAACCTGTACCTGGAGTCTTCAGTACCTGGCTGCTCTCTCAGGCTCTGCTGAG 360
DB 407 AGTGAACCTGTACCTGGAGTCTTCAGTACCTGGCTGCTCTCTCAGGCTCTGCTGAG 466
QY 361 GTGGTGTAGGAGGCGCCCTCTCTCAGTGCCTCAGTGCCTGCTGCTGCTGCTGCTG 420
DB 467 GTGGTGTAGGAGGCGCCCTCTCTCAGTGCCTCAGTGCCTGCTGCTGCTGCTGCTG 526
QY 421 TACAAGGTGATCTATTATTAAGTATGTTGAAGCTCTCAAGTACTGGTATGAGAACCAAC 480
DB 527 TACAAGGTGATCTATTATTAAGTATGTTGAAGCTCTCAAGTACTGGTATGAGAACCAAC 586
QY 481 ATCTCCATTAACATGACAGTGTGAAGACAGTGAAGTGAAGTGAAGTGAAGTGAAG 540
DB 587 ATCTCCATTAACATGACAGTGTGAAGACAGTGAAGTGAAGTGAAGTGAAGTGAAG 646
QY 541 TGGCAGCTGGACTATGAGTCTGAGCCCTCTCAACATTAAGTGAAGTGAAGTGAAG 600
DB 647 TGGCAGCTGGACTATGAGTCTGAGCCCTCTCAACATTAAGTGAAGTGAAGTGAAG 706
QY 601 AAGTACTGGCTACAAATTTTATCCCATTTGTTGGTGGTGAATCTGTTGCTGGACACA 660
DB 707 AAGTACTGGCTACAAATTTTATCCCATTTGTTGGTGGTGAATCTGTTGCTGGACACA 766
QY 661 GGATTATTTATCTCAACTCAGCAGCTCACATTTCTTTGAAGATTGAAGAACCAAG 720
DB 767 GGATTATTTATCTCAACTCAGCAGCTCACATTTCTTTGAAGATTGAAGAACCAAG 826
QY 721 AAGGCTTCAGACTTGAAGCCCACTTGAAGCCCACTTGAAGCCCACTTGAAGCCCA 774
DB 827 AAGGCTTCAGACTTGAAGCCCACTTGAAGCCCACTTGAAGCCCACTTGAAGCCCA 880

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RESULT 9

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US-08-756-387B-1
; Sequence 1, Application US/08756387B
; Patent No. 5945294
; GENERAL INFORMATION:
; APPLICANT: Frank, Glenn R.
; APPLICANT: Porter, James P.
; APPLICANT: Rushlow, Keith E.
; APPLICANT: Wasson, Donald L.
; TITLE OF INVENTION: Method to Detect Ige
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carol Talkington Verser, Ph.D.
; ADDRESSEE: Heskia Corporation
; STREET: 1825 Sharp Point Drive
; CITY: Fort Collins
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80525
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: WordPerfect for Windows, Version 7.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/756,387B
; FILING DATE: No. 5945294ember 26, 1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Verser, Carol Talkington
; REGISTRATION NUMBER: 37,459
; REFERENCE/DOCKET NUMBER: DI-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 970/493-7272
; TELEFAX: 970/484-9505
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1198 nucleotides
; TYPE: nucleic acid

```

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; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 107..877
US-08-756-387B-1

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Query Match 100.0%; Score 774; DB 2; Length 1198;
Best Local Similarity 100.0%; Pred. No. 6,8e-246;
Matches 774; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 ATGGCTCTCCCTCCCTGGAATCCCTACTACTCTGCTGCTGCTGCTGCTGCTGCTGCTG 60
DB 107 ATGGCTCTCCCTCCCTGGAATCCCTACTACTCTGCTGCTGCTGCTGCTGCTGCTGCTG 166
QY 61 GATGCGCTGTTAGCAGTCCCTCAGAAACCTTAAGGTCTCTTGAACCTCCATGGAATAGA 120
DB 167 GATGCGCTGTTAGCAGTCCCTCAGAAACCTTAAGGTCTCTTGAACCTCCATGGAATAGA 226
QY 121 ATATTTAAAGAGAGAGATGTGACTCTTACATGTAATGGGACAAATTTCTTTGAAGTCA 180
DB 227 ATATTTAAAGAGAGAGATGTGACTCTTACATGTAATGGGACAAATTTCTTTGAAGTCA 286
QY 181 TCCACCAATATGGTTCCCAATATGGCAGCTTTTCAAGAGAGACAAATTTCAAGTTTGAAT 240
DB 287 TCCACCAATATGGTTCCCAATATGGCAGCTTTTCAAGAGAGACAAATTTCAAGTTTGAAT 346
QY 241 GTGAATGCCAAATTTGAAGACAGTGAAGATACAAATGTGACCAACCAAGTTAATGAG 300
DB 347 GTGAATGCCAAATTTGAAGACAGTGAAGATACAAATGTGACCAACCAAGTTAATGAG 406
QY 301 AGTGAACCTGTGCTGCTGGAAGTCTTCAAGTCACTGGCTGCTCTTTCAGGCTCTTCTGCTGAG 360
DB 407 AGTGAACCTGTGCTGCTGGAAGTCTTCAAGTCACTGGCTGCTCTTTCAGGCTCTTCTGCTGAG 466
QY 361 GTGCTGATGAGGCGCCAGCCCTCTTCTCAGTGTGCTGCTGCTGCTGCTGCTGCTGCTG 420
DB 467 GTGCTGATGAGGCGCCAGCCCTCTTCTCAGTGTGCTGCTGCTGCTGCTGCTGCTGCTG 526
QY 421 TACAAGGTGATCTATTATTAAGGATGTGAAGCTCTCAAGTACTGTGATGAGAACCAAC 480
DB 527 TACAAGGTGATCTATTATTAAGGATGTGAAGCTCTCAAGTACTGTGATGAGAACCAAC 586
QY 481 ATCTCCATTAACATGCCACAGTGTGAAGACAGTGAAGTGAAGTGAAGTGAAGTGAAG 540
DB 587 ATCTCCATTAACATGCCACAGTGTGAAGACAGTGAAGTGAAGTGAAGTGAAGTGAAG 646
QY 541 TGGCAGCTGGACTATGAGTCTGAGCCCTCTCAACATTAAGTGAAGTGAAGTGAAGTGAAG 600
DB 647 TGGCAGCTGGACTATGAGTCTGAGCCCTCTCAACATTAAGTGAAGTGAAGTGAAGTGAAG 706
QY 601 AAGTACTGGCTACAAATTTTATCCCATTTGTTGGTGGTGAATCTGTTGCTGCTGAGACACA 660
DB 707 AAGTACTGGCTACAAATTTTATCCCATTTGTTGGTGGTGAATCTGTTGCTGCTGAGACACA 766
QY 661 GGATTATTTATCTCAACTCAGCAGCTCACATTTCTTGAAGATTGAAGAACCAAG 720
DB 767 GGATTATTTATCTCAACTCAGCAGCTCACATTTCTTGAAGATTGAAGAACCAAG 826
QY 721 AAGGCTTCAGACTTCTGAAGCCCACTTGAAGCCCACTTGAAGCCCACTTGAAGCCCA 774
DB 827 AAGGCTTCAGACTTCTGAAGCCCACTTGAAGCCCACTTGAAGCCCACTTGAAGCCCA 880

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RESULT 10

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US-08-756-387B-3/c
; Sequence 3, Application US/08756387B
; Patent No. 5945294
; GENERAL INFORMATION:
; APPLICANT: Frank, Glenn R.
; APPLICANT: Porter, James P.
; APPLICANT: Rushlow, Keith E.

```

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; APPLICANT: Wassom, Donald L.
; TITLE OF INVENTION: Method to Detect Ige
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carol Talkington Verser, Ph.D.
; ADDRESSEE: Heska Corporation
; STREET: 1825 Sharp Point Drive
; CITY: Fort Collins
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80525
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: WordPerfect for Windows, Version 7.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/756,387B
; FILING DATE: No. 5945294ember 26, 1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Verser, Carol Talkington
; REGISTRATION NUMBER: 37,459
; REFERENCE/DOCKET NUMBER: DI-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 970/493-7272
; TELEFAX: 970/484-9505
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1198 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; US-08-756-387B-3

Query Match 100.0%; Score 774; DB 2; Length 1198;
Best Local Similarity 100.0%; Pred. No. 6.8e-246;
Matches 774; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGCTCTGCTGAGTATGCTTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGT 180
DB 1 ATGCTCTGCTGAGTATGCTTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGT 180
QY 61 GATGGCTGTGTAGCAGTCCCTCAGAACCTTAAGTCTCTTGAACCCCTCAGTGAATAGA 120
DB 1092 ATGGCTCTGCTGAGTATGCTTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGT 180
QY 1032 GATGGCTGTGTAGCAGTCCCTCAGAACCTTAAGTCTCTTGAACCCCTCAGTGAATAGA 120
DB 121 ATATTTAAGGAGAGATGCTTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGT 180
QY 972 ATATTTAAGGAGAGATGCTTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGT 180
DB 181 TCACCAAAATGGTTCCAAATGGCAGCTTTTCAGAGAGACAAATTCAGTTGAATATT 240
QY 912 TCACCAAAATGGTTCCAAATGGCAGCTTTTCAGAGAGACAAATTCAGTTGAATATT 240
DB 241 GTGAATGCCAAATTTGAAGACAGTGGAGATACAAATGTCAGCACCAACAAGTTAATGAG 300
QY 852 GTGAATGCCAAATTTGAAGACAGTGGAGATACAAATGTCAGCACCAACAAGTTAATGAG 300
DB 301 AGTGAACCTGTGCTGAGTATGCTTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGT 180
QY 792 AGTGAACCTGTGCTGAGTATGCTTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGT 180
DB 361 GTGCTGATGGAGGCGCAGCCCTCTTCTCAGTGGCCATGTTGGAGAACCTGGATGTG 420
QY 732 GTGCTGATGGAGGCGCAGCCCTCTTCTCAGTGGCCATGTTGGAGAACCTGGATGTG 420
DB 421 TACAAGGTGATCTATTATTAAGGATGTTGAAGTCTCTCAAGTACTGGTATGAGAACCAAC 480
QY 672 TACAAGGTGATCTATTATTAAGGATGTTGAAGTCTCTCAAGTACTGGTATGAGAACCAAC 480
DB 481 ATCTCCATTACAAATGCCAGTTCAGACAGTGGAGAACCTACTACTGTACGGGCAAGTG 540

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DB 612 ATCTCCATTACAAATGCCAGTTGAAGACAGTGGAACTCTACTGTACGGCAAGTG 553
QY 541 TGGCAGCTGGACTATGAGTCTGAGCCCTCAACATTACTGTATATAAGCTCCGGCTGAG 600
DB 552 TGGCAGCTGGACTATGAGTCTGAGCCCTCAACATTACTGTATATAAGCTCCGGCTGAG 493
QY 601 AAGTACTGGCTACAATTTTATCCCATTTGGTGGTGAATCTGTTGCTGTGACACA 660
DB 492 AAGTACTGGCTACAATTTTATCCCATTTGGTGGTGAATCTGTTGCTGTGACACA 433
QY 661 GGATTATTTATCTCAACTCAGCAGCAGGTCACATTTCTTCAAGATTAAAGAGAACCAAG 720
DB 432 GGATTATTTATCTCAACTCAGCAGCAGGTCACATTTCTTCAAGATTAAAGAGAACCAAG 373
QY 721 AAAGCTTCAGACTTCTGAACCCACATCTAAGCCAAACCCCAAAACAACTGA 774
DB 372 AAAGCTTCAGACTTCTGAACCCACATCTAAGCCAAACCCCAAAACAACTGA 319

RESULT 11
US-09-285-873-1
; Sequence 1, Application US/09285873
; Patent No. 6309832
; GENERAL INFORMATION:
; APPLICANT: Frank, Glenn R.
; APPLICANT: Porter, James P.
; APPLICANT: Rushlow, Keith E.
; APPLICANT: Wassom, Donald L.
; TITLE OF INVENTION: Method to Detect Ige
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Heska Corporation
; STREET: 1825 Sharp Point Drive
; CITY: Fort Collins
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80525
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: WordPerfect for Windows, Version 7.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/285,873
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/756,387
; FILING DATE: No. 6309832ember 26, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Verser, Carol Talkington
; REGISTRATION NUMBER: 37,459
; REFERENCE/DOCKET NUMBER: DI-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 970/493-7272
; TELEFAX: 970/484-9505
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1198 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 107..877
; US-09-285-873-1

Query Match 100.0%; Score 774; DB 4; Length 1198;
Best Local Similarity 100.0%; Pred. No. 6.8e-246;
Matches 774; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

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QY 1 ATGGCTCTGCGAGGATCCCTACTCTACTGTGTAGCTTACTGTCTTCTCGCTCCA 60
Db 107 ATGGCTCTGCGAGGATCCCTACTCTACTGTGTAGCTTACTGTCTTCTCGCTCCA 166
QY 61 GATGCGGTGTTAGCAGTCCCTCAGAAACCTTAAGTCTCTCTTGAACCTCCATGGAATAGA 120
Db 167 GATGCGGTGTTAGCAGTCCCTCAGAAACCTTAAGTCTCTCTTGAACCTCCATGGAATAGA 226
QY 121 ATATTAAAGAGAGAGATGTGACCTCTTACATGTAAATGGAACAAATTTCTTTGAAGTCAGT 180
Db 227 ATATTAAAGAGAGAGATGTGACCTCTTACATGTAAATGGAACAAATTTCTTTGAAGTCAGT 286
QY 181 TCCACCAATGGTTCCCAATGGCAGCTTTTCAAGAGAGACAAATTCAGATTTGAATATT 240
Db 287 TCCACCAATGGTTCCCAATGGCAGCTTTTCAAGAGAGACAAATTCAGATTTGAATATT 346
QY 241 GTGAATGCCAATTTGAAGACAGTGGAGAAATACAAATGTGAGCAACCAAGTTAATGAG 300
Db 347 GTGAATGCCAATTTGAAGACAGTGGAGAAATACAAATGTGAGCAACCAAGTTAATGAG 406
QY 301 AGTGAACCTGTGTACCTGGAAGTCTTTCAGTGAAGTGGCTGTCTTTCAGGCTCTGTGTAG 360
Db 407 AGTGAACCTGTGTACCTGGAAGTCTTTCAGTGAAGTGGCTGTCTTTCAGGCTCTGTGTAG 466
QY 361 GTGGTGTAGGAGGCGCCAGCCCTCTTCTCAGGTGCCATGTTGGAGAACTGGGATGTG 420
Db 467 GTGGTGTAGGAGGCGCCAGCCCTCTTCTCAGGTGCCATGTTGGAGAACTGGGATGTG 526
QY 421 TACAAGGTGATCTATTATTAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCAAC 480
Db 527 TACAAGGTGATCTATTATTAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCAAC 586
QY 481 ATCTCCATACAAATGACAGTGTGAAGACAGTGGACCTACTACTGTACGGGCAAGTG 540
Db 587 ATCTCCATACAAATGACAGTGTGAAGACAGTGGACCTACTACTGTACGGGCAAGTG 646
QY 541 TGGCAGCTGACTATGACTCTGAGCCCTCAACATTAATCTGTAATAAAGCTCCGCGTGAG 600
Db 647 TGGCAGCTGACTATGACTCTGAGCCCTCAACATTAATCTGTAATAAAGCTCCGCGTGAG 706
QY 601 AAGTACTGGTACAAATTTTATCCCATTTGTGGTGGTGAATCTCTGTTGTGTGGACACA 660
Db 707 AAGTACTGGTACAAATTTTATCCCATTTGTGGTGGTGAATCTCTGTTGTGTGGACACA 766
QY 661 GGATTTATTTATCTCAACTCAGCAGCAGTCAATTTCTTTGAAGATTAAGAGAACCCAGG 720
Db 767 GGATTTATTTATCTCAACTCAGCAGCAGTCAATTTCTTTGAAGATTAAGAGAACCCAGG 826
QY 721 AAAGCTTTCAGACTTCTGAACCCACATCTTAAGCCAAACCCCAAAACAACTCA 774
Db 827 AAAGCTTTCAGACTTCTGAACCCACATCTTAAGCCAAACCCCAAAACAACTCA 880

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RESULT 12

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US-09-285-873-3/c
; Sequence 3, Application US/09285873
; Patent No. 6309832
; GENERAL INFORMATION:
; APPLICANT: Frank, Glenn R.
; APPLICANT: Porter, James P.
; APPLICANT: Rushlow, Keith E.
; APPLICANT: Wasson, Donald L.
; TITLE OF INVENTION: Method to Detect IgE
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carol Talkington Verser, Ph.D.
; ADDRESS: Heska Corporation
; STREET: 1825 Sharp Point Drive
; City: Fort Collins
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80525

```

```

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: WordPerfect for Windows, Version 7.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/285,873
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/756,387
; FILING DATE: No. 6309832ember 26, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Verser, Carol Talkington
; REGISTRATION NUMBER: 37,459
; REFERENCE/DOCKET NUMBER: DI-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 970/493-7272
; TELEFAX: 970/484-9505
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1198 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; US-09-285-873-3

```

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Query Match 100.0%; Score 774; DB 4; Length 1198;
Best Local Similarity 100.0%; Pred. No. 6.8e-246;
Matches 774; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 ATGGCTCTGCGAGGATCCCTACTCTACTGTGTAGCTTACTGTCTTCTCGCTCCA 60
Db 1092 ATGGCTCTGCGAGGATCCCTACTCTACTGTGTAGCTTACTGTCTTCTCGCTCCA 1033
QY 61 GATGCGGTGTTAGCAGTCCCTCAGAAACCTTAAGTCTCTTGAACCTCCATGGAATAGA 120
Db 1032 GATGCGGTGTTAGCAGTCCCTCAGAAACCTTAAGTCTCTTGAACCTCCATGGAATAGA 973
QY 121 ATATTAAAGAGAGAGATGTGACCTTACATGTAAATGGAACAAATTTCTTTGAAGTCAGT 180
Db 972 ATATTAAAGAGAGAGATGTGACCTTACATGTAAATGGAACAAATTTCTTTGAAGTCAGT 913
QY 181 TCCACCAATGGTTCCCAATGGCAGCTTTTCAAGAGAGACAAATTCAGATTTGAATATT 240
Db 912 TCCACCAATGGTTCCCAATGGCAGCTTTTCAAGAGAGACAAATTCAGATTTGAATATT 853
QY 241 GTGAATGCCAATTTGAAGACAGTGGAGAAATACAAATGTGAGCAACCAAGTTAATGAG 300
Db 852 GTGAATGCCAATTTGAAGACAGTGGAGAAATACAAATGTGAGCAACCAAGTTAATGAG 793
QY 301 AGTGAACCTGTGTACCTGGAAGTCTTTCAGTGAAGTGGCTGTCTTTCAGGCTCTGTGTAG 360
Db 792 AGTGAACCTGTGTACCTGGAAGTCTTTCAGTGAAGTGGCTGTCTTTCAGGCTCTGTGTAG 733
QY 361 GTGGTGTAGGAGGCGCCAGCCCTCTTCTCAGGTGCCATGTTGGAGAACTGGGATGTG 420
Db 732 GTGGTGTAGGAGGCGCCAGCCCTCTTCTCAGGTGCCATGTTGGAGAACTGGGATGTG 673
QY 421 TACAAGGTGATCTATTATTAAGGATGGTGAAGCTCTTCAAGTACTGTGTATGAGAACCCAAAC 480
Db 672 TACAAGGTGATCTATTATTAAGGATGGTGAAGCTCTTCAAGTACTGTGTATGAGAACCCAAAC 613
QY 481 ATCTCCATTAACAATGCCAGTGGAGCACTTACTACTGTACGGGCAAGTG 540
Db 612 ATCTCCATTAACAATGCCAGTGGAGCACTTACTACTGTACGGGCAAGTG 553
QY 541 TGGCAGCTGGAATGAGTCTGAGCCCTCAACATTAATGTAATAAAGCTCCGCGTGAG 600
Db 552 TGGCAGCTGGAATGAGTCTGAGCCCTCAACATTAATGTAATAAAGCTCCGCGTGAG 493
QY 601 AAGTACTGGCTACAAATTTTATCCCATTTGTGGTGGTGAATCTTGTGTGGACACA 660

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Db 492 AAGTACTGGCTCAAAATTTTATCCCATTTGTTGGTGAATTCCTGCTGGACACA 433
 QY 661 GGATTAATTTATCTCACTCAGCAGCAGGTACATTTCTCTTGAAGTAAGAACACAGG 720
 Db 432 GGATTAATTTATCTCACTCAGCAGCAGGTACATTTCTCTTGAAGTAAGAACACAGG 373
 QY 721 AAAGGCTTCAGACTTCTGAACCCACATCTTAAGCCAAACCCCAAAACAACTGA 774
 Db 372 AAAGGCTTCAGACTTCTGAACCCACATCTTAAGCCAAACCCCAAAACAACTGA 319

RESULT 13

US-09-944-277A-1
 ; Sequence 1, Application US/09944277A
 ; Patent No. 6682894

GENERAL INFORMATION:

APPLICANT: Frank, Glenn R.
 Porter, James P.
 Rushlow, Keith E.
 Wassom, Donald L.
 TITLE OF INVENTION: Method to Detect Ige
 NUMBER OF SEQUENCES: 13
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Carol Talkington Verser, Ph.D.
 STREET: 1825 Sharp Point Drive
 CITY: Fort Collins
 STATE: Colorado
 COUNTRY: USA
 ZIP: 80525

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: Windows 95
 SOFTWARE: WordPerfect for Windows, Version 7.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/944,277A
 FILING DATE: 30-AUG-2001
 CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/285,873
 FILING DATE: 1993-03-31
 ATTORNEY/AGENT INFORMATION:
 NAME: Verser, Carol Talkington
 REGISTRATION NUMBER: 37,459
 REFERENCE/DOCKET NUMBER: DI-1
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 970/493-7272
 TELEFAX: 970/484-9505

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:
 LENGTH: 1198 nucleotides
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 FEATURE:

NAME/KEY: CDS

LOCATION: 107..877

SEQUENCE DESCRIPTION: SEQ ID NO: 1:

US-09-944-277A-1

Query Match 100.0%; Score 774; DB 4; Length 1198;
 Best Local Similarity 100.0%; Pred. No. 6.8e-246;
 Matches 774; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGCTCTGCCATGAATCCCTACTACTGTGTAGCTTACTTCTTGGCTCCA 60
 Db 107 ATGGCTCTGCCATGAATCCCTACTACTGTGTAGCTTACTTCTTGGCTCCA 166
 QY 61 GATGGCGTGTAGCAGTCCCTCAGAAACCTAAGGTCCTCTTGAACCTCCATGAATAGA 120

Db 167 GATGGCGTGTAGCAGTCCCTCAGAAACCTAAGGTCCTCTTGAACCCCTCATGAATAGA 226
 QY 121 ATATTTAAAGGAGAGAAATGTGACTCTTACATGTAAATGGGAAACAATTTCTTTGAAGTCAGT 180
 Db 227 ATATTTAAAGGAGAGAAATGTGACTCTTACATGTAAATGGGAAACAATTTCTTTGAAGTCAGT 286
 QY 181 TCCACCAAAATGGTTCACAAATGCGACCTTTTCAAGAGAGACAAATTCAGATTTGAATAT 240
 Db 287 TCCACCAAAATGGTTCACAAATGCGACCTTTTCAAGAGAGACAAATTCAGATTTGAATAT 346
 QY 241 GTCAATGCCAAAATTTGAAGACAGTGGAGAAATACAAATGTGACCAACCAAGTTAATGAG 300
 Db 347 GTCAATGCCAAAATTTGAAGACAGTGGAGAAATACAAATGTGACCAACCAAGTTAATGAG 406
 QY 301 AGTGAACCTGTGTACTCTGGAAGTCTTTCAGTGTGCTGCTCTTCAAGCCCTCTCTGTGAG 360
 Db 407 AGTGAACCTGTGTACTCTGGAAGTCTTTCAGTGTGCTGCTCTTCAAGCCCTCTCTGTGAG 466
 QY 361 GTGGTGATGGAGGCGCAGCCCTCTTCTCAGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 420
 Db 467 GTGGTGATGGAGGCGCAGCCCTCTTCTCAGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 526
 QY 421 TACAAGGTGATCTATTATAAGGATGGTGAAGCTCTCAAGTACTGCTATGAGAACCCACAAC 480
 Db 527 TACAAGGTGATCTATTATAAGGATGGTGAAGCTCTCAAGTACTGCTATGAGAACCCACAAC 586
 QY 481 ATCTCCATTACAAATGCCACAGTTGAAGACAGTGAACCTACTACTGTACGGGAAAGTG 540
 Db 587 ATCTCCATTACAAATGCCACAGTTGAAGACAGTGAACCTACTACTGTACGGGAAAGTG 646
 QY 541 TGGCAGCTGGACTATGACTCTGAGCCCTCAACATTTACTGTAATAAAGGCTCCCGCTGAG 600
 Db 647 TGGCAGCTGGACTATGACTCTGAGCCCTCAACATTTACTGTAATAAAGGCTCCCGCTGAG 706
 QY 601 AAGTACTGGCTACAAATTTTATCCCATTTGTGGTGTGATCTGTTGCTGTGACACA 660
 Db 707 AAGTACTGGCTACAAATTTTATCCCATTTGTGGTGTGATCTGTTGCTGTGACACA 766
 QY 661 GGATTAATTTATCTCAACTCAGCAGCAGTCACTTCTCTTGAAGATTAAGAGAACCCAGG 720
 Db 767 GGATTAATTTATCTCAACTCAGCAGCAGTCACTTCTCTTGAAGATTAAGAGAACCCAGG 826
 QY 721 AAAGGCTTCAGACTTCTGAACCCACATCTTAAGCCAAACCCCAAAACAACTGA 774
 Db 827 AAAGGCTTCAGACTTCTGAACCCACATCTTAAGCCAAACCCCAAAACAACTGA 880

RESULT 14

US-09-944-277A-3/C
 ; Sequence 3, Application US/09944277A
 ; Patent No. 6682894

GENERAL INFORMATION:

APPLICANT: Frank, Glenn R.
 Porter, James P.
 Rushlow, Keith E.
 Wassom, Donald L.
 TITLE OF INVENTION: Method to Detect Ige
 NUMBER OF SEQUENCES: 13
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Carol Talkington Verser, Ph.D.
 STREET: 1825 Sharp Point Drive
 CITY: Fort Collins
 STATE: Colorado
 COUNTRY: USA
 ZIP: 80525

COMPUTER READABLE FORM:

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 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: Windows 95
 SOFTWARE: WordPerfect for Windows, Version 7.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/944,277A

;; FILING DATE: 30-Aug-2001
;; CLASSIFICATION: <Unknown>
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 09/285,873
;; FILING DATE: 1999-03-31
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Verser, Carol Talkington
;; REGISTRATION NUMBER: 37,459
;; REFERENCE/DOCKET NUMBER: DI-1
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 970/493-7272
;; TELEFAX: 970/484-9505
;; INFORMATION FOR SEQ ID NO: 3:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 1198 nucleotides
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: cDNA
;; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-944-277A-3

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QY 1 ATGGCTCTGCATCGAATCCCTACTCTACTGTGTAGCTTACTGTTCCTCGCTCCA 60
DB 1092 ATGGCTCTGCATCGAATCCCTACTCTACTGTGTAGCTTACTGTTCCTCGCTCCA 1033

QY 61 GATGCGGTGTAGCAGTCCCTCAGAAACCTAAGGTCTCTTGAACCTCCATGGAATAGA 120
DB 1032 GATGCGGTGTAGCAGTCCCTCAGAAACCTAAGGTCTCTTGAACCTCCATGGAATAGA 973

QY 121 ATATTTAAAGAGAGAAATGTGACTCTTACATGTAAATGGGAACAATTTCTTTGAAGTCAGT 180
DB 972 ATATTTAAAGAGAGAAATGTGACTCTTACATGTAAATGGGAACAATTTCTTTGAAGTCAGT 913

QY 181 TCCACCAATGGTTCACAAATGGAGAGCCCTTTCAGAGAGAGACAAATTCAGATTTGAATATT 240
DB 912 TCCACCAATGGTTCACAAATGGAGAGCCCTTTCAGAGAGAGACAAATTCAGATTTGAATATT 853

QY 241 GTGAATGCCAAATTTGAAGACAGTGGAGAGATACAAATGTGAGCAGCAGCAAGTTAATAG 300
DB 852 GTGAATGCCAAATTTGAAGACAGTGGAGAGATACAAATGTGAGCAGCAGCAAGTTAATAG 793

QY 301 AGTGAACCTGTGTACTCGAAAGTCTTCAAGTCACTGGCTGCTCTTCAAGGCTCTGTGTAG 360
DB 792 AGTGAACCTGTGTACTCGAAAGTCTTCAAGTCACTGGCTGCTCTTCAAGGCTCTGTGTAG 733

QY 361 GTGGTGTAGGAGGCGCCGCCCTCTTCTCAGGTGCCATGGTTGGAGGAACCTGGGATGTG 420
DB 732 GTGGTGTAGGAGGCGCCGCCCTCTTCTCAGGTGCCATGGTTGGAGGAACCTGGGATGTG 673

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RESULT 15

US-08-897-956A-6
; Sequence 6, Application US/08897956A
; Patent No. 6423512
; GENERAL INFORMATION:
; APPLICANT: Mary Ellen Digan
; APPLICANT: Philip Lake
; APPLICANT: Hermann Gram
; TITLE OF INVENTION: Fusion Polypeptides
; FILE REFERENCE: 600-7244/CPA
; CURRENT APPLICATION NUMBER: US/08/897,956A
; CURRENT FILING DATE: 1997-07-21
; PRIOR APPLICATION NUMBER: 60/022,689
; PRIOR FILING DATE: 1996-07-26
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 773
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Fusion Polynucleotide
US-08-897-956A-6

Query Match 99.9%; Score 773; DB 4; Length 773;
Best Local Similarity 100.0%; Pred. No. 1.1e-245;
Matches 773; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OM nucleic - nucleic search, using sw model

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Searched: 3340653 seqs, 2534783454 residues 6681306

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	774	100.0	1198	9	US-09-944-277A-3
5	774	100.0	1198	9	US-09-962-832-244
6	774	100.0	1198	17	US-10-775-169-141
7	774	99.8	898	13	US-10-236-392-27
8	699	90.3	699	9	US-09-944-277A-7
9	591	76.4	591	9	US-09-944-277A-10
10	530	68.5	757	13	US-10-236-392-29
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15	515.2	66.6	528	10	US-09-809-715-3	Sequence 3, Appli
16	438.4	56.6	1015	16	US-10-434-817-1	Sequence 1, Appli
17	438.4	56.6	1015	16	US-10-434-817-3	Sequence 3, Appli
18	435	56.2	765	16	US-10-434-817-4	Sequence 4, Appli
19	435	56.2	765	16	US-10-434-817-5	Sequence 5, Appli
20	403.8	52.2	708	16	US-10-434-817-6	Sequence 6, Appli
21	403.8	52.2	708	16	US-10-434-817-8	Sequence 8, Appli
22	329.8	42.6	603	16	US-10-434-817-11	Sequence 11, Appli
23	169.4	21.9	2202	15	US-10-198-846-13731	Sequence 13731, A
24	167.8	21.7	765	15	US-10-027-736A-8	Sequence 8, Appli
25	167.8	21.7	887	17	US-10-641-643-1287	Sequence 1287, Ap
26	166.2	21.5	887	16	US-10-191-997-124	Sequence 124, App
27	166.2	21.5	887	17	US-10-641-643-1254	Sequence 1254, Ap
28	166.2	21.5	887	17	US-10-717-597-208	Sequence 208, App
29	166.2	21.5	887	17	US-10-775-169-140	Sequence 140, App
30	166.2	21.5	2463	15	US-10-240-965-100	Sequence 100, App
31	163	21.1	1977	10	US-09-873-367C-994	Sequence 994, App
32	163	21.1	1977	13	US-10-240-425-1368	Sequence 1268, Ap
33	163	21.1	1977	13	US-10-342-887-382	Sequence 382, App
34	163	21.1	1977	13	US-10-172-118-382	Sequence 382, App
35	163	21.1	1977	17	US-10-775-169-35	Sequence 35, Appli
36	160.8	20.8	765	15	US-10-027-736A-7	Sequence 7, Appli
37	141.6	18.3	1318	12	US-10-152-319A-2037	Sequence 2037, Ap
38	141.6	18.3	1318	16	US-10-191-803-266	Sequence 266, App
39	140	18.1	1341	16	US-10-388-934-244	Sequence 244, App
40	139.6	18.0	1321	12	US-09-836-544-22	Sequence 1906, Ap
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42	139.6	18.0	1321	13	US-10-172-118-1906	Sequence 1906, Ap
43	139.2	18.0	1398	9	US-09-925-301-286	Sequence 286, App
44	138	17.8	1035	15	US-10-384-850-13	Sequence 13, Appli
45	138	17.8	1074	15	US-10-027-736A-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1
US-09-944-277A-4
; Sequence 4, Application US/09944277A
; Patent No. US2002034771A1
; GENERAL INFORMATION:
; APPLICANT: Frank, Glenn R.
; Porter, James P.
; Rushlow, Keith E.
; Wassom, Donald L.
; TITLE OF INVENTION: Method to Detect IGS
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carol Talkington Verser, Ph.D.
; Heska Corporation
; STREET: 1825 Sharp Point Drive
; CITY: Fort Collins
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80525
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: Wordperfect for Windows, version 7.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/944, 277A
; FILING DATE: 30-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/285, 873
; FILING DATE: 1999-03-31
; ATTORNEY/AGENT INFORMATION:
; NAME: Verser, Carol Talkington
; REGISTRATION NUMBER: 37,459
; REFERENCE/DOCKET NUMBER: DI-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 970/493-7272

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TELEFAX: 970/484-9505
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 774 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..774
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-944-277A-4

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Best Local Similarity 100.0%; Pred. No. 7.7e-244;
Matches 774; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 2

US-09-944-277A-5/c

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; Sequence 5, Application US/09944277A
; Patent No. US20020034771A1
; GENERAL INFORMATION:
; APPLICANT: Frank, Glenn R.
; Porter, James P.
; Rushlow, Keith E.
; Wasson, Donald L.
; TITLE OF INVENTION: Method to Detect Ige
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carol Talkington Verser, Ph.D.
; STREET: 1825 Sharp Point Drive
; CITY: Fort Collins
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80525
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: WordPerfect for Windows, Version 7.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/944,277A
; FILING DATE: 30-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/285,873
; FILING DATE: 1999-03-31
; ATTORNEY/AGENT INFORMATION:
; NAME: Verser, Carol Talkington
; REGISTRATION NUMBER: 37,459
; REFERENCE/DOCKET NUMBER: DI-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 970/493-7272
; TELEFAX: 970/484-9505
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 774 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-944-277A-5
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Query Match      100.0%; Score 774; DB 9; Length 774;
Best Local Similarity 100.0%; Pred. No. 7.7e-244;
Matches 774; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGCTCTGCGCATGGAAATCCCTACTACTGTGTGTAGCCTTACTGTCTTCGCTCCA 60
DB 774 ATGGCTCTGCGCATGGAAATCCCTACTACTGTGTGTAGCCTTACTGTCTTCGCTCCA 715
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RESULT 3

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; Patent No. US20020034771A1
; GENERAL INFORMATION:
; APPLICANT: Frank, Glenn R.
; Porter, James P.
; Rushlow, Keith E.
; Wasson, Donald L.
; TITLE OF INVENTION: Method to Detect IgE
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carol Talkington Verser, Ph.D.
; STREET: 1825 Sharp Point Drive
; CITY: Fort Collins
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80525

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: WordPerfect for Windows, Version 7.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/944,277A
; FILING DATE: 30-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/285,873
; FILING DATE: 1999-03-31
; ATTORNEY/AGENT INFORMATION:
; NAME: Verser, Carol Talkington
; REGISTRATION NUMBER: 37,459
; REFERENCE/DOCKET NUMBER: DI-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 970/493-7272
; TELEFAX: 970/484-9505
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1198 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single

RESULT 4

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; Sequence 3, Application US/09944277A
; Patent No. US20020034771A1
; GENERAL INFORMATION:
; APPLICANT: Frank, Glenn R.
; Porter, James P.
; Rushlow, Keith E.

; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 107...877
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-944-277A-1

Query Match 100.0%; Score 774; DB 9; Length 1198;

Best Local Similarity 100.0%; Pred. No. 1e-243;
Matches 774; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 707 AAGTACTGGCTACAAATTTTATCCCATTTGTTGGTGGTGAATTTCTGTGTGGACACA 766
QY 661 GGATTATTATCTCAACTCAGCAGCAGTCACTTTCTTTGAAGATTAAAGAACCAAGG 720
Db 767 GGATTATTATCTCAACTCAGCAGCAGTCACTTTCTTTGAAGATTAAAGAACCAAGG 826
QY 721 AAAGCTTCAGACTCTTGAACCCACATCTTAAAGCCCAACCCCAAACTGA 774
Db 827 AAAGCTTCAGACTCTTGAACCCACATCTTAAAGCCCAACCCCAAACTGA 880


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; FILE REFERENCE: 21402-442A
; CURRENT APPLICATION NUMBER: US/10/236,392
; CURRENT FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: US09/540,763
; PRIOR FILING DATE: 2000-03-30
; PRIOR APPLICATION NUMBER: US60/390,155
; PRIOR FILING DATE: 2002-06-19
; PRIOR APPLICATION NUMBER: US09/635,949
; PRIOR FILING DATE: 2000-08-10
; PRIOR APPLICATION NUMBER: US60/318,765
; PRIOR FILING DATE: 2001-09-12
; PRIOR APPLICATION NUMBER: US60/357,303
; PRIOR FILING DATE: 2002-02-15
; PRIOR APPLICATION NUMBER: US60/367,753
; PRIOR FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER: US60/369,479
; PRIOR FILING DATE: 2002-04-02
; PRIOR APPLICATION NUMBER: US09/659,634
; PRIOR FILING DATE: 2000-09-12
; PRIOR APPLICATION NUMBER: US60/318,120
; PRIOR FILING DATE: 2001-09-07
; PRIOR APPLICATION NUMBER: US60/318,130
; PRIOR FILING DATE: 2001-09-07
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 794
; SOFTWARE: Custom
; SEQ ID NO 27
; LENGTH: 898
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (26)..(797)
US-10-236-392-27

Query Match      99.8%; Score 772.4; DB 13; Length 898;
Best Local Similarity 99.9%; Pred. No. 2.9e-243;
Matches 773; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1  ATGCTCTGCGATGGAATCCCTACTCTAGTGTGTAGCCTACTGTCTTCGCTCCA 60
Db
Qy      26  ATGCTCTGCGATGGAATCCCTACTCTAGTGTGTAGCCTACTGTCTTCGCTCCA 85
Db
Qy      61  GATGCGGTGTAGCAGTCCCTCAGAAACCTAAGTCTCTCTTGAACCCCTCCATGGAATAGA 120
Db
Qy      86  GATGCGGTGTAGCAGTCCCTCAGAAACCTAAGTCTCTCTTGAACCCCTCCATGGAATAGA 145
Db
Qy     121  ATATTAAAGGAGAGATGTACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGT 180
Db
Qy     146  ATATTAAAGGAGAGATGTACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGT 205
Db
Qy     181  TCACCAAAATGGTTTCCAAATGGCAGCCTTTTCAGAGAGACAAATTCAGTTTGAATATT 240
Db
Qy     206  TCACCAAAATGGTTTCCAAATGGCAGCCTTTTCAGAGAGACAAATTCAGTTTGAATATT 265
Db
Qy     241  GTGAATGCCAAATTTGAAGACAGTGGAGAAATACAAATGTGAGCAACCAAGTTAATGAG 300
Db
Qy     266  GTGAATGCCAAATTTGAAGACAGTGGAGAAATACAAATGTGAGCAACCAAGTTAATGAG 325
Db
Qy     301  AGTGAACCTGTGTACTTGGAGGCTTTCAGTGTGCTGCTCTCTCAGGCTCTCTGCTGAG 360
Db
Qy     326  AGTGAACCTGTGTACTTGGAGGCTTTCAGTGTGCTGCTCTCTCAGGCTCTCTGCTGAG 385
Db
Qy     361  GTGCTGATGAGGCGCAGCCCTCTCTCTCAGTGTGCTGCTCTCTCAGGCTCTCTGCTGAG 420
Db
Qy     386  GTGCTGATGAGGCGCAGCCCTCTCTCTCAGTGTGCTGCTCTCTCAGGCTCTCTGCTGAG 445
Db
Qy     421  TACAAGTGTATCTATTATAGGATGTGAGCTCTCAAGTACTGTGTATGAGAACCAACAC 480
Db
Qy     446  TACAAGTGTATCTATTATAGGATGTGAGCTCTCAAGTACTGTGTATGAGAACCAACAC 505
Db
Qy     481  ATCTCCATTACAAATGCCACAGTTGAAGACAGTGAACCTACTGTACGGGCGGCAAGTG 540

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Db      506  ATCTCCATTACAAATGCCACAGTTGAAGACAGTGAACCTACTGTACGGGCGGCAAGTG 565
Qy      541  TGGCAGCTGGACTATGAGTCTGAGCCCTCAACATTACTGTAAATAAAGCTCCGGGTGAG 600
Db      566  TGGCAGCTGGACTATGAGTCTGAGCCCTCAACATTACTGTAAATAAAGCTCCGGGTGAG 625
Qy      601  AAGTACTGGCTACAAATTTTATCCCAATTTGGTGGTGAATTCCTTTGCTGTGACACA 660
Db      626  AAGTACTGGCTACAAATTTTATCCCAATTTGGTGGTGAATTCCTTTGCTGTGACACA 685
Qy      661  GGATTATTTATCTCACTCAGCAGCAGTCAATTTCTTTGAAGATTAAAGAACCCAGG 720
Db      686  GGATTATTTATCTCACTCAGCAGCAGTCAATTTCTTTGAAGATTAAAGAACCCAGG 745
Qy      721  AAAGCTTCAGACTTCTGAACCCACATCTTAAGCCAAACCCCAAAACAACCTGA 774
Db      746  AAAGCTTCAGACTTCTGAACCCACATCTTAAGCCAAACCCCAAAACAACCTGA 799

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RESULT 8

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US-09-944-277A-7
; Sequence 7, Application US/09944277A
; Patent No. US20020034771A1
; GENERAL INFORMATION:
; APPLICANT: Frank, Glenn R.
; Porter, James P.
; Rushlow, Keith E.
; Wasson, Donald L.
; TITLE OF INVENTION: Method to Detect Ige
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carol Talkington Verser, Ph.D.
; STREET: 1825 Sharp Point Drive
; CITY: Fort Collins
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80525

```

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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: WordPerfect for Windows, Version 7.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/944,277A
FILING DATE: 30-Aug-2001
CLASSIFICATION: <unknown>

```

```

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/285,873
FILING DATE: 1999-03-31
ATTORNEY/AGENT INFORMATION:
NAME: Verser, Carol Talkington
REGISTRATION NUMBER: 37,459
REFERENCE/DOCKET NUMBER: DI-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 970/493-7272
TELEFAX: 970/484-9505
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 699 nucleotides
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cdna
FEATURE:
NAME/KEY: CDS
LOCATION: 1..699

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; SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-09-944-277A-7
Query Match      90.3%; Score 699; DB 9; Length 699;
Best Local Similarity 100.0%; Pred. No. 3.9e-219;
Matches 699; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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SOFTWARE: WordPerfect for Windows, Version 7.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/944,277A
FILING DATE: 30-Aug-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/285,873
FILING DATE: 1999-03-31
ATTORNEY/AGENT INFORMATION:
NAME: Verser, Carol Talkington
REGISTRATION NUMBER: 37,459
REFERENCE/DOCKET NUMBER: DI-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 970/493-7272
TELEFAX: 970/484-9505
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 591 nucleotides
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..591
SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-09-944-277A-10
Query Match 76.4%; Score 591; DB 9; Length 591;
Best Local Similarity 100.0%; Pred. No. 1.4e-183;
Matches 591; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 76 GTCCCTCAGAAACCTAAGTCTCTTGAACCTCCATGGAATAGATAATTTAAAGGAG 135
Db 1 GTCCCTCAGAAACCTAAGTCTCTTGAACCTCCATGGAATAGATAATTTAAAGGAG 60
QY 136 AATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGTTCACCAAAATGGTTC 195
Db 61 AATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGTTCACCAAAATGGTTC 120
QY 196 CACAATGGCAGCTTTCAAGAGACAAATTCAGTTTGAATTTGAATGTAATGCCAAATTT 255
Db 121 CACAATGGCAGCTTTCAAGAGACAAATTCAGTTTGAATTTGAATGTAATGCCAAATTT 180
QY 256 GAAGACAGTGGAGATACAAATTCAGACCAACCAAGTTAATGAGAGTGAACCTGTGTAC 315
Db 181 GAAGACAGTGGAGATACAAATTCAGACCAACCAAGTTAATGAGAGTGAACCTGTGTAC 240
QY 316 CTGGAAGTCTTCAAGTACCTGCTCTCTTCAAGCTCTGCTGAGGTGGTGTGAGGGC 375
Db 241 CTGGAAGTCTTCAAGTACCTGCTCTCTTCAAGCTCTGCTGAGGTGGTGTGAGGGC 300
QY 376 CAGCCCTCTTCTCAGGTGCCATGGTTGGAGGAACTGGGATGTGTACAAAGTGTATCTAT 435
Db 301 CAGCCCTCTTCTCAGGTGCCATGGTTGGAGGAACTGGGATGTGTACAAAGTGTATCTAT 360
QY 436 TATAAGATGGTGAAGCTCTCAAGTACTGGTATGAGACCAACAATCTCCATTACAAAT 495
Db 361 TATAAGATGGTGAAGCTCTCAAGTACTGGTATGAGACCAACAATCTCCATTACAAAT 420
QY 496 GCCACAGTTGAGACAGTGGACCTACTACTGTACGGCAAAAGTGGCAGCTGGACTAT 555
Db 421 GCCACAGTTGAGACAGTGGACCTACTACTGTACGGCAAAAGTGGCAGCTGGACTAT 480
QY 556 GAGTCTGAGCCCTCAACATTTACTGTAAATAAAGCTCCCGCTGAGAAGTACTGGGTACAA 615
Db 481 GAGTCTGAGCCCTCAACATTTACTGTAAATAAAGCTCCCGCTGAGAAGTACTGGGTACAA 540
QY 616 TTTTATCCCATGTTGGTGTATCTGTTTGGTGTGACACAGGATTTTATCTCA 675
Db 541 TTTTATCCCATGTTGGTGTATCTGTTTGGTGTGACACAGGATTTTATCTCA 600
QY 676 ACTCAGCAGAGTGCATTTCTTTGAAGATTAAGAGAACACAGAAAGCTTCAGACTT 735
Db 601 ACTCAGCAGAGTGCATTTCTTTGAAGATTAAGAGAACACAGAAAGCTTCAGACTT 660
QY 736 CTGAACCCCATCTTAAGCCAAACCCCAAACTGA 774
Db 661 CTGAACCCCATCTTAAGCCAAACCCCAAACTGA 699

QY 1 ATGGCTCTGCTCCATGGAAATCCCTACTCTCTGCTGTAGCTTACTTGTCTTCTCGCTCCA 60
Db 1 ATGGCTCTGCTCCATGGAAATCCCTACTCTCTGCTGTAGCTTACTTGTCTTCTCGCTCCA 60
QY 61 GATGGCTGTTAGCAGTCCCTCAGAAACCTAAGTCTCTTGAACCTCCATGGAATAGA 120
Db 61 GATGGCTGTTAGCAGTCCCTCAGAAACCTAAGTCTCTTGAACCTCCATGGAATAGA 120
QY 121 ATATTTAAGAGAGATGTGACTCTTACATGTATGGGACAAATTTCTTTGAAGTCACT 180
Db 121 ATATTTAAGAGAGATGTGACTCTTACATGTATGGGACAAATTTCTTTGAAGTCACT 180
QY 181 TCCACCAATGGTTCACCAATGGCAGCTTTCAGAGACAAATTCAGTTTGAATATT 240
Db 181 TCCACCAATGGTTCACCAATGGCAGCTTTCAGAGACAAATTCAGTTTGAATATT 240
QY 241 GTGAATGCCAAATTTGAAGACAGTGGAGATACAAATGTGAGCACCAACAAAGTTAATGAG 300
Db 241 GTGAATGCCAAATTTGAAGACAGTGGAGATACAAATGTGAGCACCAACAAAGTTAATGAG 300
QY 301 AGTGAACCTGTGTACCTGGAAATCTTCACTGACCTGGCTGCTCTTCAAGGCTCTGCTGAG 360
Db 301 AGTGAACCTGTGTACCTGGAAATCTTCACTGACCTGGCTGCTCTTCAAGGCTCTGCTGAG 360
QY 361 GTGTGTATGGAGGCGCAGCCCTCTTCTCAGGTGCCATGTGAGGAAATGGGATGTG 420
Db 361 GTGTGTATGGAGGCGCAGCCCTCTTCTCAGGTGCCATGTGAGGAAATGGGATGTG 420
QY 421 TACAAGTGTATCTATTATAAGAGTGGTGAAGCTCTCAAGTACTGTATGAGACCAAC 480
Db 421 TACAAGTGTATCTATTATAAGAGTGGTGAAGCTCTCAAGTACTGTATGAGACCAAC 480
QY 481 ATCTCCATTACAATGGCCACAGTTCAGACAGTGGAACTTACTACTGTACGGGCAAGTG 540
Db 481 ATCTCCATTACAATGGCCACAGTTCAGACAGTGGAACTTACTACTGTACGGGCAAGTG 540
QY 541 TGGCAGCTGGACTATGAGTCTGAGCCCTCAACATTACTGTATATAAAGCT 591
Db 541 TGGCAGCTGGACTATGAGTCTGAGCCCTCAACATTACTGTATATAAAGCT 591

RESULT 9
US-09-944-277A-10
Sequence 10, Application US/09944277A
Patent No. US2002034771A1
GENERAL INFORMATION:
APPLICANT: Frank, Glenn R.
Porter, James P.
Rushlow, Keith E.
Wassom, Donald L.
TITLE OF INVENTION: Method to Detect Ige
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Carol Talkington Verser, Ph.D.
STREET: 1825 Sharp Point Drive
CITY: Fort Collins
STATE: Colorado
COUNTRY: USA
ZIP: 80525
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95


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; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 528
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(528)
US-09-809-715-1

Query Match
Best Local Similarity 68.2%; Score 528; DB 10; Length 528;
Matches 528; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 76 GTCCCTCAGAAACCTAAGGTCCTCTTGAACCCCTCCATGGAATAGATAATTTAAAGGAGAG 135
Db 1 GTCCCTCAGAAACCTAAGGTCCTCTTGAACCCCTCCATGGAATAGATAATTTAAAGGAGAG 60

QY 136 AATGTGACTCTTACATGTAATGGGACAAATTTCTTGAAGTCAGTCCACCAATGGTTC 195
Db 61 AATGTGACTCTTACATGTAATGGGACAAATTTCTTGAAGTCAGTCCACCAATGGTTC 120

QY 196 CACAATGGCAGCCTTTTCAAGAGAGACAAATTTCAAGTTTGAATTTGTAATGCCAAATTT 255
Db 121 CACAATGGCAGCCTTTTCAAGAGAGACAAATTTCAAGTTTGAATTTGTAATGCCAAATTT 180

QY 256 GAAGACAGTGGAGATACAAATTTGAGCAGCAACCAAGTTTAATGAGAGTGAACCTGTGTAC 315
Db 181 GAAGACAGTGGAGATACAAATTTGAGCAGCAACCAAGTTTAATGAGAGTGAACCTGTGTAC 240

QY 316 CTGGAAGTCTTCAAGTGGCTGCTCTTCAAGGCTCTGCTGAGGCTCTGCTGAGGCTGAGGAGGC 375
Db 241 CTGGAAGTCTTCAAGTGGCTGCTCTTCAAGGCTCTGCTGAGGCTCTGCTGAGGCTGAGGAGGC 300

QY 376 CAGCCCTCTTCTCAGTGGCTGCTCTTCAAGGCTCTGCTGAGGCTGCTGAGGCTGAGGAGGC 435
Db 301 CAGCCCTCTTCTCAGTGGCTGCTCTTCAAGGCTCTGCTGAGGCTGCTGAGGCTGAGGAGGC 360

QY 436 TATAGGATGGTGAAGCTCTCAAGTGGCTGCTCTTCAAGGCTCTGCTGAGGCTGCTGAGGCTGAGGAGGC 495
Db 361 TATAGGATGGTGAAGCTCTCAAGTGGCTGCTCTTCAAGGCTCTGCTGAGGCTGCTGAGGCTGAGGAGGC 420

QY 496 GCCACAGTTGAAGACAGTGGACCTTACTACTGACGGGCAAGTGTGGCAGCTGGAGTAT 555
Db 421 GCCACAGTTGAAGACAGTGGACCTTACTACTGACGGGCAAGTGTGGCAGCTGGAGTAT 480

QY 556 GAGTCTGAGCCCTCAACATTTACTGTATAAAGCTCCCGTGGAGAG 603
Db 481 GAGTCTGAGCCCTCAACATTTACTGTATAAAGCTCCCGTGGAGAG 528

RESULT 12
US-10-293-992-1
; Sequence 1, Application US/10293992
; Publication No. US20040033527A1
; GENERAL INFORMATION:
; APPLICANT: Jardtzy, Theodore S.
; APPLICANT: Garman, Scott Clayton
; APPLICANT: Kinet, Jean-Pierre
; TITLE OF INVENTION: METHODS OF USING A THREE-DIMENSIONAL MODEL OF A PC EPSILON RECEPTOR
; FILE REFERENCE: AL-3-C1-1
; CURRENT APPLICATION NUMBER: US/10/293,992
; PRIOR FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: 09/434,193
; PRIOR FILING DATE: 1999-11-04
; PRIOR APPLICATION NUMBER: 60/107,219
; PRIOR FILING DATE: 1998-11-05
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 528
; TYPE: DNA
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; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(528)
; OTHER INFORMATION:
US-10-293-992-1

Query Match
Best Local Similarity 68.2%; Score 528; DB 13; Length 528;
Matches 528; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 76 GTCCCTCAGAAACCTAAGGTCCTCTTGAACCCCTCCATGGAATAGATAATTTAAAGGAGAG 135
Db 1 GTCCCTCAGAAACCTAAGGTCCTCTTGAACCCCTCCATGGAATAGATAATTTAAAGGAGAG 60

QY 136 AATGTGACTCTTACATGTAATGGGACAAATTTCTTGAAGTCAGTCCACCAATGGTTC 195
Db 61 AATGTGACTCTTACATGTAATGGGACAAATTTCTTGAAGTCAGTCCACCAATGGTTC 120

QY 196 CACAATGGCAGCCTTTTCAAGAGAGACAAATTTCAAGTTTGAATTTGTAATGCCAAATTT 255
Db 121 CACAATGGCAGCCTTTTCAAGAGAGACAAATTTCAAGTTTGAATTTGTAATGCCAAATTT 180

QY 256 GAAGACAGTGGAGATACAAATTTGAGCAGCAACCAAGTTTAATGAGAGTGAACCTGTGTAC 315
Db 181 GAAGACAGTGGAGATACAAATTTGAGCAGCAACCAAGTTTAATGAGAGTGAACCTGTGTAC 240

QY 316 CTGGAAGTCTTCAAGTGGCTGCTCTTCAAGGCTCTGCTGAGGCTCTGCTGAGGCTGAGGAGGC 375
Db 241 CTGGAAGTCTTCAAGTGGCTGCTCTTCAAGGCTCTGCTGAGGCTCTGCTGAGGCTGAGGAGGC 300

QY 376 CAGCCCTCTTCTCAGTGGCTGCTCTTCAAGGCTCTGCTGAGGCTGCTGAGGCTGAGGAGGC 435
Db 301 CAGCCCTCTTCTCAGTGGCTGCTCTTCAAGGCTCTGCTGAGGCTGCTGAGGCTGAGGAGGC 360

QY 436 TATAGGATGGTGAAGCTCTCAAGTGGCTGCTCTTCAAGGCTCTGCTGAGGCTGCTGAGGCTGAGGAGGC 495
Db 361 TATAGGATGGTGAAGCTCTCAAGTGGCTGCTCTTCAAGGCTCTGCTGAGGCTGCTGAGGCTGAGGAGGC 420

QY 496 GCCACAGTTGAAGACAGTGGACCTTACTACTGACGGGCAAGTGTGGCAGCTGGAGTAT 555
Db 421 GCCACAGTTGAAGACAGTGGACCTTACTACTGACGGGCAAGTGTGGCAGCTGGAGTAT 480

QY 556 GAGTCTGAGCCCTCAACATTTACTGTATAAAGCTCCCGTGGAGAG 603
Db 481 GAGTCTGAGCCCTCAACATTTACTGTATAAAGCTCCCGTGGAGAG 528

RESULT 13
US-09-944-277A-12
; Sequence 12, Application US/09944277A
; Patent No. US20020034771A1
; GENERAL INFORMATION:
; APPLICANT: Frank, Glenn R.
; APPLICANT: Porter, James P.
; APPLICANT: Rushlow, Keith E.
; APPLICANT: Wassom, Donald L.
; TITLE OF INVENTION: Method to Detect Ige
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carol Talkington Verser, Ph.D.
; STREET: 1825 Sharp Point Drive
; CITY: Fort Collins
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80525
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: Wordperfect for Windows, Version 7.0
; CURRENT APPLICATION DATA:
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APPLICATION NUMBER: US/09/944,277A
FILING DATE: 30-Aug-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/285,873
FILING DATE: 1999-03-31
ATTORNEY/AGENT INFORMATION:
NAME: Verser, Carol Talkington
REGISTRATION NUMBER: 37,459
REFERENCE/DOCKET NUMBER: DI-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 970/493-7272
TELEFAX: 970/484-9505
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 516 nucleotides
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..516
SEQUENCE DESCRIPTION: SEQ ID NO: 12:

US-09-944-277A-12

Query Match 66.7%; Score 516; DB 9; Length 516;
Best Local Similarity 100.0%; Pred. No. 6.8e-159;
Matches 516; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	76	GTCCCTCAGAAACCTAAGGTCCTCTGAACCCCTCCATGGAATAGATAATTTAAAGGAGAG	135
DB	1	GTCCCTCAGAAACCTAAGGTCCTCTGAACCCCTCCATGGAATAGATAATTTAAAGGAGAG	60
QY	136	AATGTGACTCTTACATGTAAATGGGAACAATTTCTTTGAAGTCAGTTCCACCAAAATGGTTC	195
DB	61	AATGTGACTCTTACATGTAAATGGGAACAATTTCTTTGAAGTCAGTTCCACCAAAATGGTTC	120
QY	196	CACAATGGCAGCCTTTTCAGAGAGACAAATTCAGTTTGAATTTGAATGCCAAATTT	255
DB	121	CACAATGGCAGCCTTTTCAGAGAGACAAATTCAGTTTGAATTTGAATGCCAAATTT	180
QY	256	GAAGACAGTGGAGAAATCAAAATGTGAGAGACAAATTCAGTTTGAATTTGAATGCCAAATTT	315
DB	181	GAAGACAGTGGAGAAATCAAAATGTGAGAGACAAATTCAGTTTGAATTTGAATGCCAAATTT	180
QY	316	CTGGAAGTCTTCAAGTACTGCTCTCTCAGGCTCTCTGAGGTGGTGTGAGGGGC	375
DB	241	CTGGAAGTCTTCAAGTACTGCTCTCTCAGGCTCTCTGAGGTGGTGTGAGGGGC	300
QY	376	CAGCCCTCTTCTCAGGTGCCATGGTGGAGAACTGGGATGTGTACAAAGTGATCTAT	435
DB	301	CAGCCCTCTTCTCAGGTGCCATGGTGGAGAACTGGGATGTGTACAAAGTGATCTAT	360
QY	436	TATAAGGATGGTGAAGCTCTCAAGTACTGTATGAGAACCAACATCTCCATTACAAAT	495
DB	361	TATAAGGATGGTGAAGCTCTCAAGTACTGTATGAGAACCAACATCTCCATTACAAAT	420
QY	496	GCCACAGTTGAAGACAGTGGAACTTACTACTGTACGGGCAAAAGTGGGAGCTGGACTAT	555
DB	421	GCCACAGTTGAAGACAGTGGAACTTACTACTGTACGGGCAAAAGTGGGAGCTGGACTAT	480
QY	556	GAGTCTGAGCCCTCAACATTTACTGTAAATAAAGCT	591
DB	481	GAGTCTGAGCCCTCAACATTTACTGTAAATAAAGCT	516

RESULT 14

US-10-293-992-3
Sequence 3, Application US/10293992
Publication No. US20040033527A1
GENERAL INFORMATION:
APPLICANT: Jardtzy, Theodore S.

APPLICANT: Garman, Scott Clayton
APPLICANT: Kinet, Jean-Pierre
TITLE OF INVENTION: METHODS OF USING A THREE-DIMENSIONAL MODEL OF A FC EPSILON RECEPTOR
TITLE OF INVENTION: CHAIN
FILE REFERENCE: AL-3-CL-1
CURRENT APPLICATION NUMBER: US/10/293,992
CURRENT FILING DATE: 2002-11-13
PRIOR APPLICATION NUMBER: 09/434,193
PRIOR FILING DATE: 1999-11-04
PRIOR APPLICATION NUMBER: 60/107,219
PRIOR FILING DATE: 1998-11-05
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patent in version 3.1
SEQ ID NO 3
LENGTH: 516
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(516)
OTHER INFORMATION:
US-10-293-992-3

Query Match 66.7%; Score 516; DB 13; Length 516;

Best Local Similarity 100.0%; Pred. No. 6.8e-159;
Matches 516; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	76	GTCCCTCAGAAACCTAAGGTCCTCTGAACCCCTCCATGGAATAGATAATTTAAAGGAGAG	135
DB	1	GTCCCTCAGAAACCTAAGGTCCTCTGAACCCCTCCATGGAATAGATAATTTAAAGGAGAG	60
QY	136	AATGTGACTCTTACATGTAAATGGGAACAATTTCTTTGAAGTCAGTTCCACCAAAATGGTTC	195
DB	61	AATGTGACTCTTACATGTAAATGGGAACAATTTCTTTGAAGTCAGTTCCACCAAAATGGTTC	120
QY	196	CACAATGGCAGCCTTTTCAGAGAGACAAATTCAGTTTGAATTTGAATGCCAAATTT	255
DB	121	CACAATGGCAGCCTTTTCAGAGAGACAAATTCAGTTTGAATTTGAATGCCAAATTT	180
QY	256	GAAGACAGTGGAGAAATCAAAATGTGAGAGACAAATTCAGTTTGAATTTGAATGCCAAATTT	315
DB	181	GAAGACAGTGGAGAAATCAAAATGTGAGAGACAAATTCAGTTTGAATTTGAATGCCAAATTT	240
QY	316	CTGGAAGTCTTCAAGTACTGCTCTCTCAGGCTCTCTGAGGTGGTGTGAGGGGC	375
DB	241	CTGGAAGTCTTCAAGTACTGCTCTCTCAGGCTCTCTGAGGTGGTGTGAGGGGC	300
QY	376	CAGCCCTCTTCTCAGGTGCCATGGTGGAGAACTGGGATGTGTACAAAGTGATCTAT	435
DB	301	CAGCCCTCTTCTCAGGTGCCATGGTGGAGAACTGGGATGTGTACAAAGTGATCTAT	360
QY	436	TATAAGGATGGTGAAGCTCTCAAGTACTGTATGAGAACCAACATCTCCATTACAAAT	495
DB	361	TATAAGGATGGTGAAGCTCTCAAGTACTGTATGAGAACCAACATCTCCATTACAAAT	420
QY	496	GCCACAGTTGAAGACAGTGGAACTTACTACTGTACGGGCAAAAGTGGGAGCTGGACTAT	555
DB	421	GCCACAGTTGAAGACAGTGGAACTTACTACTGTACGGGCAAAAGTGGGAGCTGGACTAT	480
QY	556	GAGTCTGAGCCCTCAACATTTACTGTAAATAAAGCT	591
DB	481	GAGTCTGAGCCCTCAACATTTACTGTAAATAAAGCT	516

RESULT 15

US-05-809-715-3
Sequence 3, Application US/09809715
Publication No. US20030003502A1
GENERAL INFORMATION:
APPLICANT: Jardtzy, Theodore S.
APPLICANT: Garman, Scott Clayton
APPLICANT: Wurzburg, Beth A.
APPLICANT: Kinet, Jean-Pierre

;; TITLE OF INVENTION: THREE-DIMENSIONAL MODEL OF A COMPLEX BETWEEN A FC
;; TITLE OF INVENTION: EPSILON RECEPTOR ALPHA CHAIN AND A FC REGION OF AN IGE
;; TITLE OF INVENTION: ANTIBODY AND USES THEREOF
;; FILE REFERENCE: AL-8
;; CURRENT APPLICATION NUMBER: US/09/809,715
;; CURRENT FILING DATE: 2001-03-14
;; PRIOR APPLICATION NUMBER: 60/189,853
;; PRIOR FILING DATE: 2000-03-15
;; NUMBER OF SEQ ID NOS: 6
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO 3
;; LENGTH: 528
;; TYPE: DNA
;; ORGANISM: Homo sapiens
;; FEATURE:
;; NAME/KEY: CDS
;; LOCATION: (1)..(528)
US-09-809-715-3

Query Match 66.6%; Score 515.2; DB 10; Length 528;
Best Local Similarity 98.5%; Pred. No. 1.3e-158;
Matches 520; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

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QY	136	AATGTGACTCTTACATGTAATGGGAACAAATTTCTTTGAAGTCAGTTCCACCAAAATGGTTC	195
Db	61	AATGTGACTCTTACATGTAATGGGAACAAATTTCTTTGAAGTCAGTTCCACCAAAATGGTTC	120
QY	196	CACAATGGCAGCCCTTTCAGAGAGACAAATTCAGTTTGAATATTTGAATGCCAAATTT	255
Db	121	CACAATGGCAGCCCTTTCAGAGAGACAAATTCAGTTTGAATATTTGAATGCCAAATTT	180
QY	256	GAAGACAGTGGAGATACAAATGTCAGCACCAACAGTTAATGAGAGTGAACCTGTGTAC	315
Db	181	GAAGACAGTGGAGATACAAATGTCAGCACCAACAGTTAATGAGAGTGAACCTGTGTAC	240
QY	316	CTGGAGTCTTCAGTGACTGGTGTCTCTTCAGGCTCTGCTGAGGTGGTGTATGGAGGGC	375
Db	241	CTGGAGTCTTCAGTGACTGGTGTCTCTTCAGGCTCTGCTGAGGTGGTGTATGGAGGGC	300
QY	376	CAGCCCTCTTCTCAGTGCCATGGTTGGAGGAACCTGGATGTGTACAAGTGATCTAT	435
Db	301	CAGCCCTCTTCTCAGTGCCATGGTTGGAGGAACCTGGATGTGTACAAGTGATCTAT	360
QY	436	TATAAGGATGGTGAAGCTCTCAAGTACTGTTATGAGAACCAACATCTCCATTACAAT	495
Db	361	TATAAGGATGGTGAAGCTCTCAAGTACTGTTATGAGAACCAACATCTCCATTACAAT	420
QY	496	GCCACAGTTGAAGACAGTGGAACTACTACTCTACGGGCAAAAGTGTGGCAGCTGGACTAT	555
Db	421	GCCGCAAGTGAAGACAGTGGAACTACTACTCTACGGGCAAAAGTGTGGCAGCTGGACTAT	480
QY	556	GAGTCTGAGCCCTCAACATTAATTAATTAAGCTCCGCTGAGAAG	603
Db	481	GAGTCTGAGCCCTCAACATTAATTAATTAAGCTCCGCTGAGAAG	528

Search completed: October 11, 2004, 01:41:40
Job time : 451.92 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 10, 2004, 11:14:29 ; Search time 2611.69 Seconds
(without alignments)
8849.962 Million cell updates/sec

Title: US-10-763-400-4
Perfect score: 774
Sequence: 1 atggctctgcctgaatc.....caaaccccaaaactga 774

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: em_esthum:*
3: em_estin:*
4: em_estnu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hic:*
9: gb_est1:*
10: gb_est2:*
11: gb_hic:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
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18: em_gss_inv:*
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20: em_gss_vrt:*
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27: em_gss_vrl:*
28: gb_gss1:*
29: gb_gss2:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	690.8	89.3	810	12	BG542554
2	608	78.6	834	10	BF679057
3	559.4	72.3	760	12	BG542157
4	555.6	71.8	840	12	BG548515

5	500.6	64.7	846	10	BF678252
6	475.4	61.4	768	13	BQ573778
7	417	53.9	707	14	CA448745
8	411.6	53.2	712	14	CA419024
9	406.4	52.5	818	10	BF677190
10	367.6	47.5	669	10	AW612525
11	337.4	43.6	660	14	CF362072
12	326.4	42.2	615	12	BM991911
13	308.4	39.8	488	13	EX110472
14	272.6	35.2	652	13	BY752906
15	254	32.8	570	9	AI676114
16	250	32.3	651	14	CF363368
17	244.2	31.6	540	9	AI685796
18	225.4	29.1	641	14	CB429248
19	222.8	28.8	394	10	AW357271
20	216.8	28.3	422	10	BF603113
21	186	24.0	479	10	BF593204
22	184	23.8	478	12	BQ005218
23	180.4	23.3	757	14	CA508723
24	175.8	22.7	403	14	CB768694
25	174.4	22.5	1201	9	AL514096
26	173	22.4	446	9	AI676097
27	172.4	22.3	429	13	BY228345
28	169.8	21.9	848	14	CB958187
29	169.4	21.9	1033	9	AL549464
30	169.4	21.9	1201	9	AL531122
31	167.8	21.7	874	14	CD244068
32	167.8	21.7	1201	13	BX399366
33	164.8	21.3	528	14	CB152997
34	163.8	21.2	823	12	BI768140
35	163	21.1	1201	13	BX402696
36	162.6	21.0	403	13	BY228552
37	162.6	21.0	404	13	BY227642
38	162.6	21.0	1201	9	AL588081
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40	162.2	21.0	987	13	BX345202
41	161.8	20.9	373	13	BY041924
42	161.2	20.8	852	12	BI821954
43	160	20.7	221	14	CD696486
44	158.4	20.5	551	12	BM364531
45	155.6	20.1	571	14	CD693938

ALIGNMENTS

RESULT 1
BG542554
LOCUS 602572052P1 NIH_MGC_77 Homo sapiens CDNA clone IMAGE:4696381 5',
DEFINITION 810 bp mRNA linear EST 03-APR-2001
ACCESSION BG542554
VERSION BG542554
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 810)
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov
Tissue Procurement: CLONTECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LCM1523 row: h column: 14
High quality sequence stop: 667.

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/db_xref="taxon:9606"
/clone="IMAGE:4696381"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NIH_MGC 77"
/notes="Organ: lung; Vector: pDNR-LIB (Clontech); Site 1:
SfiI (ggcgctcgcc); Site 2: SfiI (ggcattatggc); 5' and
3' adaptors were used in cloning as follows: 5' adaptor
sequence: 5'-CAGGCCATTATGGCC-3' and 3' adaptor sequence:
5'-ATTCTAGAGCGGCGGCAGATG-3' (30)BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size 1.9
kb (range 0.5-4.0 kb). 12/15 colonies contained inserts
by PCR. This library was enriched for full-length clones
and was constructed by Clontech Laboratories (Palo Alto,
CA). Note: this is a NIH_MGC Library."

ORIGIN
Query Match 89.3%; Score 690.8; DB 12; Length 810;
Best Local Similarity 97.0%; Pred. No. 4.5e-196;
Matches 747; Conservative 0; Mismatches 17; Indels 6; Gaps 4;

QY 1 ATGGCTCTGCGCATGGAAATCCCTACTCTACTGTGTAGCCTTACTGTCTTCGCTCCA 60
DB 31 ATGGCTCTGCGCATGGAAATCCCTACTCTACTGTGTAGCCTTACTGTCTTCGCTCCA 90
QY 61 GATGGCGTGTAGCAGTCCCTCAGAACTTAAAGTCTCTCTTGAACCCCTCCATGGAATAGA 120
DB 91 GATGGCGTGTAGCAGTCCCTCAGAACTTAAAGTCTCTCTTGAACCCCTCCATGGAATAGA 150
QY 121 ATATTTAAAGAGAGATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGT 180
DB 151 ATATTTAAAGAGAGATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGT 210
QY 181 TCCACCAAAATGGTTCCCAATGGCAGCTTTCAGAGAGACAATTCAGTTTGAATATT 240
DB 211 TCCACCAAAATGGTTCCCAATGGCAGCTTTCAGAGAGACAATTCAGTTTGAATATT 270
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4294467"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NIH_MGC_83"
/notes="Organ: prostate; Vector: pDNR-LIB (Clontech);
Site 1: SfiI (ggcgctcgcc); Site 2: SfiI
(ggcattatggc); 5' and 3' adaptors were used in cloning
as follows: 5' adaptor sequence: 5'-CAGGCCATTATGGCC-3'
and 3' adaptor sequence:
5'-ATTCTAGAGCGGCGGCAGATG-3' (30)BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size 1.4
kb (range 0.5-4.0 kb). 14/15 colonies contained inserts
by PCR. This library was enriched for full-length clones
and was constructed by Clontech Laboratories (Palo Alto,
CA)."

ORIGIN
Query Match 78.6%; Score 608; DB 10; Length 834;
Best Local Similarity 95.8%; Pred. No. 3.7e-171;
Matches 657; Conservative 0; Mismatches 25; Indels 4; Gaps 3;

QY 1 ATGGCTCTGCGCATGGAAATCCCTACTCTACTGTGTAGCCTTACTGTCTTCGCTCCA 60
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QY 61 GATGGCGTGTAGCAGTCCCTCAGAAACCTTAAGTCTCTTGAACCCCTCCATGGAATAGA 120
DB 91 GATGGCGTGTAGCAGTCCCTCAGAAACCTTAAGTCTCTTGAACCCCTCCATGGAATAGA 150
QY 121 ATATTTAAAGAGAGATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGT 180
DB 151 ATATTTAAAGAGAGATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGT 210
QY 181 TCCACCAAAATGGTTCCCAATGGCAGCTTTCAGAGAGACAATTCAGTTTGAATATT 240
DB 211 TCCACCAAAATGGTTCCCAATGGCAGCTTTCAGAGAGACAATTCAGTTTGAATATT 270
QY 241 GTGAATGCCAAATTTGAAGCAGTGGAGATAACAATGTCTAGCACCACCAAGTTAATGAG 300

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Tissue Procurement: CLONTECH Laboratories, Inc.
 cDNA Library Preparation: CLONTECH Laboratories, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Cloning Distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
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 High quality sequence stop: 590.
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 /db_xref="taxon:9606"
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 /lab_host="DH10B (T1 phage-resistant)"
 /clone_lib="NIH_MGC_77"
 /note="Organ: lung; Vector: pDNR-LIB (Clontech); Site 1: SfiI (ggccattatggcc); Site 2: SfiI (ggccattatggcc); 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGCCATATGGCC-3' and 3' adaptor sequence: 5'-ATTCTAGAGCGCGGCGGCATG-dt(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.9 kb (range 0.5-4.0 kb). 12/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH_MGC Library."

ORIGIN

Query Match 71.8%; Score 555.6; DB 12; Length 840;
 Best Local Similarity 88.3%; Pred. No. 2.1e-155;
 Matches 701; Conservative 0; Mismatches 69; Indels 24; Gaps 8;

Qy 1 ATGGCTCTGCGCATGGAATCCCTTACTACTGTGTAGCCCTTACTTCTCGTCCA 60
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 Qy 61 GATGCGGTGTAGCAGTCCCTCAGAACCTTAAGTCTCTTGAACCTCCATGGAATAG 120
 Db 91 GATGCGGTGTAGCAGTCCCTCAGAACCTTAAGTCTCTTGAACCTCCATGGAATAG 150
 Qy 121 ATATTAAAGAGAGAAATGTACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGT 180
 Db 151 ATATTAAAGAGAGAAATGTACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGT 210
 Qy 181 TCCACCAAAATGGTTCACATATGGCAGCTTTCAGAGAGACAATTCAGTTGAATAT 240
 Db 211 TCCACCAAAATGGTTCACATATGGCAGCTTTCAGAGAGACAATTCAGTTGAATAT 270
 Qy 241 GTGAATGCCAAATTTGAAGACAGTGGAGAAATACAAATGTGAGCACCACCAAGTTAATGAG 300
 Db 271 GTGAATGCCAAATTTGAAGACAGTGGAGAAATACAAATGTGAGCACCACCAAGTTAATGAG 330
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 Qy 361 GTGTGTATGAGGCGCAGCCCTCTTCTCAGTGTGCTGCTGAGGAGTGGAGTGG 420
 Db 391 GTGTGTATGAGGCGCAGCCCTCTTCTCAGTGTGCTGCTGAGGAGTGGAGTGG 450
 Qy 421 TACAAGTGATCTATTATAGGATGGTGAAGCTCTCAAGTACTGTGTATGAGAACCAAC 480
 Db 451 TACAAGTGATCTATTATAGGATGGTGAAGCTCTCAAGTACTGTGTATGAGAACCAAC 510
 Qy 481 ATCTCCATTAACAAT--GCCACAGTTGACAGAGTGAACCTTAC--TACTGTACGGCAAA 537
 Db 511 ATCTCCATTAACAATTTGACAGAGTGAACCTTACTTACTGTACGGCAAA 570
 Qy 538 GTGTGGCAGCTGGAC-----TATGAGTCTGAGGCCCTCTCAACATTACTGTAA---T 584
 Db 571 GTGTGGCAGCTGGACCTTATGAAGTTCTTGAAGGCCCTCTCAACATTACTGTAAATTTA 630

Qy 585 AAAAGCTCCGCT---GAGAACTACTGGTACAAATTTTATCCCATTTGGTGGTGTAT 641
 Db 631 AAATGCTCCGAGTGAAGAAAGTACTTGGTACAAATTTTATATCAATTTGGTGGGCTGAA 690
 Qy 642 T--CTGTTTGTGTGGACACAGGA--TTATTTATCTCAACTCAGCA--CGAGGTCAATTT 696
 Db 691 TCCCTGTTTGTGTGGACACCGGATTTATTTATCTCAACTCAGCAAGCGTCCCATTT 750
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 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 846)
 AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: CLONTECH Laboratories, Inc.
 cDNA Library Preparation: CLONTECH Laboratories, Inc.
 DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Cloning Distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Plate: LLCMI071 row: j column: 15
 High quality sequence stop: 609.
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 /clone_lib="NIH_MGC_83"
 /note="Organ: prostate; Vector: pDNR-LIB (Clontech); Site 1: SfiI (ggccattatggcc); Site 2: SfiI (ggccattatggcc); 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGCCATTAATGGCC-3' and 3' adaptor sequence: 5'-ATTCTAGAGCGCGGCGGCATG-dt(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.4 kb (range 0.5-4.0 kb). 14/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA)."

ORIGIN

Query Match 64.7%; Score 500.6; DB 10; Length 846;
 Best Local Similarity 92.8%; Pred. No. 7.6e-139;
 Matches 636; Conservative 0; Mismatches 34; Indels 15; Gaps 10;

Qy 12 CATGGAATCCCTACTACTGTGTGTAGCCTTACTTCTTCGCTCCAGATGGCGTGT 71
 Db 36 CATGGAATCCCTACTACTGTGTGTAGCCTTACTTCTTCGCTCCAGATGGCGTGT 95

FEATURES
 source

UI-H-E10-ayo-p-24-0-UI 3', mRNA sequence.
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 CA448745.1 GI:24813165
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 Homo sapiens (human)
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 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 707)
 NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index.
 Unpublished (1997)
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: Dr. Jose Mercuende
 cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
 cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: Clone distribution information can be obtained
 from Dr. M. Bento Soares, bento-soares@uiowa.edu
 The following repetitive elements were found in this cDNA
 sequence: 93-129, >LINE2 (matched complement)
 Seg primer: M13 FORWARD
 POLYA=Yes.
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 /lab_host="DHI0B (Life Technologies)"
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 with a modified polylinker; Site 1: EcoR I; Site 2: Not I;
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 according to Bonaldo, Lennon and Soares, Genome Research,
 6:791-806, 1996. First strand cDNA synthesis was primed
 with an oligo-dT primer containing a Not I site. Double
 stranded cDNA was ligated to an EcoR I adaptor, digested
 with Not I, and cloned directionally into pT7T3-Pac
 vector. The oligonucleotide used to prime the synthesis of
 first-strand cDNA contains a library tag sequence that is
 located between the Not I site and the (dT)18 tail. The
 sequence tag for this library is ACATTGCGAC.
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 TAG_SEQ=ACATTGCGAC"
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 Matches 417; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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 DB 347 AGGAAGGCTTCAGACTTCTGNAACCCACATCTCTAGCCCAACCCCAACCAACTGA 291
 RESULT 8
 CA419024/c
 LOCUS
 DEFINITION
 UI-H-E21-bbj-e-19-0-UI.s1 NCI_CGAP_Ch2 Homo sapiens cDNA clone
 UI-H-E21-bbj-e-19-0-UI 3', mRNA sequence.
 CA419024
 CA419024.1 GI:24781675
 EST.
 Homo sapiens (human)
 ORGANISM
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 712)
 NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index.
 Unpublished (1997)
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: Dr. Steven Gitelis/ Rush Presbyterian, Dept. of
 Orthopaedics
 cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
 cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: Clone distribution information can be obtained
 from Dr. M. Bento Soares, bento-soares@uiowa.edu
 The following repetitive elements were found in this cDNA
 sequence: 1-42, >(TAAA)n#Simple repeat (matched complement)
 94-130, >LINE2 (matched complement)
 Seg primer: M13 FORWARD
 POLYA=Yes.
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 /dev_stage="Adult"
 /lab_host="DHI0B (Life Technologies)"
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 /note="Organ: Left Pelvis; Vector: pT7T3-Pac (Pharmacia)
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 NCI CGAP Ch2 is a normalized cDNA library containing the
 following tissue(s): Chondrosarcoma Grade II. The library
 was constructed according to Bonaldo, Lennon and Soares,
 Genome Research, 6:791-806, 1996. First strand cDNA
 synthesis was primed with an oligo-dT primer containing a
 Not I site. Double stranded cDNA was ligated to an EcoR I
 adaptor, digested with Not I, and cloned directionally
 into pT7T3-Pac vector. The oligonucleotide used to prime
 the synthesis of first-strand cDNA contains a library tag
 sequence that is located between the Not I site and the
 (dT)18 tail. The sequence tag for this library is
 TGATCAGCT.
 TAG LIB=UI-H-E21
 TAG_SEQ=ATCTAATATG"
 ORIGIN

Query Match 53.2%; Score 411.6; DB 14; Length 712;
 Best Local Similarity 98.3%; Pred. No. 4e-112;
 Matches 414; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 354 TGCTGAGTGTGATGAGGCGGAGCCCTCTCTCTCAGTGGCATGGTGGAGGAACGTG 413
 DB 712 TGCTGAGTGTGATGAGGCGGAGCCCTCTCTCAGTGGCATGGTGGAGGAACGTG 653

QY 414 GGATGTGTACAGGTGTATCTATTATAAGGATGGTGAAGCTCTCAAGTACTGTGATGAGAA 473
 DB 652 GGATGTGTACAGGTGTATCTATTATAAGGATGGTGAAGCTCTCAAGTACTGTGATGAGAA 593

QY 474 CCACAGATCTCCATTACAAATGCCAGTGTGAAGAGAGTGGACCTACTACTGTACGGG 533
 DB 592 CCACAGATCTCCATTACAAATGCCAGTGTGAAGAGAGTGGACCTACTACTGTACGGG 533

QY 534 CAAGTGTGGCAGCTGAGTATGATCTGAGCCCTCAACATTAAGTCTGTAATAAAGCTCC 593
 DB 532 CAAGTGTGGCAGCTGAGTATGATCTGAGCCCTCAACATTAAGTCTGTAATAAAGCTCC 473

QY 594 GCGTGAGAGTACTGGCTACAAATTTTATCCCATTTGTTGGTGATCTGTTTCTGT 653
 DB 472 GCGTGAGAGTACTGGCTACAAATTTTATCCCATTTGTTGGTGATCTGTTTCTGT 413

QY 654 GGACACAGGATTTATTTATCTCAACTGACGACAGCTCACATTTCTCTGAAAGATTAAAG 713
 DB 412 GGACACAGGATTTATTTATCTCAACTGACGACAGCTCACATTTCTCTGAAAGATTAAAG 353

QY 714 AACAGGAAGGCTTGAGCTTCTGAACCCACATCTTAAGCCAAAACCCAAAACAACTG 773
 DB 352 AACAGGAAGGCTTGAGCTTCTGAACCCACATCTTAAGCCAAAACCCAAAACAACTG 293

QY 774 A 774
 DB 292 A 292

RESULT 9
 BF677190
 LOCUS
 DEFINITION 602087255F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4251469 5',
 mRNA sequence.
 ACCESSION BF677190
 VERSION BF677190.1 GI:11951085
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 818)
 NIH-MGC <http://mgi.uci.nih.gov/>.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: CLONETECH Laboratories, Inc.
 cDNA Library Preparation: CLONETECH Laboratories, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: LLCM1074 row: n column: 14
 High quality sequence stop: 616.
 Location/Qualifiers
 1..818
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:4251469"
 /lab_host="DH10B (T1 phage-resistant)"
 /clone_lib="NIH_MGC_83"
 /note="Organ: prostate; Vector: pDNR-LIB (Clontech);

FEATURES

source

Site 1: SfiI (ggccgctcgcc); Site 2: SfiI (ggccattatggc); 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGCCATTATGGCC-3' and 3' adaptor sequence: 5'-ATTCTAGAGCCGAGGCGGACATG-QT(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.4 kb (range 0.5-4.0 kb). 14/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA)."

ORIGIN

Query Match 52.5%; Score 406.4; DB 10; Length 818;
 Best Local Similarity 53.3%; Pred. No. 1.6e-110;
 Matches 583; Conservative 0; Mismatches 101; Indels 16; Gaps 10;

QY 1 ATGCTCTCTCCATGGGAATCCCTACTCTACTGTGTAGCCCTTACTGTCTCGCTCA 60
 DB 35 ATGCTCTCTCCATGGGAATCCCTACTCTACTGTGTAGCCCTTACTGTCTCGCTCA 94

QY 61 GATGGCTGTGTAGCAGTCCCTCAGAAACCTAAGGTCTCTTGAAACCTCATGGAATAGA 120
 DB 95 GATGGCTGTGTAGCAGTCCCTCAGAAACCTAAGGTCTCTTGAAACCTCATGGAATAGA 154

QY 121 ATATTTAAAGGAGAGATGTGACTCTTACATGTAAATGGGAACAATTTCTT-TGAAGTCAG 179
 DB 155 ATATTTAAAGGAGAGATGTGACTCTTACATGTAAATGGGAACAATTTCTTGTGAAGTCAG 214

QY 180 TTCCACCAATATGGTTCACAAATGGGAGCCCTTTCAGAAAGAGACAAATTCAGTTTGAATA- 238
 DB 215 TTCCACCAATATGGTTCACAAATGGGAGCCCTTTCAGAAAGAGACAAATTTCAAGTTTGAAC 274

QY 239 ---TTGTGAATGCCAAAT--TTGAAGACAGTGGAGAAAT-ACAATGTCAAGCACCAACAAG 292
 DB 275 TACTGTGTATGTCNAATTTGTGAAGCAGTGGCGAATAACAATGTCAAGCACCAACAAG 334

QY 293 TTAATGAGTGAACCTGTGTACTCTGGAAGTCTTCAAGTCTCTGCTGCTCTTCAGGCCCT 352
 DB 335 TTAATGAGTGAACCTGTGTACTCTGGAAGTCTTCAAGTCTCTGCTGCTCTTCAGGCCCT 394

QY 353 CTGCTGAGGTGGTGTATGGAGGCGCAGCCCTCTTCTCAGGTGCCATGGTTGGAGGAAC 412
 DB 395 CTGCTGAGGTGGTGTATGGAGGCGCAGCCCTCTTCTCAGGTGCCATGGTTGGAGGACAC 454

QY 413 GGGATGTGTAC-AAGTGTATCTATTATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAG 471
 DB 455 TGGATGTGTACAAAGGTGATCTATTATAAGGATGGTGAAGCTCTCAAGTACT-GTATGAG 513

QY 472 AACCAACATCTCCATTACAAATGCCAGTGTGAAGACAGTGGAAACC--TACTACTGT 528
 DB 514 AACCA-AAAATTTCCATTACAAATGCCAGTGTGAAGACAGTGGAAACCCTAAGTACTTGT 572

QY 529 ACGGGCAAA-GTGTGGCAGCTGGAATA-TGAGTCTGAGCCCTCAACATTAAGTAAATAA 586
 DB 573 ACGGGCAAAAGGTGTGGCAAGTGAATTTGAGTCTTGGAGCCCTCAACATTAAGTAAATA 632

QY 587 AAGCTCCGCTGAGAGTACTGCTCAAAATTTTATCCATTTGTTGGTGGTGAATCTGT 646
 DB 633 AAGCTCCGCTGAGAGTACTGCTCAAAATTTTATCCATTTGTTGGTGGTGAATCTGT 692

QY 647 TTGCTGTGGACACAGGATTAATTTATCTCAACTCAGCAGCA 686
 DB 693 TTGCTGTGGAAAGGATTAATTTATCAATCGAAGGGCA 732

RESULT 10

AW612525/c

LOCUS

DEFINITION

ACCESSION

VERSION

AW612525

AW612525.1

GI:7317711

669 bp

mrna

linear

EST 23-MAR-2000

hm03f07.x1

NCI CGAP Kid11

Homo sapiens

cDNA clone

IMAGE:2954053

3'

similar to gb:X06948

HIGH AFFINITY IMMUNOGLOBULIN EPSILON RECEPTOR

ALPHA-SUBUNIT (HUMAN);

mRNA sequence.

AW612525

AW612525.1

GI:7317711

KEYWORDS
SOURCE EST.
ORGANISM Homo sapiens (human)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 659)
 NCI-CCGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
 Email: c9apbs-remail.nih.gov
 Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
 Emmert-Buck, M.D., Ph.D.
 cDNA Library Preparation: M. Bento Soares, Ph.D.
 cDNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CCGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
image.llnl.gov/image/html/iresources.shtml
 Seq primer: -40UP from Gibco
 High quality sequence stop: 438.
FEATURES
 Location/Qualifiers
 1..669
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:2954053"
 /lab_host="DH10B"
 /clone_lib="NCI_CGAP_Kid11"
 /note="Organ: kidney; Vector: pTT3D-Pac (Pharmacia) with
 a modified polylinker; Site 1: Not 1; Site 2: Eco RI;
 Plasmid DNA from the normalized library NCI_CGAP_Kid3 was
 prepared, and ss circles were made in vitro. Following HAP
 purification, this DNA was used as tracer in a subtractive
 hybridization reaction. The driver was PCR-amplified cDNAs
 from a pool of 5,000 clones made from the same library
 (cloneIDs 1322376-1323911, 1456007-1456775, and
 1500552-1502855). Subtraction by Bento Soares and M.
 Fatima Bonaldo."
ORIGIN
 Query Match 47.5%; Score 367.6; DB 10; Length 669;
 Best Local Similarity 97.2%; Pred. No. 6.7e-99;
 Matches 384; Conservative 0; Mismatches 10; Indels 1; Gaps 1;
 QY 381 CCTCTTCCTCAGTGCCATGGTTGGAGGAAGTGGATGTACAGGTGATCTATTATAA 440
 Db |||||
 669 CCTCTTCCTCAGTGCCATGGTTGGAGGAAGTGGATGTACAGGTGATCTATTATAA 610
 QY 441 GGATGGTGAAGCTCTCAAGTACTGGTATGAGACCAACATCTCCATTACAAATGCCAC 500
 Db |||||
 609 GGATGGTGAAGCTCTCAAGTACTGGTATGAGACCAACATCTCCATTACATATGCCAC 550
 QY 501 AGTTGAAGACAGTGGAACTTACTGTACGGGCAAGTGTGGCAGCTGGATATGAGTC 560
 Db |||||
 549 AGTTGAAGACAGTGGAACTTACTGTACGGGCAAGTGTGGCAGCTGGATATGAGTC 490
 QY 561 TGAGCCCTCAACATTACTGTAATANAAGCTCCGGTGAGAGTACTGGCTACAA-TTTT 619
 Db |||||
 489 TGAGCCCTCAACATTACTGTAATANAAGCTCCGGTGAGAGTACTGGCTACAA-TTTT 430
 QY 620 TTATCCCATTTGTTGGTGAATCTCTGTTGGACACAGGATTAATTATCTCAACTC 679
 Db |||||
 429 TTATCCCATTTGTTGGTGAATCTCTGTTGGACACAGGATTAATTATCTCAACTC 370
 QY 680 AGCAGAGCTGCATTTCTCTTGAAGATTAAGAGAACAGGAAAGCTTCAGCTTCGA 739
 Db |||||
 369 AGCAGAGCTGCATTTCTCTTGAAGATTAAGAGAACAGGAAAGCTTCAGCTTCGA 310
 QY 740 ACCCATCTCTTAAGCCAAACCCCAAAACAACTGA 774
 Db |||||
 309 ACCCATCTCTTAAGCCAAACCCCAAAACAACTGA 275

RESULT 11
CF362072 660 bp mRNA linear EST 25-AUG-2003
LOCUS 828457 MARC 3PIG Sus scrofa cDNA 5', mRNA sequence.
DEFINITION CF362072
ACCESSION CF362072.1 GI:34161364
VERSION EST.
KEYWORDS Sus scrofa (pig)
SOURCE Sus scrofa
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE 1 (bases 1 to 660)
AUTHORS Smith, T.P.L., Freking, B.A., Ford, J.J., Vallet, J.L., Fox, J.,
 Wise, T.A., Nonnen, D.J., Wray, J.E. and Keele, J.W.
TITLE A second set of porcine ESTs from a pooled-tissue normalized
 library
JOURNAL Unpublished (2003)
COMMENT Contact: Smith TPL
 USDA, ARS, US Meat Animal Research Center
 PO Box 166, Clay Center, NE 68933-0166, USA
 Tel: 402 762 4366
 Fax: 402 762 4390
 Email: smith@mail.marc.usda.gov
 Single pass sequencing. Bases called with phred v0.020425.c and
 trimmed with the aid of the trim_alt option. Vector identified with
 cross_match v0.990329.
 Plate: SRG8018, row: L, column: 4
 Seq primer: GTAATACGACTCACTATAGG.
FEATURES
 Location/Qualifiers
 1..660
 /organism="Sus scrofa"
 /mol_type="mRNA"
 /db_xref="taxon:9823"
 /tissue_type="pooled"
 /lab_host="DH10B"
 /clone_lib="MARC 3PIG"
 /note="Vector: pCDNA3.1; Site 1: EcoRI; Site 2: NotI;
 Library made with RNA pooled from multiple tissues
 including brain, liver, muscle, placenta/endometrium,
 ovary, testes, and bone marrow."
ORIGIN
 Query Match 43.6%; Score 337.4; DB 14; Length 660;
 Best Local Similarity 71.6%; Pred. No. 8.1e-90;
 Matches 462; Conservative 0; Mismatches 171; Indels 12; Gaps 1;
 QY 1 ATGGCTCTCCATGGATCCCTACTCTACTGTGTAGCTTACTGTTCGCTCCA 60
 Db |||||
 16 ATGCTCTCTCCATGGATCCCTACTCTACTGTGTAGCTTACTGTTCGCTCCA 75
 QY 61 GATGGCGTGTAGCAGTCCCTCAGAAACCTAAGGTCTCTTGAACCTCCATGGAATAGA 120
 Db |||||
 76 GATGGCATGGCAGTCTATCCAGGATCTCAGGTGCTCTTGAATCCCATCGAATCGA 135
 QY 121 ATATTTAAGAGAGAGATGTACTCTTACATGTAAATGGGAACAATTTCTTTGAAGTCAGT 180
 Db |||||
 136 ATATTTAAGAGAGAGATGTACTCTTACATGTAAATGGGAACAATTTCTTTGAAGTCAGT 195
 QY 181 TCCACCAAAATGGTTCCAAATGGCAGCTTTTCAAGAGAGACAATTTCAAGTTTGAATATT 240
 Db |||||
 196 CCCACCAATTTGGACACACACACAACTTTTGAAGTGAATCTTCGATTTGGGACCTT 255
 QY 241 GTGAATGCCAAATTTGAAGACAGTGGAGAAATCAAAATGTACACCAACAAGTTAATAG 300
 Db |||||
 256 AAGAAATGCAAAACCTGGGACAGCGCAAAATACAGATGCCAAAGCAAGACTTACAATG 315
 QY 301 AGTGAACCTGTGTACCTGGAAGTCTTCACTGAGTGGCTCTCTTCAGGCTCTGCTGAG 360
 Db |||||
 316 AGTGAACCTGTGTACCTGGAAGTCTTCACTGAGTGGCTCTCTTCAGGCTCTGCTGAG 375
 QY 361 GTGGTGAAGAGGGCCAGCCCTCTTCTCAGGTGCCATGTTGGAGGAACCTGGATGTG 420


```

/sex="male"
/dev stage="adult"
/lab host="DH10B"
/clone lib="NCI CGAP Pr28"
/notes="Organ: prostate; Vector: pTT3D-Pac (Pharmacia)
with a modified polylinker; Plasmid DNA from the
normalized library NCI CGAP Pr22 was prepared, and ss
circles were made in vitro. Following HAP purification,
this DNA was used as tracer in a subtractive hybridization
reaction. The driver was PCR-amplified cDNAs from a pool
of 5,000 clones made from the same library (cloned IDs
985608-986759, 1101192-1101959, and 1217328-1220615).
Subtraction by Bento Soares and M. Fatima Bonaldo."

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ORIGIN

Query Match 39.8%; Score 308.4; DB 13; Length 488;
Best Local Similarity 99.7%; Pred. No. 3.6e-81;
Matches 309; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 465 GTATGAGAACACACATCTCCATTACAAATGCCACAGTTGAAGACAGTGGAACTACTA 524
Db 1 GTATGAGAACACACATCTCCATTACAAATGCCACAGTTGAAGACAGTGGAACTACTA 60

QY 525 CTGTACGGGCAAGTGTGGAGCTGGAGTATGATGCTGAGCCCTCAACATTACTGTAAT 584
Db 61 CTGTACGGGCAAGTGTGGAGCTGGAGTATGATGCTGAGCCCTCAACATTACTGTAAT 120

QY 585 AAAGCTCCGGTGAAGTACTGGCTACATTTTATCCATTTGTGGTGGATCT 644
Db 121 AAAGCTCCGGTGAAGTACTGGCTACATTTTATCCATTTGTGGTGGATCT 180

QY 645 GTTGTCTGTGACACAGGATTTATCTCAACTCAGCAGCTGACATTTCTTTGAA 704
Db 181 GTTGTCTGTGACACAGGATTTATCTCAACTCAGCAGCTGACATTTCTTTGAA 240

QY 705 GATTAAGAACACAGGAAAGCTTCAGACTTCTGAACCCATCTTAAGCCAAACCCCA 764
Db 241 GATTAAGAACACAGGAAAGCTTCAGACTTCTGAACCCATCTTAAGCCAAACCCCA 300

QY 765 AAAACAATGA 774
Db 301 AAAACAATGA 310

RESULT 14
BY752906
LOCUS
DEFINITION BY752906 652 bp mRNA linear EST 17-DEC-2002
CNA clone F930034C11 5', mRNA sequence.

ACCESSION BY752906
VERSION
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 652)
Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S.,
Nikaido, I., Osato, N., Saito, R., Suzuki, H., Yamanaka, I.,
Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A.,
Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D.P., Bult, C.,
Hume, D.A., Quackenbush, J., Schriml, L.M., Kanapin, A., Matsuda, H.,
Batalov, S., Beisel, K.W., Blake, J.A., Bradt, D., Brusio, V.,
Chothia, C., Corbani, L.E., Cousins, S., Dalla, E., Dragani, T.A.,
Fletcher, C.F., Forrest, A., Frazer, K.S., Gaasterland, T.,
Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S.,
Gustincich, S., Hirokawa, N., Jackson, I.J., Jarvis, E.D., Kanai, A.,
Kawai, H., Kawasawa, Y., Kedierski, R.M., King, B.L., Konagaya, A.,
Kurochkin, I.V., Lee, X., Lenhard, B., Lyons, P.A., Maglott, D.R.,
Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T.,
Numata, K., Okido, T., Pavan, W.J., Pertea, G., Pesole, G.,
Petrovsky, N., Pillai, R., Pontius, J.U., Qi, D., Ramachandran, S.,
Ravasi, T., Reed, J.C., Reed, D.J., Reid, J., Ring, B.Z., Ringwald, M.,

Sandelin, A., Schneider, C., Semple, C.A., Setou, M., Shimada, K.,
Sultana, R., Takenaka, Y., Taylor, M.S., Teasdale, R.D., Tomita, M.,
Verardo, R., Wagner, L., Wahlestedt, C., Wang, Y., Watanabe, Y.,
Wells, C., Wilming, L.G., Wynshaw-Boris, A., Yanagisawa, M., Yang, I.,
Yang, L., Yang, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P.,
Hayatsu, N., Hirozane-Kishikawa, T., Konno, H., Nakamura, M.,
Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K.,
Akawa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Ishii, Y.,
Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, B., Shibata, K.,
Shingawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E.S.,
Rogers, J., Birney, E. and Hayashizaki, Y.
Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)

JOURNAL 22354683
MEDLINE 12466851
PUBMED

COMMENT
Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gsc.riken.go.jp,
URL: http://genome.gsc.riken.go.jp/
Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Carninci, P.,
Fukuda, S., Hashizume, W., Hayashida, K., Hirozane, T., Hori, F.,
Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kawai, J., Kojima, Y.,
Kondo, S., Konno, H., Koya, S., Miyazaki, A., Murata, M., Nakamura, M.,
Nomura, K., Numazaki, R., Ohno, M., Osato, N., Saito, R., Sakazume, N.,
Sano, H., Sasaki, B., Sato, K., Shibata, K., Shiraki, T., Tagami, M.,
Takeda, Y., Waki, K., Watahiki, A., Muramatsu, M. and Hayashizaki, Y.
Direct Submision
Computational Analysis of Full-Length Mouse cDNAs Compared with
Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
Genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer. Genome Res.
10 (11), 1757-1771 (2000)
Computer-based methods for the mouse full-length cDNA
encyclopedia: real-time sequence clustering for construction of a
nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.
Tissues were provided by Kirk W. Beisel (Boys Town National
Research Hospital 555 North 30th Street Omaha, NE 68131 USA) whose
assistance we gratefully acknowledge.
Please visit our web site (http://genome.gsc.riken.go.jp) for
further details.
Location/Qualifiers
1 . 652
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="F930034C11"
/tissue_type="inner ear"
/dev stage="adult"
/clone_lib="RIKEN full-length enriched, adult inner ear"

ORIGIN

Query Match 35.2%; Score 272.6; DB 13; Length 652;
Best Local Similarity 68.6%; Pred. No. 2.5e-70;
Matches 406; Conservative 0; Mismatches 180; Indels 6; Gaps 2;

QY 3 GGCTCTCGCCATCGAATCCCTACTTCTACTGTGTAGCTTACTTCTTCTCGTCCGAG 62
Db 29 GGGGATGGTCACTGGAGAGGTCTGCCAGCTGTGCTAGCAGCTGCTTCTTCTTGA 89


```

QY 63 TGGCGTGTAGCAGTCCCTCAGAAACCTAAGGTCTCTTGAACTCCATGGAATAGAAT 122
Db 89 TGTCACTTCGACGCCACTGAGAAATCTGTACTGACCTTGGACCCACCATGATAGAAT 148
QY 123 ATTAAAGGAGAGAAATGACTCTTACATGTAATGGAACAATTTCTTCAAGT---CAG 179
Db 149 ATTTACAGAGAGAAGTGAACCTTTCTGTATGGAACATCACCTTCAATGAATC 208
QY 180 TTCACCAATAGTTTCCAAATGGCAGCTTTTCAAGAGAGACAAATTCAGTTTGAATAT 239
Db 209 TACTACTAAATGGATCCCAATGATGCTCTCTGAGTGAATCTTTCACATTTGGTCAAT 268
QY 240 TGTGAATGCCAAATTTGAAGACAGTGGAGAAATACAAATGTTCAGCACCACAAAGTTAATGA 299
Db 269 TGTGAGTCCACCGCTTCAAGACAGTGGAAATACATATGTCAGAGCAAGATGTTTAA 328
QY 300 GAGTGAACCTGTGTACTGTGAAGTCTTCAGTGAAGTGGCTGCTCTTCAGGCCCTCTGCTGA 359
Db 329 GAGTAAACCTGTGTACTTGAATGTAACCAAGATTGGCTGCTCTTCAGACATCTGCTGA 388
QY 360 GGTGTGTATGAGGCCAGCCCTCTTCTCAGGTGCCATGTTGGAGGAACCTGGATGT 419
Db 389 CATGATCTTATGATGATGATCTTTCATGATGATGATGATGATGATGATGATGATGAT 448
QY 420 GTACAGGTGATCTATTAATAGGATGTTGAAGCTCTCAAGTACTGTGTATGAGAACCAAA 479
Db 449 CGCAAGGTGATCTACTACAGGAATGACCATGCTTTCAACTACAGTATGAGAGCC---C 505
QY 480 CATCTCCATTAACAATGCCAGTGAAGACAGTGAACCTTACTTGTACGGGGCAAGT 539
Db 506 CGTCTCCATTAAGAGGCCACACTGAATGACAGTGGCACCTTACCATGNCAGAGGCTATCT 565
QY 540 GTGGCAGCTGCACTATGATGCTGAGCCCTCAACATTAATGCTTAAATAAAGCT 591
Db 566 TAGGCAGTGAATATGAATCTGCAAAATTCAGAAATGCTGTAGTAAAGCT 617

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RESULT 15

```

LOCUS AI676114 570 bp mRNA linear EST 17-DEC-1999
DEFINITION wc05e12.x1 NCI CGAP Pr28 Homo sapiens cdna clone IMAGE:2314318 3'
similar to gb:X06948 HIGH AFFINITY IMMUNOGLOBULIN EPSILON RECEPTOR
ALPHA-SUBUNIT (HUMAN); mRNA sequence.
ACCESSION AI676114
VERSION AI676114.1 GI:4876594
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 570)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Michael J. Brownstein, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html

```

Trace considered overall poor quality

Insert Length: 625 Std Error: 0.00

Seq primer: -400P from Gibco

High quality sequence stop: 1.

Location/Qualifiers

1. .570

FEATURES
source

```

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2314318"
/sex="male"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="NCI-CGAP Pr28"
/note="Organ: prostate; Vector: p773D-Pac (Pharmacia)
with a modified polylinker; Plasmid DNA from the
normalized library NCI CGAP Pr28 was prepared, and ss
circles were made in vitro. Following HAP purification,
this DNA was used as tracer in a subtractive hybridization
reaction. The driver was PCR-amplified cDNAs from a pool
of 5,000 clones made from the same library (clones IDs
985608-986759, 1101192-1101959, and 1217928-1220615).
Subtraction by Bento Soares and M. Fatima Bonaldo."

```

ORIGIN

```

Query Match 32.8%; Score 254; DB 9; Length 570;
Best Local Similarity 88.7%; Pred. No. g.1e-65;
Matches 275; Conservative 0; Mismatches 35; Indels 0; Gaps 0;

QY 465 GTATGAGAACCAACATCTCCATTACAAATGCCACAGTTGAAGACAGTGGAACTACTA 524
Db 570 GTATGAGAAATCGCATCTGTGCCATAGCGAATGCCAGGTGATAGACAGTAGGCGCTATTG 511
QY 525 CTGTACGGGCAAAAGTGTGGCAGCTGGACTATGATCTGAGCCCTCAACATTACTGTAAT 584
Db 510 CTGTGGGGCAAAAGTGTGGCAGCTGGCTATTAGTCTGAGCCCTCGAACATTGATGTAAT 451
QY 585 AAAAGCTCCGGTGAGAAAGTACTGGGTACAAATTTTATCCCATTTGTTGGTGGTATCT 644
Db 450 AAAAGCTCCGGTGAGAAAGTACTGGGTACAAATTTTATCCCATTTGTTGGTGGTATCT 391
QY 645 GTTTGCTGTGGACACAGGATTTATCTCAACTCAGCAGCAGGTGCACATTTCTCTTGAA 704
Db 390 GTTTGCTGTGGACACAGGATTTATCTCAACTCAGCAGCAGGTGCACATTTCTCTTGAA 331
QY 705 GATTAAGAGAACCGGAAAGGCTTCAGACTTCTGAACCCACATCTTAAGCCAAACCCAA 764
Db 330 GATTAAGAGAACCGGAGAGGCTTCAGACTTCTGAACCCACATCTTAAGCCAAACCCAA 271
QY 765 AAACAACCTGA 774
Db 270 AAACAGCTGA 261

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Search completed: October 10, 2004, 19:44:37
Job time : 2613.69 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: October 6, 2004, 08:59:38 ; Search time 52.4569 Seconds
(without alignments)
1249.617 Million cell updates/sec

Title: US-10-763-400-6
Perfect score: 1264
Sequence: 1 VPKQKVSLSNPPWNRIFKGE.....RTRKGRLLNPPKPNPKN 232

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database : A_Geneseq_29Jan04.*
- 1: Geneseq1980s.*
 - 2: Geneseq1990s.*
 - 3: Geneseq2000s.*
 - 4: Geneseq2001s.*
 - 5: Geneseq2002s.*
 - 6: Geneseq2003as.*
 - 7: Geneseq2003bs.*
 - 8: Geneseq2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1264	100.0	232	4	AAB31585 Amino aci
2	1264	100.0	257	1	AAP90385 Alpha sub
3	1264	100.0	257	2	AAR05025 Alpha sub
4	1264	100.0	257	2	AAR14772 Human Fc(
5	1264	100.0	257	2	AAR42336 Human Fce
6	1264	100.0	257	2	AAR24066 Alpha sub
7	1264	100.0	257	2	AAW61190 The alpha
8	1264	100.0	257	4	AAB74667 Human imm
9	1264	100.0	257	4	AAB31584 Amino aci
10	1264	100.0	257	5	ABG32801 Human IGE
11	1264	100.0	257	6	ABO01301 Human pro
12	1264	100.0	257	7	ADD48674 Human Fc
13	1264	100.0	260	3	RAY96230 Human Fc
14	1259	99.6	257	2	AAW48094 Human IGE
15	1251	99.0	257	7	ADB85536 Human imm
16	1113.5	88.1	247	2	AAR30483 Human hig
17	1031.5	81.6	218	6	ABO01302 Human pro
18	1002	79.3	182	3	RAY96234 Recombina
19	1002	79.3	183	3	RAY96232 Recombina
20	991	78.4	978	2	AAW48096 Human ser
21	991	78.4	978	5	ABG32803 Human IGE
22	981.5	77.7	235	2	AAR26064 Human Fce
23	969	76.7	176	3	RAY94210 Human PhF
24	969	76.7	176	4	AAG65597 Amino aci
25	947	74.9	172	2	RAY33185 Human sFC

26	947	74.9	172	3	AA94211 Human PhF
27	947	74.9	172	4	AAB31587 A Fc epsi
28	947	74.9	197	2	AAR45778 Human diH
29	947	74.9	197	4	AAB31586 A Fc epsi
30	947	74.9	635	4	AAB31594 Fc epsilo
31	947	74.9	660	4	AAB31593 Fc epsilo
32	947	74.9	731	4	AAB31591 Amino aci
33	947	74.9	756	4	AAB31590 Amino aci
34	944	74.7	175	4	AAG65598 Amino aci
35	938	74.2	193	2	AAR89281 IGE high
36	785.5	62.1	236	2	AA927060 Equine Fc
37	785.5	62.1	255	2	AA927058 Equine Fc
38	775	61.3	281	2	AAR13867 Hybrid FC
39	679	53.7	281	2	AAR13870 Hybrid FC
40	676	53.5	229	2	AAW81114 Canine FC
41	676	53.5	253	2	AAW81113 Canine FC
42	639	50.6	281	2	AAR13872 Fc(gamma)
43	606	47.9	281	2	AAR13869 Hybrid FC
44	576.5	45.6	245	1	AAP90386 Alpha sub
45	570	45.1	201	2	AA927061 Recombina

ALIGNMENTS

RESULT 1:
AAB31585
ID AAB31585 standard; protein; 232 AA.
XX
AC AAB31585;
XX
DT 30-APR-2001 (first entry)
XX
DE Amino acid sequence of Fc epsilon receptor alpha-chain mature protein.
XX
KW Fc epsilon receptor; FcepsilonR; immunoglobulin E; IGE; atopic disease;
KW luminescence inducing protein; allergy; hyper IGE syndrome;
KW internal parasite infection; B cell neoplasia.
XX
OS Homo sapiens.
XX
PN WO200104310-A1.
XX
PD 18-JAN-2001.
XX
PF 13-JUL-2000; 2000WO-US019070.
XX
PR 13-JUL-1999; 99US-0143612P.
PR 02-VAR-2000; 2000US-0186412P.
PR (HESK-) HESKA CORP.
PR (PROV-) PROMEGA CORP.
PI Weber ER, Wood KV, Hall MP;
XX
WPI: 2001-103082/11.
DR N-PSDB; AA924913.
XX
PT A fusion protein, comprising an Fc epsilon receptor domain and a
PT luminescence inducing protein domain that induces a LP substrate to emit
PT light when contacted with the LP domain, useful for detecting
PT immunoglobulin (Ig) E.
XX
XX Claim 16; Page 62-63; 105pp; English.
PS
XX The present sequence represents a human Fc epsilon receptor (FcepsilonR)
XX alpha-chain mature protein, that binds to immunoglobulin (Ig) E. The
CC FcepsilonR domain is used to produce a fusion protein, which also
CC comprises a luminescence inducing protein domain that induces a substrate
CC to emit light when contacted with the luminescence inducing protein
CC domain. The fusion protein may be used to detect IgE. It may also be used
CC to identify a compound capable of inhibiting FcepsilonR protein activity.
CC IgE antibody production is indicative of diseases such as allergies,

CC atopic disease, hyper IgE syndrome, internal parasite infections and B
 CC cell neoplasia. Detection of IgE production in an animal following
 CC therapy is indicative of the efficacy of the treatment, for example when
 CC using treatments intended to disrupt IgE production
 XX
 SQ Sequence 232 AA;

Query Match 100.0%; Score 1264; DB 4; Length 232;
 Best Local Similarity 100.0%; Pred. No. 4.5e-93;
 Matches 232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 VPQKPKVSLNPPWNRIFKGENVTLCNGNPFVSVSTKWFHNGSLSEETNSLNINNAKF 60
 DB 1 VPQKPKVSLNPPWNRIFKGENVTLCNGNPFVSVSTKWFHNGSLSEETNSLNINNAKF 60
 QY 61 EDSGEYKCOHQVNESEPVYLEVFSDDLLOQASAEVVMGQPLFLRCHGWRNWDVYKVIY 120
 DB 61 EDSGEYKCOHQVNESEPVYLEVFSDDLLOQASAEVVMGQPLFLRCHGWRNWDVYKVIY 120
 QY 121 YKDGALKYWNHNHNSITNATVDSGTYYCTGKWQLDYSEPLNITVIKAPREKYWLQ 180
 DB 121 YKDGALKYWNHNHNSITNATVDSGTYYCTGKWQLDYSEPLNITVIKAPREKYWLQ 180
 QY 181 FFIPLLVILFAVDTGFLISTQQQVTFLLKIKRTRKGFRLNPHKPNPKNN 232
 DB 181 FFIPLLVILFAVDTGFLISTQQQVTFLLKIKRTRKGFRLNPHKPNPKNN 232

RESULT 2

AAP90385
 ID AAP90385 standard; protein; 257 AA.

AC AAP90385;
 DT 24-OCT-2003 (revised)
 DT 25-MAR-2003 (revised)
 DT 01-NOV-1989 (first entry)
 XX
 XX Alpha subunit of human mast cell IgE surface receptor.
 XX Immunoglobulin E receptor alpha subunit; allergies;
 KW non-peptide drug design; human.
 KW Homo sapiens; (Human); mast cell line.
 OS KUB12.
 OS W08905352-A.
 PN 15-JUN-1989.
 PD 29-NOV-1988; 88WO-US004255.
 PF 01-DEC-1987; 87US-00127214.
 PR (HARD) HARVARD COLLEGE
 PA (USSH) NAT INST OF HEALTH.
 XX
 XX Leder P, Benfey P;
 PI WPI; 1989-192698/26.
 DR N-PSDB; AAN90126.
 DR
 XX CDNA encoding IgE receptor alpha-sub-unit - used to treat allergies.
 PT
 XX
 XX Disclosure; Fig 4; 17pp; English.

Immunoglobulin E receptor alpha subunit of human mast cell IgE surface
 receptor (see corresp. AAN90126). Used to produce antibodies which can
 diagnose IgE receptor levels, measure and treat allergies, and design non
 -peptide drugs. (Updated on 25-MAR-2003 to correct PA field.) (Updated on
 24-OCT-2003 to standardise OS field)

SQ Sequence 257 AA;

Query Match 100.0%; Score 1264; DB 1; Length 257;
 Best Local Similarity 100.0%; Pred. No. 5.1e-93;
 Matches 232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPQKPKVSLNPPWNRIFKGENVTLCNGNPFVSVSTKWFHNGSLSEETNSLNINNAKF 60
 DB 26 VPQKPKVSLNPPWNRIFKGENVTLCNGNPFVSVSTKWFHNGSLSEETNSLNINNAKF 85
 QY 61 EDSGEYKCOHQVNESEPVYLEVFSDDLLOQASAEVVMGQPLFLRCHGWRNWDVYKVIY 120
 DB 86 EDSGEYKCOHQVNESEPVYLEVFSDDLLOQASAEVVMGQPLFLRCHGWRNWDVYKVIY 145
 QY 121 YKDGALKYWNHNHNSITNATVDSGTYYCTGKWQLDYSEPLNITVIKAPREKYWLQ 180
 DB 146 YKDGALKYWNHNHNSITNATVDSGTYYCTGKWQLDYSEPLNITVIKAPREKYWLQ 205
 QY 181 FFIPLLVILFAVDTGFLISTQQQVTFLLKIKRTRKGFRLNPHKPNPKNN 232
 DB 206 FFIPLLVILFAVDTGFLISTQQQVTFLLKIKRTRKGFRLNPHKPNPKNN 257

RESULT 3

AAR05025
 ID AAR05025 standard; protein; 257 AA.

AC AAR05025;
 DT 02-OCT-1990 (first entry)
 XX
 XX Alpha subunit of human high affinity IgE receptor.
 DE high affinity IgE receptor; alpha subunit of IgE receptor; human;
 KW allergic response; ss.
 XX
 XX Synthetic.
 OS
 XX W09004640-A.
 PN 03-MAY-1990.
 PD 18-OCT-1988; 88US-00259065.
 PF 18-OCT-1988; 88US-00259065.
 PR (USDC) US SEC OF COMMERCE.
 XX
 XX Kinet JP, Metzger H;
 PI WPI; 1990-164023/21.
 DR N-PSDB; AAQ04644.
 DR

DNA sequences for sub-unit peptide(s) of high affinity IgE receptor - and
 derived polypeptides, for therapy and diagnosis of allergies, and studies
 of IgE receptor interaction.

PS Disclosure; Page ?; -pp; English.

XX The high affinity receptor is a tetrameric complex consisting of 2 gamma
 CC subunits and one each of subunits alpha and beta. It is expressed on mast
 CC cells and is involved in the allergic response. COS-7 cells cotransfected
 CC with cDNA for all 3 intact subunit types (derived from rat basophilic
 CC leukaemia cells) express receptor on their surfaces. Detailed study of
 CC the receptors is now possible. See also AAQ04643 and AAQ04645-6

SQ Sequence 257 AA;

Query Match 100.0%; Score 1264; DB 2; Length 257;
 Best Local Similarity 100.0%; Pred. No. 5.1e-93;
 Matches 232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPQKPKVSLNPPWNRIFKGENVTLCNGNPFVSVSTKWFHNGSLSEETNSLNINNAKF 60

CC	Government-owned NTIS applications to prevent clashes with ongoing US
CC	granted patent numbers. For further information please visit the Derwent
CC	web site at www.derwent.com/dwpi/updates/ntis_us.html .) (Updated on 25-
CC	MAR-2003 to correct PF field.)
XX	Sequence 257 AA;
Qy	Query Match 100.0%; Score 1264; DB 2; Length 257;
Db	Best Local Similarity 100.0%; Pred. No. 5.1e-93;
Matches 232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Qy	1 VPOKPKVSLNPPWNRIFKGENVTLTGNNFFVSTKFWHNGSLSEETNSSLNIVNAKF 60
Db	26 VPOKPKVSLNPPWNRIFKGENVTLTGNNFFVSTKFWHNGSLSEETNSSLNIVNAKF 85
Qy	61 EDSGEYKCOHQVNESEPVYLEVFSDDLLOASAEVVMGQPLFLRCHGWRNWDVYKVIY 120
Db	86 EDSGEYKCOHQVNESEPVYLEVFSDDLLOASAEVVMGQPLFLRCHGWRNWDVYKVIY 145
Qy	121 YKDGEALKYWEYENHNISITNATVEDSGTYCTGKWQLDYSEPLNITVIKAPREKYWLQ 180
Db	146 YKDGEALKYWEYENHNISITNATVEDSGTYCTGKWQLDYSEPLNITVIKAPREKYWLQ 205
Qy	181 FFIPLLWVILFAVDTGFLFISTQQQVTFLLKIKRTRKGFRLNPHPKPNKNN 232
Db	206 FFIPLLWVILFAVDTGFLFISTQQQVTFLLKIKRTRKGFRLNPHPKPNKNN 257
RESULT 5	
AAR42336	
ID	AAR42336 standard; protein; 257 AA.
XX	AAR42336;
XX	25-MAR-2003 (revised)
DT	21-JUN-1994 (first entry)
DE	Human FcεRI alpha.
XX	IGE; immunoglobulin E receptor; beta subunit; basophils; allergy;
KW	aggregation; signal transduction; diagnosis; antagonist.
XX	Homo sapiens.
OS	WO9321317-A1.
PN	28-OCT-1993.
PD	16-APR-1993; 93WO-US003419.
PF	16-APR-1992; 92US-00869933.
PR	(USSH) US DEPT HEALTH & HUMAN SERVICE.
PA	Kinet JP;
PI	WPI; 1993-351727/44.
DR	N-PSDB; AAQ51020.
XX	Immunoglobulin E receptor human beta sub-unit isolation - using 1st
PT	strand reverse transcripts from human basophils as templates for a
PT	polymerase chain reaction, used to treat and diagnose allergic diseases.
XX	Claim 5; Fig 1; 154pp; English.
PS	The sequence is that of the human FcεRI alpha subunit, isolated by using
CC	first strand reverse transcriptase from human basophils by PCR. The gene
CC	and its prod. can be used to identify human beta subunit FcεRI inhibitors
CC	(immunoglobulin E receptor) which inhibit the binding of IGE to its
CC	receptor and inhibit the aggregation function of the receptor or the
CC	signal transducing function related to allergic response. Such inhibitors
CC	can be used for the treatment or prevention of allergic disease. See also
CC	AAR42337-42. (Updated on 25-MAR-2003 to correct PN field.)

26	VPOKPKVSLNPPWNRIFKGENVTLTGNNFFVSTKFWHNGSLSEETNSSLNIVNAKF	85
61	EDSGEYKCOHQVNESEPVYLEVFSDDLLOASAEVVMGQPLFLRCHGWRNWDVYKVIY	120
86	EDSGEYKCOHQVNESEPVYLEVFSDDLLOASAEVVMGQPLFLRCHGWRNWDVYKVIY	145
121	YKDGEALKYWEYENHNISITNATVEDSGTYCTGKWQLDYSEPLNITVIKAPREKYWLQ	180
146	YKDGEALKYWEYENHNISITNATVEDSGTYCTGKWQLDYSEPLNITVIKAPREKYWLQ	205
181	FFIPLLWVILFAVDTGFLFISTQQQVTFLLKIKRTRKGFRLNPHPKPNKNN	232
206	FFIPLLWVILFAVDTGFLFISTQQQVTFLLKIKRTRKGFRLNPHPKPNKNN	257
RESULT 4		
AAR14772		
ID	AAR14772 standard; protein; 257 AA.	
XX	AAR14772;	
XX	25-MAR-2003 (revised)	
DT	17-DEC-2001 (revised)	
DT	03-FEB-1992 (first entry)	
DE	Human Fc(εpsilon)RI alpha subunit.	
XX	Immunoglobulin; receptor; high affinity receptor.	
XX	Homo sapiens.	
Key	Location/Qualifiers	
Peptide	1..25	
Protein	26..257	
Domain	80..104	
Domain	163..190	
Region	205..224	
Region	225..257	
USN7626704-N.		
15-OCT-1991.		
14-DEC-1990;	90US-00626704.	
14-DEC-1990;	90US-00626704.	
(USSH) NAT INST OF HEALTH.		
Kinet JP, Metzger H;		
WPI; 1991-346755/47.		
N-PSDB; AAQ14736.		
DNA coding alpha, beta and gamma-units of ige high affinity receptor -		
are used to prepare recombinant polypeptide(s) for treating allergy, drug		
screening or monitoring ige level.		
Disclosure; Fig 1; 58pp; English.		
A lambda gtl1 library was prepared from poly-A RNA isolated from KUB12		
cells. Screening was by a cDNA fragment from the rat Fc(εpsilon)RI alpha		
cDNA corresponding to nucleotides 119-781. Positive clones were subcloned		
and sequenced. This amino acid sequence was deduced from the cDNA clone		
(Note: Revised entry submitted to correct the patent number format of US		

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XX SQ Sequence 257 AA;
Query Match 100.0%; Score 1264; DB 2; Length 257;
Best Local Similarity 100.0%; Pred. No. 5.1e-93;
Matches 232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 VPQPKVSLNPPNRIKGENVTITCNGNFFEVSSTKWFHNGSLSEBTSSSLNIVNAKF 60
Db 26 VPQPKVSLNPPNRIKGENVTITCNGNFFEVSSTKWFHNGSLSEBTSSSLNIVNAKF 85
QY 61 EDSGEYKCOHQOVNESEPVYLEVSDWLLLOQASAEVVMGQPLFLRCHGWRNWDVVKVIY 120
Db 86 EDSGEYKCOHQOVNESEPVYLEVSDWLLLOQASAEVVMGQPLFLRCHGWRNWDVVKVIY 145
QY 121 YKDGALKYWNHNSITNATVEDSGTYCTGKVMOLDYSEPLNITVIKAPREKYWLQ 180
Db 146 YKDGALKYWNHNSITNATVEDSGTYCTGKVMOLDYSEPLNITVIKAPREKYWLQ 205
QY 181 FFIPLLVILFAVDTGFLISTQQQVTELLKIKTRKGFRLLNHPKPNPKNN 232
Db 206 FFIPLLVILFAVDTGFLISTQQQVTELLKIKTRKGFRLLNHPKPNPKNN 257

RESULT 6
AAW24066
ID AAW24066 standard; protein; 257 AA.
XX
AC AAW24066;
XX
DT 04-FEB-1998 (first entry)
XX
DE Alpha subunit of human high affinity receptor for IgE (human FcERI).
KW alpha subunit; human high affinity receptor; IgE; FcERI; antigen;
KW preformed mediator; histamine; serotonin; leukotriene; IgE level;
KW allergic condition; therapy; allergic response; drug screening;
KW DNA probe; diagnostic assay.
XX
OS Homo sapiens.
XX
FH Location/Qualifiers
FT Peptide
FT 1..25 /label= signal_peptide
FT 26..257 /label= mature_peptide
FT 26..204 /label= extracellular_portion_of_protein
FT 80..104 /label= homologous_domain_1
FT /note= "this region is homologous with amino acids 163-190"
FT 163..190 /label= homologous_domain_2
FT /note= "this region is homologous with amino acids 80-104"
FT 205..224 /label= transmembrane_segment
FT 225..257 /label= cytoplasmic_domain
XX
US5639660-A.
XX
PD 17-JUN-1997.
XX
PF 24-FEB-1988; 88US-00160457.
XX
PR 24-FEB-1988; 88US-00160457.
XX
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.
PA (HOFF ) HOFFMANN LA ROCHE INC.
XX
PI Kochan JP, Kinet JP;

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XX DR WPI; 1997-332052/30.
XX DR N-PSDB; AAT85615.
XX
PT DNA encoding alpha sub-unit of high affinity receptor for immunoglobulin
PT E - used for producing polypeptide(s) which can be used for therapy or to
PT prevent allergic responses or in diagnostic and screening assays.
XX
PS Claim 7; Fig 1A-B; 15pp; English.
XX
CC This sequence represents the alpha subunit of the human high affinity
CC receptor for IgE (FcERI). FcERI is found exclusively on mast cells,
CC basophils and related cells. Aggregation of IgE occupied FcERI by antigen
CC triggers both the release of preformed mediators such as histamine and
CC serotonin, as well as stimulating the synthesis of leukotrienes. It is
CC the release of these mediators that results in an allergic condition. The
CC DNA can be used to produce the human FcERI alpha polypeptides which can
CC be used for therapy or to prevent allergic responses, in drug screening
CC assays or for monitoring IgE levels in patients. The DNA encoding this
CC protein can also be used to produce DNA probes useful in diagnostic
CC assays
XX
SQ Sequence 257 AA;
Query Match 100.0%; Score 1264; DB 2; Length 257;
Best Local Similarity 100.0%; Pred. No. 5.1e-93;
Matches 232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 VPQPKVSLNPPNRIKGENVTITCNGNFFEVSSTKWFHNGSLSEBTSSSLNIVNAKF 60
Db 26 VPQPKVSLNPPNRIKGENVTITCNGNFFEVSSTKWFHNGSLSEBTSSSLNIVNAKF 85
QY 61 EDSGEYKCOHQOVNESEPVYLEVSDWLLLOQASAEVVMGQPLFLRCHGWRNWDVVKVIY 120
Db 86 EDSGEYKCOHQOVNESEPVYLEVSDWLLLOQASAEVVMGQPLFLRCHGWRNWDVVKVIY 145
QY 121 YKDGALKYWNHNSITNATVEDSGTYCTGKVMOLDYSEPLNITVIKAPREKYWLQ 180
Db 146 YKDGALKYWNHNSITNATVEDSGTYCTGKVMOLDYSEPLNITVIKAPREKYWLQ 205
QY 181 FFIPLLVILFAVDTGFLISTQQQVTELLKIKTRKGFRLLNHPKPNPKNN 232
Db 206 FFIPLLVILFAVDTGFLISTQQQVTELLKIKTRKGFRLLNHPKPNPKNN 257

RESULT 7
AAW61190
ID AAW61190 standard; protein; 257 AA.
XX
AC AAW61190;
XX
DT 07-OCT-1998 (first entry)
XX
DE The alpha chain of a Fc epsilon receptor.
XX
KW Alpha chain; human; Fc epsilon receptor; canine; equine; feline;
KW immunoglobulin E; IgE; detection; diagnose; allergy; atopic disease;
KW hyper-IgE syndrome; internal parasitic infection; B cell neoplasia;
KW flea allergy; heartworm infection.
XX
OS Homo sapiens.
XX
FN WO9823964-A1.
XX
PD 04-JUN-1998.
XX
PF 24-NOV-1997; 97WO-US021651.
XX
PR 26-NOV-1996; 96US-00756387.
XX
PA (HESK-) HESKA CORP.
XX
PI Frank RG, Porter JP, Rushlow KE, Wassom DL;

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XX WPI; 1998-322873/28.
 DR N-PSDB; AAF36343.
 XX
 PT Detection of non-human immunoglobulin E - by complex formation with human
 PT Fc epsilon receptor, used for, e.g. diagnosis of allergy and atopic
 PT disease.
 XX
 XX Disclosure; Page 37-38; 70pp; English.
 XX
 CC The present sequence represents the alpha chain of the human Fc epsilon
 CC receptor. Detection of canine, equine or feline immunoglobulin E (IgE)
 CC comprises reacting isolated human Fc epsilon receptor with the test
 CC sample and detecting formation of a IgE-receptor complex. Detection of
 CC IgE is used to diagnose allergy, atopic disease, hyper-IgE syndrome,
 CC internal parasitic infections or B cell neoplasia, and for measuring
 CC effect of treatments. Most particularly flea allergy in dogs and cats is
 CC detected, and also heartworm infection
 XX
 SQ Sequence 257 AA;
 Query Match 100.0%; Score 1264; DB 2; Length 257;
 Best Local Similarity 100.0%; Pred. No. 5.1e-93;
 Matches 232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 QY 1 VPQPKVSLNPPNRIKGENVLTTCNGNPFVSVSTKWFHNGSLSEETNSSLINVNAKF 60
 Db 26 VPQPKVSLNPPNRIKGENVLTTCNGNPFVSVSTKWFHNGSLSEETNSSLINVNAKF 85
 QY 61 EDSEYKCOHQVNESEPVYLEVFSDWLLQASAEVVMGQPLFLRCHGWRNWDVYKVIY 120
 Db 86 EDSEYKCOHQVNESEPVYLEVFSDWLLQASAEVVMGQPLFLRCHGWRNWDVYKVIY 145
 QY 121 YKDGKALKYWEHNHISITNATVEDSGTYCTGKWQLDYSEPLNITVIKAPREKYWLQ 180
 Db 146 YKDGKALKYWEHNHISITNATVEDSGTYCTGKWQLDYSEPLNITVIKAPREKYWLQ 205
 QY 181 FPIPLVILFAVDTGFIQTQQVTFLLKIKRTRKGFRLNPHKPNPKNN 232
 Db 206 FPIPLVILFAVDTGFIQTQQVTFLLKIKRTRKGFRLNPHKPNPKNN 257
 XX
 RESULT 8
 AAB74667
 ID AAB74667 standard; protein; 257 AA.
 XX
 AC AAB74667;
 XX
 DT 19-JUN-2001 (first entry)
 XX
 DE Human immunoglobulin E receptor I alpha subunit protein.
 XX
 KW Human; polymorphism; immunoglobulin E receptor I alpha subunit; IGERA;
 KW single nucleotide polymorphism; SNP; allele specific oligonucleotide;
 KW immunoassay; detection.
 XX
 OS Homo sapiens.
 XX
 PN WO200111010-A2.
 XX
 PD 15-FEB-2001.
 XX
 PF 02-AUG-2000; 2000WO-US021097.
 XX
 PR 09-AUG-1999; 99US-0147860P.
 XX
 PA (GENA-) GENAISSANCE PHARM INC.
 XX
 PI Chew A. Denton RR, Duda A, Kliem SE, Lanz EM, Nandabalan K;
 PI Stephens JC;
 XX
 XX WPI; 2001-202766/20.
 DR N-PSDB; AAF97964.

XX New polynucleotide for gene therapy, comprises nucleotide polymorphisms
 PT in the immunoglobulin E receptor I alpha subunit gene.
 XX
 XX Claim 10; Fig 3; 99pp; English.
 XX
 CC The present invention describes an isolated polynucleotide (I) comprising
 CC a nucleotide sequence (S) which is a polymorphic variant of a reference
 CC sequence for the human immunoglobulin E receptor I alpha subunit (IGERA)
 CC gene or its fragment. The polymorphic variant comprises at least one
 CC polymorphism selected from guanine (G) at PS2, PS3, PS6, PS12, PS18 or PS9,
 CC PS10 or PS21, cytosine (C) at PS7, PS3, PS6, PS12, PS18 or PS20, adenine
 CC (A) at PS5, PS7, PS11, PS13, PS14, PS15, PS19, or PS22 and thymine (T) at
 CC PS4, PS8, PS16 or PS17, or (G) at a position corresponding to nucleotide
 CC 251. (A) at a position corresponding to nucleotide 302 or 741, and (T) at
 CC a position corresponding to nucleotide 530. (I) can be used in gene
 CC therapy. (I) is useful for therapeutic purposes. A polypeptide (II)
 CC encoded by (I) is useful in drug screening assays and in assays to
 CC measure the binding affinity of one or more candidate drugs targeting
 CC (II). An antibody (III) to (II) is useful to immunoprecipitate (II) from
 CC solution and also reacts with (II) on Western or immunoblots of
 CC polyacrylamide gels on membrane supports or substrates. (III) is also
 CC useful in immunoassays to detect (II) in biological samples. AAF97965 to
 CC AAF98096 represent IGERA allele specific oligonucleotide probes; AAF98097
 CC to AAF98140 represent IGERA gene polymorphism detection primers; and
 CC AAF98141 to AAF98180 represent IGERA gene PCR primers which are used in
 CC the exemplification of the present invention. The present sequence
 CC represents the human IGERA protein used in the present invention
 XX
 SQ Sequence 257 AA;
 Query Match 100.0%; Score 1264; DB 4; Length 257;
 Best Local Similarity 100.0%; Pred. No. 5.1e-93;
 Matches 232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 VPQPKVSLNPPNRIKGENVLTTCNGNPFVSVSTKWFHNGSLSEETNSSLINVNAKF 60
 Db 26 VPQPKVSLNPPNRIKGENVLTTCNGNPFVSVSTKWFHNGSLSEETNSSLINVNAKF 85
 QY 61 EDSEYKCOHQVNESEPVYLEVFSDWLLQASAEVVMGQPLFLRCHGWRNWDVYKVIY 120
 Db 86 EDSEYKCOHQVNESEPVYLEVFSDWLLQASAEVVMGQPLFLRCHGWRNWDVYKVIY 145
 QY 121 YKDGKALKYWEHNHISITNATVEDSGTYCTGKWQLDYSEPLNITVIKAPREKYWLQ 180
 Db 146 YKDGKALKYWEHNHISITNATVEDSGTYCTGKWQLDYSEPLNITVIKAPREKYWLQ 205
 QY 181 FPIPLVILFAVDTGFIQTQQVTFLLKIKRTRKGFRLNPHKPNPKNN 232
 Db 206 FPIPLVILFAVDTGFIQTQQVTFLLKIKRTRKGFRLNPHKPNPKNN 257

RESULT 9
 AAB31584
 ID AAB31584 standard; protein; 257 AA.
 XX
 AC AAB31584;
 XX
 DT 30-APR-2001 (first entry)
 XX
 DE Amino acid sequence of a human Fc epsilon receptor alpha-chain.
 XX
 KW Fc epsilon receptor; Fc epsilonR; immunoglobulin E; IgE; atopic disease;
 KW luminescence inducing protein; allergy; hyper IgE syndrome;
 KW internal parasite infection; B cell neoplasia.
 XX
 OS Homo sapiens.
 XX
 PN WO200104310-A1.
 XX
 PD 18-JAN-2001.
 XX
 PF 13-JUL-2000; 2000WO-US019070.

XX 13-JUL-1999; 99US-0143612P.
 PR 02-MAR-2000; 2000US-0186412P.
 XX (HESK-) HESKA CORP.
 PA (PROM-) PROMEGA CORP.
 XX Weber ER, Wood KV, Hall MP;
 XX WPI; 2001-103082/11.
 DR N-PSDB; AAF24911.
 XX A fusion protein, comprising an Fc epsilon receptor domain and a
 PT luminescence inducing protein domain that induces a LP substrate to emit
 PT light when contacted with the LP domain, useful for detecting
 PT immunoglobulin (Ig) E.
 XX Claim 16; Page 60; 105pp; English.
 PS The present sequence represents a human Fc epsilon receptor (FcepsilonR)
 XX alpha-chain protein, that binds to immunoglobulin (Ig) E. The FcepsilonR
 CC domain is used to produce a fusion protein, which also comprises a
 CC luminescence inducing protein domain that induces a substrate to emit
 CC light when contacted with the luminescence inducing protein domain. The
 CC fusion protein may be used to detect IgE. It may also be used to identify
 CC a compound capable of inhibiting FcepsilonR protein activity. IgE
 CC antibody production is indicative of diseases such as allergies, atopic
 CC disease, hyper IgE syndrome, internal parasite infections and B cell
 CC neoplasia. Detection of IgE production in an animal following therapy is
 CC indicative of the efficacy of the treatment, for example when using
 CC treatments intended to disrupt IgE production
 XX Sequence 257 AA;
 SQ
 Query Match 100.0%; Score 1264; DB 4; Length 257;
 Best Local Similarity 100.0%; Pred. No. 5.1e-93;
 Matches 232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 VPQPKVSLNPPNRIKGENVLTTCNGNFFVSSSTKWFHNGSLSEETNSSLINVNAKF 60
 Db 26 VPQPKVSLNPPNRIKGENVLTTCNGNFFVSSSTKWFHNGSLSEETNSSLINVNAKF 85
 QY 61 EDGSEYKCOHQVNESEPVYLEVFSDWLLLLQASAEVVMGQPLFLRCHGRNWDVYKVIY 120
 Db 86 EDGSEYKCOHQVNESEPVYLEVFSDWLLLLQASAEVVMGQPLFLRCHGRNWDVYKVIY 145
 QY 121 YKDGKALKYVYENHISITNATVEDSGTYCTGKWOLDYSESEPLNITTVIKAPREKYWLQ 180
 Db 146 YKDGKALKYVYENHISITNATVEDSGTYCTGKWOLDYSESEPLNITTVIKAPREKYWLQ 205
 QY 181 FFIPLLVILFAVDTGFLFISTQQQVTLTKIKTRKGRFLLNPHKPNKN 232
 Db 206 FFIPLLVILFAVDTGFLFISTQQQVTLTKIKTRKGRFLLNPHKPNKN 257
 RESULT 10
 ABG32801
 ID ABG32801 standard; protein; 257 AA.
 XX AC ABG32801;
 XX 29-NOV-2002 (first entry)
 XX Human IgE receptor FcepsilonRIalpha.
 XX Human; IgE; receptor; FcepsilonRIalpha; HSA; human serum albumin;
 XX anti-allergic; dermatological; anti-inflammatory; antiasthmatic;
 XX IgE binding domain; systemic allergy; IgE-receptor-mediated disorder;
 XX atopic dermatitis; atopic asthma; chronic urticaria.
 XX Homo sapiens.
 XX Location/Qualifiers
 FH Key

FT Peptide 1..25
 FT Protein /label= Signal_peptide
 FT 26..257
 FT Region /label= Mature_FcepsilonRIalpha
 FT 26..204
 FT /label= IgE_binding_domain
 FT /note= "This region is specifically claimed in claim 5"
 XX US6423512-B1.
 XX 23-JUL-2002.
 XX 21-JUL-1997; 97US-00897956.
 XX 26-JUL-1996; 96US-0023689P.
 XX (NOVS) NOVARTIS AG.
 XX Digan ME, Lake P, Gram H;
 XX WPI; 2002-672940/72.
 XX N-PSDB; ABS2959.
 XX New fusion IgE-binding polypeptide, useful for the prevention and
 PT treatment of systemic allergy and/or other IgE-receptor-mediated
 PT disorders such as atopic dermatitis, atopic asthma and chronic urticaria.
 XX Claim 5; Fig 13; 49pp; English.
 XX The invention relates to a new fusion polypeptide or its pharmaceutically
 CC acceptable salt comprises at least one IgE-binding domain fused to at
 CC least one human serum albumin (HSA) component, where the IgE-binding
 CC domain is the sequence (a) defined residues Val26-Leu204 of the protein
 CC sequence appearing as ABG32801, or a truncation at the carboxy terminus
 CC by 1-12 amino acids. Also included are: (1) a fusion polypeptide defined
 CC by residues Val26-Leu978 of the protein appearing as ABG32803; (2) a
 CC polynucleotide sequence encoding the fusion protein; (3) a host cell
 CC transformed with the polynucleotide; (4) a method of preparing the fusion
 CC protein comprising transforming a host cell with a vector comprising a
 CC polynucleotide encoding the fusion polypeptide, expressing the fusion
 CC polypeptide in the cell, and recovering the fusion polypeptide from the
 CC host cell, optionally in the form of its salt; and (5) a vector for
 CC expressing a polynucleotide sequence encoding a fusion polypeptide of
 CC formula (I), (II), (III), (IV), or (V) or its salts (R1-L-R2 (I), R2-
 CC L-R1 (II), R1-L-R2-L-R1 (III), R1-L-R1-L-R2 (IV), R2-L-R1-L-R1
 CC (V), where R1 = the polypeptide (a) or its truncation at the carboxy
 CC terminus by 1-12 amino acids and R2 = a polypeptide selected from the
 CC sequence defined by residues Asp25-Leu609 the human HSA sequence
 CC appearing as ABG32802, or its truncation at the carboxy terminus by 1-10
 CC amino acids and L = independently a chemical bond, where the vector is
 CC PXMT3-Rla-HAS-Rla). The compositions and methods of the present invention
 CC are useful for the prevention and treatment of systemic allergy and other
 CC IgE-receptor-mediated disorders such as atopic dermatitis, atopic asthma
 CC and chronic urticaria. The IgE-binding polypeptide have a more prolonged
 CC effective serum life, more improved clinical utility in the treatment of
 CC allergy, as well as improved activity in a more efficient and cost-
 CC effective manner. The present sequence is the human IgE receptor
 CC FcepsilonRIalpha used to make the fusion protein of the invention
 XX Sequence 257 AA;
 SQ

Query Match 100.0%; Score 1264; DB 5; Length 257;
 Best Local Similarity 100.0%; Pred. No. 5.1e-93;
 Matches 232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 VPQPKVSLNPPNRIKGENVLTTCNGNFFVSSSTKWFHNGSLSEETNSSLINVNAKF 60
 Db 26 VPQPKVSLNPPNRIKGENVLTTCNGNFFVSSSTKWFHNGSLSEETNSSLINVNAKF 85
 QY 61 EDGSEYKCOHQVNESEPVYLEVFSDWLLLLQASAEVVMGQPLFLRCHGRNWDVYKVIY 120
 Db 86 EDGSEYKCOHQVNESEPVYLEVFSDWLLLLQASAEVVMGQPLFLRCHGRNWDVYKVIY 145

QY 121 YKGEALKYWNHNISITNATVEDSGTYCTGKVMQLDYSEBPLNITVIKAPREKYWLQ 180
 DB 146 YKGEALKYWNHNISITNATVEDSGTYCTGKVMQLDYSEBPLNITVIKAPREKYWLQ 205
 QY 181 FFIPLLVVILFAVDTGFIQTQQVTFLLKIKTRKGRFLLNPHBKPKN 232
 DB 206 FFIPLLVVILFAVDTGFIQTQQVTFLLKIKTRKGRFLLNPHBKPKN 257

RESULT 11
 ABO01301
 ID ABO01301 standard; protein; 257 AA.
 XX ABO01301;
 AC ABO01301;
 XX
 DT 07-AUG-2003 (first entry)
 XX
 DE Human protein NOV8a.
 XX
 KW Human; NOVX; cardiomyopathy; atherosclerosis; hypertension;
 KW congenital heart defect; prostate cancer; diabetes; metabolic disorder;
 KW neoplasm; graft versus host disease; AIDS; bronchial asthma;
 KW Crohn's disease; multiple sclerosis; infectious disease; anorexia;
 KW cancer-associated cachexia; neurodegenerative disorder;
 KW Alzheimer's disease; Parkinson's disease; immune disorder;
 KW haematopoietic disorder; dyslipidaemia; wasting disorder; gene therapy.
 XX
 OS Homo sapiens.
 XX
 FN WO2003023008-A2.
 XX
 PD 20-MAR-2003.
 XX
 FF 09-SEP-2002; 2002WO-US028596.
 XX
 PR 07-SEP-2001; 2001US-0318120P.
 PR 07-SEP-2001; 2001US-0318130P.
 PR 10-SEP-2001; 2001US-0318430P.
 PR 12-SEP-2001; 2001US-0318765P.
 PR 17-SEP-2001; 2001US-0322781P.
 PR 17-SEP-2001; 2001US-0322816P.
 PR 19-SEP-2001; 2001US-0323519P.
 PR 20-SEP-2001; 2001US-0323631P.
 PR 20-SEP-2001; 2001US-0323636P.
 PR 25-SEP-2001; 2001US-0324969P.
 PR 25-SEP-2001; 2001US-0325031P.
 PR 26-SEP-2001; 2001US-0324990P.
 PR 15-FEB-2002; 2002US-0357303P.
 PR 28-FEB-2002; 2002US-0360973P.
 PR 20-MAR-2002; 2002US-0366131P.
 PR 25-MAR-2002; 2002US-0367753P.
 PR 02-APR-2002; 2002US-0369479P.
 PR 10-MAY-2002; 2002US-0379532P.
 PR 17-MAY-2002; 2002US-0381664P.
 PR 17-MAY-2002; 2002US-0381672P.
 PR 28-MAY-2002; 2002US-0383651P.
 PR 29-MAY-2002; 2002US-0384012P.
 PR 19-JUN-2002; 2002US-0390155P.
 PR 06-SEP-2002; 2002US-00390155.
 XX
 FA (CURA-) CURAGEN CORP.
 XX
 PI Zhong M, Li L, Gorman L, Spytek KA, Kekuda R, Taupier RJ;
 PI Anderson DW, Vernet CAM, Catterton E, Miller CE, Shenoy SG;
 PI Patturajan M, Pena CE, Tchernev VT, Padigar M, Gusev VY;
 PI Malyankar UM, Burgess CE, Gerlach VL, Gasman SJ, Rieger DK;
 PI Grosse WM, Smithson G, Feyman JA, Stirling G, Rothenberg NE;
 PI Larochelele WJ, Shmukles RA, Crabtree J, Rastelli L, Voss EZ;
 PI Boldog FL, Edinger SR, Millet I, Macdougall JR, Ellerman K;
 PI Chapoval A;
 XX
 DR WPI; 2003-313246/30.
 DR N-PSDB; ACD06182.

XX New polypeptides and polynucleotides having properties related to
 PT stimulation of biochemical or physiological responses in a cell or
 PT tissue, useful for diagnosing or preventing e.g. atherosclerosis,
 PT hypertension, prostate cancer.
 XX
 PS Claim 2; Page 133; 849pp; English.
 XX
 CC The invention relates to an isolated polypeptide comprising one of 127
 CC sequences (appearing as ABO1288-ABO1414) designated as NOVX, a mature
 CC form of NOVX, an amino acid sequence which is at least 95% identical to
 CC NOVX or an amino acid sequence comprising one or more conservative
 CC substitutions in NOVX. Also included are nucleic acids encoding NOVX
 CC proteins, determining the presence or amount of NOVX or NOVX DNA in a
 CC sample (by introducing the sample to an antibody that binds
 CC immunospecifically to the polypeptide), determining the presence of
 CC amount of antibody bound to the polypeptide), determining the presence of
 CC or predisposition to a disease associated with altered levels of
 CC expression of NOVX or NOVX DNA in a first mammalian subject, identifying
 CC an agent that binds to NOVX, identifying a potential therapeutic agent
 CC for treatment of a pathology related to aberrant expression or aberrant
 CC physiological interactions of NOVX, screening for a modulator of activity
 CC of or of latency or predisposition to a pathology associated with NOVX, a
 CC vector comprising NOVX DNA, a cell comprising the vector (used to produce
 CC NOVX) and an anti-NOVX antibody. The NOVX nucleic acids and polypeptides
 CC are useful as a marker for cell or tissue type, and in diagnosing and
 CC treating pathologies, diseases, conditions or disorders associated with
 CC NOVX sequences, including cardiomyopathy, atherosclerosis, hypertension,
 CC congenital heart defects, prostate cancer, diabetes, metabolic disorders,
 CC neoplasm, graft versus host disease, AIDS, bronchial asthma, Crohn's
 CC disease, multiple sclerosis, infectious diseases, anorexia, cancer-
 CC associated cachexia, neurodegenerative disorders (e.g. Alzheimer's
 CC disease or Parkinson's disease), immune disorders, haematopoietic
 CC disorders, dyslipidaemias, and wasting disorders associated with chronic
 CC diseases. These may also be used to screen for molecules which inhibit or
 CC enhance NOVX activity or function, and for detecting specific cell types.
 CC These may also be used in chromosome mapping, gene therapy, tissue
 CC typing, and in forensic biology. The present sequence represents a NOVX
 CC protein
 XX
 SQ Sequence 257 AA;
 XX

Query Match 100.0%; Score 1264; DB 6; Length 257;
 Best Local Similarity 100.0%; Pred. No. 5.1e-93;
 Matches 232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPQKPKVSLNPPWNRIFKGENVLTTCNGNPFVSSTKWFNGSLSEETNSLNIVNAKF 60
 DB 26 VPQKPKVSLNPPWNRIFKGENVLTTCNGNPFVSSTKWFNGSLSEETNSLNIVNAKF 85
 QY 61 EDGGEYKQHQVNESEPVYLEVFSDDLQASAEVVMVEGQPLFLRCHGWRNDVYKVIY 120
 DB 86 EDGGEYKQHQVNESEPVYLEVFSDDLQASAEVVMVEGQPLFLRCHGWRNDVYKVIY 145
 QY 121 YKGEALKYWNHNISITNATVEDSGTYCTGKVMQLDYSEBPLNITVIKAPREKYWLQ 180
 DB 146 YKGEALKYWNHNISITNATVEDSGTYCTGKVMQLDYSEBPLNITVIKAPREKYWLQ 205
 QY 181 FFIPLLVVILFAVDTGFIQTQQVTFLLKIKTRKGRFLLNPHBKPKN 232
 DB 206 FFIPLLVVILFAVDTGFIQTQQVTFLLKIKTRKGRFLLNPHBKPKN 257

RESULT 12
 ADD48674
 ID ADD48674 standard; protein; 257 AA.
 XX ADD48674;
 AC ADD48674;
 XX
 DT 29-JAN-2004 (first entry)
 XX
 DE Human Protein P12319, SEQ ID NO 14381.
 XX

KW Human; pain; neuronal tissue; gene therapy;
 KW spinal segmental nerve injury; chronic constriction injury; CCI;
 KW spared nerve injury; SNI; Chung.
 OS Homo sapiens.
 XX WO2003016475-A2.
 PN 27-FEB-2003.
 XX 14-AUG-2002; 2002WO-US025765.
 XX 14-AUG-2001; 2001US-0312147P.
 PR 01-NOV-2001; 2001US-0346382P.
 PR 26-NOV-2001; 2001US-0333347P.
 XX (GEO) GEN HOSPITAL CORP.
 PA (FARB) BAYER AG.
 XX Woolf C, D'urso D, Befort K, Costigan M;
 DR WPI; 2003-268312/26.
 DR GENBANK; F12319.
 XX New composition comprising two or more isolated polypeptides, useful for
 PT preparing a medicament for treating pain in an animal.
 XX Claim 1; Page; 1017pp; English.
 XX The invention discloses a composition comprising two or more isolated rat
 CC or human polynucleotides or a polynucleotide which represents a fragment,
 CC derivative or allelic variation of the nucleic acid sequence. Also
 CC claimed are a vector comprising the novel polynucleotide, a host cell
 CC comprising the vector, a method for identifying a nucleotide sequence
 CC which is differentially regulated in an animal subjected to pain and a
 CC kit to perform the method, an array, a method for identifying an agent
 CC that increases or decreases the expression of the polynucleotide sequence
 CC that is differentially expressed in neuronal tissue of a first animal
 CC subjected to pain, a method for identifying a compound which regulates
 CC the expression of a polynucleotide sequence which is differentially
 CC expressed in an animal subjected to pain, a method for identifying a
 CC compound that regulates the activity of one or more of the
 CC polynucleotides, a method for producing a pharmaceutical composition, a
 CC method for identifying a compound or small molecule that regulates the
 CC activity in an animal of one or more of the polypeptides given in the
 CC specification, a method for identifying a compound useful in treating
 CC pain and a pharmaceutical composition comprising the one or more
 CC polypeptides or their antibodies. The polynucleotide or the compound that
 CC modulates its activity is useful for preparing a medicament for treating
 CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
 CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. Gene
 CC therapy). The sequence presented is a human protein (shown in Table 2 of
 CC the specification) which is differentially expressed during pain. Note:
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic form directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.
 XX Sequence 257 AA;
 SQ

Query Match 100.0%; Score 1264; DB 7; Length 257;
 Best Local Similarity 100.0%; Pred. No. 5.1e-93;
 Matches 232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPQKPKVSLNPPWNRIFKGENVTITCNGNFFVSSSTKWFHNGSLSEETNSLAINVNAKF 60
 DB 26 VPQKPKVSLNPPWNRIFKGENVTITCNGNFFVSSSTKWFHNGSLSEETNSLAINVNAKF 85
 QY 61 EDSGEYKQHQOQVNESEPVYLEVFSDDLLOQSAEAVVMGQPLFLRCHGRNWDYKVIY 120
 DB 86 EDSGEYKQHQOQVNESEPVYLEVFSDDLLOQSAEAVVMGQPLFLRCHGRNWDYKVIY 145
 QY 121 YKDGALKYKYYENHNISITNATVDSGTYYCTGKWQOLDYSEPLNITVIKAPREKYWLQ 180

DB 146 YKDGALKYKYYENHNISITNATVDSGTYYCTGKWQOLDYSEPLNITVIKAPREKYWLQ 205
 QY 181 FFIPLLVLVILFAVDITGLFISTQQVTFLLKIKRTRKGFRLNPNPKPKN 232
 DB 206 FFIPLLVLVILFAVDITGLFISTQQVTFLLKIKRTRKGFRLNPNPKPKN 257

RESULT 13
 AAY96230
 ID AAY96230 standard; protein; 260 AA.
 XX
 AC AAY96230;
 XX
 DT 11-SEP-2000 (first entry)
 XX
 DE Human Fc receptor, Fcpsi1onRia.
 XX
 KW Human; Fc receptor; Fcpsi1onRia; immunoglobulin; infection;
 KW immune response; HIV; IgG; immunosuppressive; anti-rheumatic;
 KW anti-inflammatory; AIDS; SLE; multiple myeloma; rheumatoid arthritis;
 KW systemic lupus erythematosus; tumour.
 XX
 OS Homo sapiens.
 XX
 PN EP1006183-A1.
 XX
 PD 07-JUN-2000.
 XX
 PF 03-DEC-1998; 98EP-00122969.
 XX
 PR 03-DEC-1998; 98EP-00122969.
 XX
 PA (PLAC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
 XX
 DR WPI; 2000-367968/32.
 DR N-PSDB; AAA27470.
 XX
 PT Novel Fc receptor lacking transmembrane domains, a signal peptide, and
 PT glycosylation, useful for diagnosing and treating immune disorders and
 PT cancer.
 XX
 PS Disclosure; Page 40-41; 60pp; English.
 XX
 CC The present sequence is the human Fc receptor, Fcpsi1onRia. Fc receptors
 CC play an important role in defending the body against infections. First,
 CC pathogens are opsonised by serum immunoglobulins. The resulting complex
 CC then binds to cells expressing Fc receptors. Upon Fc receptor activation,
 CC immune effector pathways are activated, leading to immune response. The
 CC present sequence may be modified to produce recombinant versions. The
 CC recombinant Fc receptor consist only of the extracellular portion of the
 CC receptor and are not glycosylated i.e. they do not have transmembrane
 CC domains or signal peptides. The recombinant proteins may be used in
 CC immunoassays to determine the immune status of patients with chronic
 CC diseases of the immune system, e.g. AIDS, systemic lupus erythematosus
 CC (SLE), multiple myeloma (MM), or rheumatoid arthritis. In addition,
 CC pharmaceutical compositions containing recombinant proteins may be used
 CC to treat or prevent autoimmune diseases, allergies or tumours, especially
 CC AIDS, rheumatoid arthritis or MM
 XX
 SQ Sequence 260 AA;
 Query Match 100.0%; Score 1264; DB 3; Length 260;
 Best Local Similarity 100.0%; Pred. No. 5.2e-93;
 Matches 232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPQKPKVSLNPPWNRIFKGENVTITCNGNFFVSSSTKWFHNGSLSEETNSLAINVNAKF 60
 DB 29 VPQKPKVSLNPPWNRIFKGENVTITCNGNFFVSSSTKWFHNGSLSEETNSLAINVNAKF 88
 QY 61 EDSGEYKQHQOQVNESEPVYLEVFSDDLLOQSAEAVVMGQPLFLRCHGRNWDYKVIY 120
 DB 89 EDSGEYKQHQOQVNESEPVYLEVFSDDLLOQSAEAVVMGQPLFLRCHGRNWDYKVIY 148

QY 121 YKGEALKYWNHNISITNATVEDSGTYCTGKQWQLDYSEPLNITVTKAPREKYLQ 180
Db 149 YKGEALKYWNHNISITNATVEDSGTYCTGKQWQLDYSEPLNITVTKAPREKYLQ 208
QY 181 FPIPLLVILFAVDTLGTFSTQOQVTFLLKIKRTKGFELLPKPKPN 232
Db 209 FPIPLLVILFAVDTLGTFSTQOQVTFLLKIKRTKGFELLPKPKPN 260

RESULT 14
AAW48094
ID AAW48094 standard; protein; 257 AA.
XX AAW48094;
XX 20-JUL-1998 (first entry)
DE Human IGE receptor Fc-epsilon-RI alpha chain.

XX Fc-epsilon RI alpha chain; IGE receptor; human serum albumin;
KW fusion protein; allergy; atopic dermatitis; asthma; urticaria; hay fever;
KW eczema; anaphylaxis; gene therapy; diagnosis; transgenic animal.

OS Homo sapiens.
XX
XX Key Location/Qualifiers
FH Peptide 1..25
FT /label= Sig_peptide
FT Protein 26..257
FT /label= Mat_protein
FT Domain 26..204
FT /note= "extracellular domain"

XX WO9804718-A1.
XX 05-FEB-1998.
XX 25-JUL-1997; 97WO-EP004066.
XX 26-JUL-1996; 96US-00690216.
XX (NOVS) NOVARTIS AG.

XX Digan ME, Lake P, Gram H;
XX WPI; 1998-130705/12.
XX N-PSDB; AAV20402.
XX New fusion polypeptide for, e.g. diagnosing allergies - comprises
XX immunoglobulin E-binding domain fused to human serum albumin.

XX Claim 2; Page 44; 77pp; English.
XX
XX This is the amino acid sequence of the dominant form of full-length
XX native human IGE receptor Fc-epsilon RI alpha chain. A claimed fusion
XX protein (FP) comprises an IGE binding domain fused to at least one human
XX serum albumin (HSA) component (see AAW38095), optionally via a peptide
XX linker, and is especially a dimeric FP (see AAW48096) comprising HSA
XX fused, at each of its N- and C-termini, to the extracellular domain of Fc
XX -epsilon RI alpha chain. Also claimed are: nucleic acids encoding the FP
XX (see AAV20404); a vector; a process for preparing the FP; a method of
XX performing gene therapy in humans that comprises removing somatic cells
XX from a patient, genetically modifying them in culture by insertion of a
XX polynucleotide that encodes the FP, and reintroducing the modified cells
XX into the patient so that the FP is expressed by the cells of the patient;
XX and use of the FP in an in vitro diagnostic assay to determine the level
XX of IGE or auto-antibodies to Fc epsilon RI in a sample. The products can
XX be used in the prevention and/or treatment of IGE-mediated allergic
XX diseases and related disorders such as atopic dermatitis, atopic asthma,
XX chronic urticaria, hayfever and eczema. Compared with using IGE binding
XX domain alone, the FP has a longer serum life, and thus greater activity,
XX without a loss of ability to bind serum IGE or circulating auto-
XX antibodies

XX Sequence 257 AA;
SQ Query Match 99.6%; Score 1259; DB 2; Length 257;
Best Local Similarity 99.6%; Pred. No. 1.3e-92;
Matches 231; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 VPQPKVSLNPPNRIKFGENVTLTCNGNFFFEVSSTKWFHNGSLSEETNSSLNIVNAKF 60
Db 26 VPQPKVSLNPPNRIKFGENVTLTCNGNFFFEVSSTKWFHNGSLSEETNSSLNIVNAKF 85
QY 61 EDSGEYKCOHQVNESEPVYLEVFSDFWLLQASAEVVMGQPLFLRCHGWRNMDVYKVIY 120
Db 86 EDSGEYKCOHQVNESEPVYLEVFSDFWLLQASAEVVMGQPLFLRCHGWRNMDVYKVIY 145
QY 121 YKGEALKYWNHNISITNATVEDSGTYCTGKQWQLDYSEPLNITVTKAPREKYLQ 180
Db 146 YKGEALKYWNHNISITNATVEDSGTYCTGKQWQLDYSEPLNITVTKAPREKYLQ 205
QY 181 FPIPLLVILFAVDTLGTFSTQOQVTFLLKIKRTKGFELLPKPKPN 232
Db 206 FPIPLLVILFAVDTLGTFSTQOQVTFLLKIKRTKGFELLPKPKPN 257

RESULT 15
ADB85536
ID ADB85536 standard; protein; 257 AA.
XX ADB85536;
XX 04-DEC-2003 (first entry)
DE Human immunoglobulin E high affinity receptor alpha subunit protein.
XX alpha subunit; high affinity receptor for immunoglobulin E; FcERI;
KW mast cell; basophil; histamine; serotonin; allergic condition;
KW antiallergic; allergic response; drug screening assay; immunoglobulin E;
human.
XX Homo sapiens.
XX
XX Key Location/Qualifiers
FH Misc-difference 221 /note= "Encoded by GGA"
FT Misc-difference 253 /note= "Encoded by AAC"
FT
FT
FT
FT
FN US6602983-B1.
XX
XX 05-AUG-2003.
XX
XX 22-SEP-1994; 94US-00310902.
XX
XX 24-FEB-1988; 88US-00160457.
XX 30-OCT-1991; 91US-00785127.
XX 29-MAY-1993; 93US-00066640.
XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
XX Kinet JP, Kochan JP;
XX WPI; 2003-669612/63.
XX N-PSDB; ADB85535.
XX New alpha subunit of the human high affinity receptor for immunoglobulin
XX E polypeptides, useful as antagonists to prevent allergic response, as
XX reagents in drug screening assays, or for monitoring immunoglobulin E
XX levels in patients.
XX Claim 1; Fig 1; 9pp; English.
XX This invention relates to a novel purified polypeptide corresponding to
XX the alpha subunit of the human high affinity receptor for immunoglobulin

CC E (FcERI) and the DNA sequence which encodes it. The receptor of the
 CC invention is found exclusively on mast cells, basophils and related
 CC cells. Activation of the receptor triggers the release of preformed
 CC mediators such as histamine and serotonin which may result in allergic
 CC conditions. Compounds which modulate FcERI activity may have anti-allergic
 CC activity. The polypeptide of the invention may be useful as an antagonist
 CC for preventing allergic response, as a reagent in drug screening assays,
 CC as a therapeutic or for monitoring immunoglobulin E levels in patients.
 CC The DNA sequences may be useful for producing the polypeptide or for
 CC synthesizing cDNA sequences to construct DNA probes used in diagnostic
 CC assays. The present sequence is the amino acid sequence of the alpha
 CC subunit of the human FcERI receptor of the invention.

XX
 SQ Sequence 257 AA;

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Query Match          99.0%; Score 1251; DB 7; Length 257;
Best Local Similarity 99.1%; Pred No. 5.6e-92;
Matches 230; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 VPQKPKVSLNPPWNRIFKGENVTLCNGNPFVVSSTKWFHNGSLSBETNSSLNIVNAKF 60
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Db 26 VPQKPKVSLNPPWNRIFKGENVTLCNGNPFVVSSTKWFHNGSLSBETNSSLNIVNAKF 85
   |||||

QY 61 EDSGEYKCOHOQVNESEPVYLEVFSDDLQLQASAEVVMGQPLFIRCHGWRNWDVYKVIY 120
   |||||
Db 86 EDSGEYKCOHOQVNESEPVYLEVFSDDLQLQASAEVVMGQPLFIRCHGWRNWDVYKVIY 145
   |||||

QY 121 YKDGEALKYWEHNHNSITNATVEDSGTYCTGKQWQLDYSEPLNITVIKAPREKYWLQ 180
   |||||
Db 146 YKDGEALKYWEHNHNSITNATVEDSGTYCTGKQWQLDYSEPLNITVIKAPREKYWLQ 205
   |||||

QY 181 FPIPLLVILFAVDTLGLFISTQQQVTFLLKIKRTRKGFRLNPHPKPNPKNN 232
   |||||
Db 206 FPIPLLVILFAVDTELFISTQQQVTFLLKIKRTRKGFRLNPHPKPNPKNN 257
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Search completed: October 6, 2004, 09:03:06
 Job time : 54.4569 secs